

Resource Summary Report

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WebMGA

RRID:SCR_011951

Type: Tool

Proper Citation

WebMGA (RRID:SCR_011951)

Resource Information

URL: <http://weizhong-lab.ucsd.edu/metagenomic-analysis/>

Proper Citation: WebMGA (RRID:SCR_011951)

Description: A customizable web server for fast metagenomic analysis.

Abbreviations: WebMGA

Resource Type: analysis service resource, service resource, data analysis service, production service resource

Resource Name: WebMGA

Resource ID: SCR_011951

Alternate IDs: OMICS_01524

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260728T043401+0000

Ratings and Alerts

No rating or validation information has been found for WebMGA.

No alerts have been found for WebMGA.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 196 mentions in open access literature.

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

Ranesan AC, et al. (2025) Whole genome surveying and metabolomic profiling aided navigation of therapeutic plethora of *Streptomyces melanogenes* WPF1 isolated from *Pinus patula* rhizosphere. *Bioresources and bioprocessing*, 12(1), 149.

Sánchez-Torres P, et al. (2024) Discovery and Transcriptional Profiling of *Penicillium digitatum* Genes That Could Promote Fungal Virulence during Citrus Fruit Infection. *Journal of fungi* (Basel, Switzerland), 10(4).

Sosa-Jiménez VM, et al. (2024) Discovery of a novel symbiotic lineage associated with a hematophagous leech from the genus *Haementeria*. *Microbiology spectrum*, 12(7), e0428623.

Haidar R, et al. (2024) Two *Paenibacillus* spp. strains promote grapevine wood degradation by the fungus *Fomitiporia mediterranea*: from degradation experiments to genome analyses. *Scientific reports*, 14(1), 15779.

Zerouki C, et al. (2023) Whole-genome sequence and mass spectrometry study of the snow blight fungus *Phacidium infestans* (Karsten) DSM 5139 growing at freezing temperatures. *Molecular genetics and genomics* : MGG, 298(6), 1449.

Benigno V, et al. (2023) Diversity and evolution of an abundant ICEclc family of integrative and conjugative elements in *Pseudomonas aeruginosa*. *mSphere*, 8(6), e0051723.

Del Campo EM, et al. (2023) Comparative Transcriptomic and Proteomic Analyses Provide New Insights into the Tolerance to Cyclic Dehydration in a Lichen Phycobiont. *Microbial ecology*, 86(3), 1725.

Nguyen TTH, et al. (2023) Three marine species of the genus *Fulvivirga*, rich sources of carbohydrate-active enzymes degrading alginate, chitin, laminarin, starch, and xylan. *Scientific reports*, 13(1), 6301.

Chanama M, et al. (2023) *Streptomyces antimicrobicus* sp. nov., a novel clay soil-derived actinobacterium producing antimicrobials against drug-resistant bacteria. *PloS one*, 18(5), e0286365.

Lin YT, et al. (2023) Interactions among deep-sea mussels and their epibiotic and endosymbiotic chemoautotrophic bacteria: Insights from multi-omics analysis. *Zoological research*, 44(1), 106.

Naizabekov S, et al. (2023) Comparative genomic analysis of *Methylocystis* sp. MJC1 as a platform strain for polyhydroxybutyrate biosynthesis. *PloS one*, 18(5), e0284846.

Lee Y, et al. (2023) Characterization of a Potential Probiotic *Lactiplantibacillus plantarum* LRCC5310 by Comparative Genomic Analysis and its Vitamin B6 Production Ability. *Journal of microbiology and biotechnology*, 33(5), 644.

Pogoreutz C, et al. (2022) Coral holobiont cues prime *Endozoicomonas* for a symbiotic lifestyle. *The ISME journal*, 16(8), 1883.

Levi Mortera S, et al. (2022) A metaproteomic-based gut microbiota profiling in children affected by autism spectrum disorders. *Journal of proteomics*, 251, 104407.

Chen CL, et al. (2022) Sexual Crossing, Chromosome-Level Genome Sequences, and Comparative Genomic Analyses for the Medicinal Mushroom *Taiwanofungus camphoratus* (Syn. *Antrodia cinnamomea*, *Antrodia camphorata*). *Microbiology spectrum*, 10(1), e0203221.

Guzmán-Moreno J, et al. (2022) *Bacillus megaterium* HgT21: a Promising Metal Multiresistant Plant Growth-Promoting Bacteria for Soil Bioremediation. *Microbiology spectrum*, 10(5), e0065622.

Sengupta K, et al. (2022) Genomic architecture of three newly isolated unclassified *Butyrivibrio* species elucidate their potential role in the rumen ecosystem. *Genomics*, 114(2), 110281.

Wen Y, et al. (2022) Genomic Investigation of Desert *Streptomyces huasconensis* D23 Reveals Its Environmental Adaptability and Antimicrobial Activity. *Microorganisms*, 10(12).

Lata KS, et al. (2022) A core and pan gene map of *Leptospira* genus and its interactions with human host. *Microbial pathogenesis*, 162, 105347.

Jiao J, et al. (2022) The zinc-finger bearing xenogeneic silencer MucR in γ -proteobacteria balances adaptation and regulatory integrity. *The ISME journal*, 16(3), 738.