Resource Summary Report

Generated by dkNET on May 16, 2025

Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis

RRID:SCR_002676
Type: Tool

Proper Citation

Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis (RRID:SCR_002676)

Resource Information

URL: http://camera.calit2.net/

Proper Citation: Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis (RRID:SCR_002676)

Description: THIS RESOURCE IS NO LONGER IN SERVICE, documented May 26, 2016; however, the URL provides links to associated projects and data. A suite of data query, download, upload, analysis and sharing tools serving the needs of the microbial ecology research community, and other scientists using metagenomics data.

Abbreviations: CAMERA

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

Defining Citation: PMID:21045053

Keywords: ecology, energy, environment, gene, analysis, bioinformatics, biological, biology, community, cyberinfrastructure, data, dna, genome, genomics, health care, map, marine, metadata, metagenomic, microbial, microbiology, molecular biology, organism, research, scientific, sequence, sequencing, software, tool, training, viral

Funding: Gordon and Betty Moore Foundation

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis

Resource ID: SCR_002676

Alternate IDs: SCR_011924, OMICS_01476, nif-0000-23292

Record Creation Time: 20220129T080214+0000

Record Last Update: 20250516T053640+0000

Ratings and Alerts

No rating or validation information has been found for Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis.

No alerts have been found for Community Cyberinfrastructure for Advanced Marine Microbial Ecology Research and Analysis.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 83 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Figueroa JL, et al. (2024) MerCat2: a versatile k-mer counter and diversity estimator for database-independent property analysis obtained from omics data. Bioinformatics advances, 4(1), vbae061.

Zhang W, et al. (2021) Characterization and genomic analysis of the first Oceanospirillum phage, vB_OliS_GJ44, representing a novel siphoviral cluster. BMC genomics, 22(1), 675.

Pang Z, et al. (2021) Linking Plant Secondary Metabolites and Plant Microbiomes: A Review. Frontiers in plant science, 12, 621276.

Moreno PS, et al. (2017) Characterisation of the canine faecal virome in healthy dogs and dogs with acute diarrhoea using shotgun metagenomics. PloS one, 12(6), e0178433.

Zou B, et al. (2017) MIPE: A metagenome-based community structure explorer and SSU primer evaluation tool. PloS one, 12(3), e0174609.

Tapia JE, et al. (2016) Microbiota Influences Morphology and Reproduction of the Brown

Alga Ectocarpus sp. Frontiers in microbiology, 7, 197.

Ichinomiya M, et al. (2016) Diversity and oceanic distribution of the Parmales (Bolidophyceae), a picoplanktonic group closely related to diatoms. The ISME journal, 10(10), 2419.

Carvalho E, et al. (2016) Discovery of A-type procyanidin dimers in yellow raspberries by untargeted metabolomics and correlation based data analysis. Metabolomics : Official journal of the Metabolomic Society, 12(9), 144.

Fondi M, et al. (2016) "Every Gene Is Everywhere but the Environment Selects": Global Geolocalization of Gene Sharing in Environmental Samples through Network Analysis. Genome biology and evolution, 8(5), 1388.

Rinaudo P, et al. (2016) biosigner: A New Method for the Discovery of Significant Molecular Signatures from Omics Data. Frontiers in molecular biosciences, 3, 26.

Dudhagara P, et al. (2015) Web Resources for Metagenomics Studies. Genomics, proteomics & bioinformatics, 13(5), 296.

Noda-García L, et al. (2015) Insights into the evolution of enzyme substrate promiscuity after the discovery of (??)? isomerase evolutionary intermediates from a diverse metagenome. BMC evolutionary biology, 15, 107.

von Dassow P, et al. (2015) Life-cycle modification in open oceans accounts for genome variability in a cosmopolitan phytoplankton. The ISME journal, 9(6), 1365.

Groussman RD, et al. (2015) Diversity and Evolutionary History of Iron Metabolism Genes in Diatoms. PloS one, 10(6), e0129081.

Puxty RJ, et al. (2015) Spontaneous Deletion of an "ORFanage" Region Facilitates Host Adaptation in a "Photosynthetic" Cyanophage. PloS one, 10(7), e0132642.

Martin M, et al. (2015) The Cultivable Surface Microbiota of the Brown Alga Ascophyllum nodosum is Enriched in Macroalgal-Polysaccharide-Degrading Bacteria. Frontiers in microbiology, 6, 1487.

Smith MW, et al. (2015) Metagenomic evidence for reciprocal particle exchange between the mainstem estuary and lateral bay sediments of the lower Columbia River. Frontiers in microbiology, 6, 1074.

Kumar S, et al. (2015) Metagenomics: Retrospect and Prospects in High Throughput Age. Biotechnology research international, 2015, 121735.

Lara E, et al. (2015) Life-style and genome structure of marine Pseudoalteromonas siphovirus B8b isolated from the northwestern Mediterranean Sea. PloS one, 10(1), e0114829.

Coolen MJ, et al. (2015) The transcriptional response of microbial communities in thawing Alaskan permafrost soils. Frontiers in microbiology, 6, 197.