

Resource Summary Report

Generated by [NIF](#) on Aug 29, 2026

AmphoraNet

RRID:SCR_005009

Type: Tool

Proper Citation

AmphoraNet (RRID:SCR_005009)

Resource Information

URL: <http://amphoranet.pitgroup.org/>

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Description: Webserver implementation of the AMPHORA2 workflow for phylogenetic analysis of metagenomic shotgun sequencing data. It is capable of assigning a probability-weighted taxonomic group for each phylogenetic marker gene found in the input metagenomic sample.

Abbreviations: AmphoraNet

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

Defining Citation: [PMID:24144838](#)

Keywords: dna sequence, amino acid sequence, dna, sequence, amino acid, phylogenetic, reliability score, nucleotide, protein, nucleotide sequence, protein sequence, phylogenetic analysis, metagenomic, metagenomics, phylotyping, bio.tools

Availability: Acknowledgement requested, Free, Public

Resource Name: AmphoraNet

Resource ID: SCR_005009

Alternate IDs: biotools:amphoranet, OMICS_01450

Alternate URLs: <https://bio.tools/amphoranet>

Record Creation Time: 20220129T080227+0000

Record Last Update: 20260829T182932+0000

Ratings and Alerts

No rating or validation information has been found for AmphoraNet.

No alerts have been found for AmphoraNet.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

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.

Wassermann B, et al. (2022) The microbiome and resistome of apple fruits alter in the post-harvest period. *Environmental microbiome*, 17(1), 10.

Lee JY, et al. (2021) Characterization of *Marteella soudanensis* sp. nov., Isolated from a Mine Sediment. *Microorganisms*, 9(8).

Siupka P, et al. (2021) Antifungal Activity and Biosynthetic Potential of New *Streptomyces* sp. MW-W600-10 Strain Isolated from Coal Mine Water. *International journal of molecular sciences*, 22(14).

Siupka P, et al. (2020) Genome Mining Revealed a High Biosynthetic Potential for Antifungal *Streptomyces* sp. S-2 Isolated from Black Soot. *International journal of molecular sciences*, 21(7).

Dos Santos Melo-Nascimento AO, et al. (2020) Complete genome reveals genetic repertoire and potential metabolic strategies involved in lignin degradation by environmental ligninolytic *Klebsiella variicola* P1CD1. *PloS one*, 15(12), e0243739.

Mohapatra B, et al. (2019) Comparative genome analysis of arsenic reducing, hydrocarbon metabolizing groundwater bacterium *Achromobacter* sp. KAs 3-5T explains its competitive edge for survival in aquifer environment. *Genomics*, 111(6), 1604.

Cui J, et al. (2019) Metagenomic Insights Into a Cellulose-Rich Niche Reveal Microbial Cooperation in Cellulose Degradation. *Frontiers in microbiology*, 10, 618.

Li Z, et al. (2019) Genome-Resolved Proteomic Stable Isotope Probing of Soil Microbial Communities Using $^{13}\text{CO}_2$ and ^{13}C -Methanol. *Frontiers in microbiology*, 10, 2706.

Luedin SM, et al. (2019) Draft Genome Sequence of *Chromatium okenii* Isolated from the Stratified Alpine Lake Cadagno. *Scientific reports*, 9(1), 1936.

Patil PP, et al. (2018) Taxonogenomics reveal multiple novel genomospecies associated with clinical isolates of *Stenotrophomonas maltophilia*. *Microbial genomics*, 4(8).

Thiel V, et al. (2017) The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. II. Metabolic Functions of Abundant Community Members Predicted from Metagenomic Analyses. *Frontiers in microbiology*, 8, 943.

Sant'Anna FH, et al. (2017) Reclassification of *Paenibacillus riograndensis* as a Genomovar of *Paenibacillus sonchi*: Genome-Based Metrics Improve Bacterial Taxonomic Classification. *Frontiers in microbiology*, 8, 1849.

Tripathi C, et al. (2017) Complete Genome Analysis of *Thermus parvatiensis* and Comparative Genomics of *Thermus* spp. Provide Insights into Genetic Variability and Evolution of Natural Competence as Strategic Survival Attributes. *Frontiers in microbiology*, 8, 1410.

Thiel V, et al. (2016) The Dark Side of the Mushroom Spring Microbial Mat: Life in the Shadow of Chlorophototrophs. I. Microbial Diversity Based on 16S rRNA Gene Amplicons and Metagenomic Sequencing. *Frontiers in microbiology*, 7, 919.

Muller EE, et al. (2014) Community-integrated omics links dominance of a microbial generalist to fine-tuned resource usage. *Nature communications*, 5, 5603.