

Resource Summary Report

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VAMPS

RRID:SCR_004483

Type: Tool

Proper Citation

VAMPS (RRID:SCR_004483)

Resource Information

URL: <http://vamps.mbl.edu/overview.php>

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Description: A publicly-accessible website to measure and visualize similarities and differences between molecular profiles of complex microbial communities. The project includes visualization tools such as heat maps that simultaneously compare the taxonomic distributions of multiple datasets and 3-D charts of the frequency distributions of 16S rRNA tags. Analytical tools include Chao diversity estimates and rarefaction curves. As a service to the community, researchers have the opportunity to upload their own data to the site for private viewing with the full range of data and analysis tools. Public data can be downloaded for further analysis locally.

Abbreviations: VAMPS

Synonyms: VAMPS Project, Visualization and Analysis of Microbial Population Structure

Resource Type: data analysis service, data or information resource, data repository, storage service resource, database, service resource, production service resource, analysis service resource

Defining Citation: [PMID:24499292](#)

Funding: Alfred P. Sloan Foundation ;
NSF ;
NASA Astrobiology Institute

Availability: Public, The community can contribute to this resource

Resource Name: VAMPS

Resource ID: SCR_004483

Alternate IDs: OMICS_01501

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260801T190236+0000

Ratings and Alerts

No rating or validation information has been found for VAMPS.

No alerts have been found for VAMPS.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 28 mentions in open access literature.

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

Chaouni B, et al. (2023) Spatio-temporal patterns of *Synechococcus* oligotypes in Moroccan lagoonal environments. *Scientific reports*, 13(1), 110.

Shapiro T, et al. (2021) Revealing of Non-Cultivable Bacteria Associated with the Mycelium of Fungi in the Kerosene-Degrading Community Isolated from the Contaminated Jet Fuel. *Journal of fungi* (Basel, Switzerland), 7(1).

Sheik CS, et al. (2021) Novel Microbial Groups Drive Productivity in an Archean Iron Formation. *Frontiers in microbiology*, 12, 627595.

Baron NC, et al. (2021) Black Fungi and Hydrocarbons: An Environmental Survey for Alkylbenzene Assimilation. *Microorganisms*, 9(5).

Hunter-Cevera KR, et al. (2021) Seasonal environmental variability drives microdiversity within a coastal *Synechococcus* population. *Environmental microbiology*, 23(8), 4689.

Purkamo L, et al. (2020) Ultradeep Microbial Communities at 4.4 km within Crystalline Bedrock: Implications for Habitability in a Planetary Context. *Life* (Basel, Switzerland), 10(1).

Janouškovec J, et al. (2019) Apicomplexan-like parasites are polyphyletic and widely but selectively dependent on cryptic plastid organelles. *eLife*, 8.

Teske A, et al. (2019) Characteristics and Evolution of sill-driven off-axis hydrothermalism in Guaymas Basin - the Ringvent site. *Scientific reports*, 9(1), 13847.

Fernandes S, et al. (2018) Enhanced carbon-sulfur cycling in the sediments of Arabian Sea oxygen minimum zone center. *Scientific reports*, 8(1), 8665.

- Brazelton WJ, et al. (2017) Metagenomic identification of active methanogens and methanotrophs in serpentinite springs of the Voltri Massif, Italy. *PeerJ*, 5, e2945.
- Schmidt V, et al. (2017) Subtle Microbiome Manipulation Using Probiotics Reduces Antibiotic-Associated Mortality in Fish. *mSystems*, 2(6).
- Freeman MA, et al. (2017) X-Cells Are Globally Distributed, Genetically Divergent Fish Parasites Related to Perkinsids and Dinoflagellates. *Current biology : CB*, 27(11), 1645.
- Labonté JM, et al. (2017) Influence of Igneous Basement on Deep Sediment Microbial Diversity on the Eastern Juan de Fuca Ridge Flank. *Frontiers in microbiology*, 8, 1434.
- Trojan D, et al. (2016) A taxonomic framework for cable bacteria and proposal of the candidate genera *Electrothrix* and *Electronema*. *Systematic and applied microbiology*, 39(5), 297.
- Walsh EA, et al. (2016) Relationship of Bacterial Richness to Organic Degradation Rate and Sediment Age in Subseafloor Sediment. *Applied and environmental microbiology*, 82(16), 4994.
- Gorvitovskaia A, et al. (2016) Interpreting *Prevotella* and *Bacteroides* as biomarkers of diet and lifestyle. *Microbiome*, 4, 15.
- Fernandez-Gonzalez N, et al. (2016) Microbial Communities Are Well Adapted to Disturbances in Energy Input. *mSystems*, 1(5).
- Reveillaud J, et al. (2016) Subseafloor microbial communities in hydrogen-rich vent fluids from hydrothermal systems along the Mid-Cayman Rise. *Environmental microbiology*, 18(6), 1970.
- Valverde JR, et al. (2016) Looking for Rhizobacterial Ecological Indicators in Agricultural Soils Using 16S rRNA metagenomic Amplicon Data. *PloS one*, 11(10), e0165204.
- Schmidt V, et al. (2016) Influence of Fishmeal-Free Diets on Microbial Communities in Atlantic Salmon (*Salmo salar*) Recirculation Aquaculture Systems. *Applied and environmental microbiology*, 82(15), 4470.