

Resource Summary Report

Generated by [kravitz2](#) on Sep 18, 2026

PhyloPythiaS

RRID:SCR_011923

Type: Tool

Proper Citation

PhyloPythiaS (RRID:SCR_011923)

Resource Information

URL: <http://phylopythias.bifo.helmholtz-hzi.de/index.php?phase=wait>

Proper Citation: PhyloPythiaS (RRID:SCR_011923)

Description: Web Server for Taxonomic Assignment of Metagenome Sequences that is a fast and accurate sequence composition-based classifier that utilizes the hierarchical relationships between clades. Taxonomic assignments with the web server can be made with a generic model, or with sample-specific models that users can specify and create. Several interactive visualization modes and multiple download formats allow quick and convenient analysis and downstream processing of taxonomic assignments.

Abbreviations: PPS

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

Defining Citation: [PMID:22745671](#), [PMID:21358620](#)

Keywords: metagenome, sequence, taxonomy, classification

Resource Name: PhyloPythiaS

Resource ID: SCR_011923

Alternate IDs: OMICS_01460

Old URLs: <http://phylopythias.cs.uni-duesseldorf.de/index.php?phase=wait>

Record Creation Time: 20220129T080307+0000

Record Last Update: 20260912T200207+0000

Ratings and Alerts

No rating or validation information has been found for PhyloPythiaS.

No alerts have been found for PhyloPythiaS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 12 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Galván V, et al. (2023) High wax ester and triacylglycerol biosynthesis potential in coastal sediments of Antarctic and Subantarctic environments. PloS one, 18(7), e0288509.

Jensen S, et al. (2021) Endozoicomonadaceae symbiont in gills of Acrea clam encodes genes for essential nutrients and polysaccharide degradation. FEMS microbiology ecology, 97(6).

Tauzin AS, et al. (2020) Investigating host-microbiome interactions by droplet based microfluidics. Microbiome, 8(1), 141.

Laville E, et al. (2019) Investigating Host Microbiota Relationships Through Functional Metagenomics. Frontiers in microbiology, 10, 1286.

Westmann CA, et al. (2018) Mining Novel Constitutive Promoter Elements in Soil Metagenomic Libraries in Escherichia coli. Frontiers in microbiology, 9, 1344.

Calderoli PA, et al. (2018) Predominance and high diversity of genes associated to denitrification in metagenomes of subantarctic coastal sediments exposed to urban pollution. PloS one, 13(11), e0207606.

Wei Y, et al. (2018) Diversity of Gene Clusters for Polyketide and Nonribosomal Peptide Biosynthesis Revealed by Metagenomic Analysis of the Yellow Sea Sediment. Frontiers in microbiology, 9, 295.

Festa S, et al. (2017) Assigning ecological roles to the populations belonging to a phenanthrene-degrading bacterial consortium using omic approaches. PloS one, 12(9), e0184505.

Ufarté L, et al. (2017) Discovery of carbamate degrading enzymes by functional metagenomics. PloS one, 12(12), e0189201.

Gregor I, et al. (2016) PhyloPythiaS+: a self-training method for the rapid reconstruction of low-ranking taxonomic bins from metagenomes. PeerJ, 4, e1603.

Zhang W, et al. (2016) Genomic and Transcriptomic Evidence for Carbohydrate Consumption among Microorganisms in a Cold Seep Brine Pool. Frontiers in microbiology,

7, 1825.

Denman SE, et al. (2015) Metagenomic analysis of the rumen microbial community following inhibition of methane formation by a halogenated methane analog. *Frontiers in microbiology*, 6, 1087.