Resource Summary Report

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RDPipeline

RRID:SCR_001192
Type: Tool

Proper Citation

RDPipeline (RRID:SCR_001192)

Resource Information

URL: http://pyro.cme.msu.edu/

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Description: Software to simplify the processing of large rRNA sequence libraries (including single-strand and paired-end reads) obtained through high-throughput sequencing technology. Tools for assembly, quality filtering, taxonomy based analysis and taxonomy independent analysis tools, and tools to convert the data to formats suitable for common ecological and statistical packages are available. For extremely large datasets, command line tools are available.

Abbreviations: RDPipeline

Synonyms: RDP Pipeline, RDP Amplicon Sequence Pipeline

Resource Type: software resource, software application, data processing software

Defining Citation: PMID:24288368

Keywords: amplicon sequencing, high-throughput sequencing, rrna, assembly, quality filtering, taxonomy, analysis, FASEB list

Funding:

Availability: Acknowledgement requested, Creative Commons Attribution-ShareAlike License, v3 Unported

Resource Name: RDPipeline

Resource ID: SCR_001192

Alternate IDs: OMICS_02158

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250519T204453+0000

Ratings and Alerts

No rating or validation information has been found for RDPipeline.

No alerts have been found for RDPipeline.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 39 mentions in open access literature.

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

Williams HE, et al. (2018) Effects of dietary supplementation of formaldehyde and crystalline amino acids on gut microbial composition of nursery pigs. Scientific reports, 8(1), 8164.

Lee HJ, et al. (2018) Effects of cosmetics on the skin microbiome of facial cheeks with different hydration levels. MicrobiologyOpen, 7(2), e00557.

Li Q, et al. (2018) Influence of Altered Microbes on Soil Organic Carbon Availability in Karst Agricultural Soils Contaminated by Pb-Zn Tailings. Frontiers in microbiology, 9, 2062.

Lian T, et al. (2018) Rhizobacterial community structure in response to nitrogen addition varied between two Mollisols differing in soil organic carbon. Scientific reports, 8(1), 12280.

Dong W, et al. (2018) Warming deferentially altered multidimensional soil legacy induced by past land use history. Scientific reports, 8(1), 1546.

Yan YW, et al. (2018) Microbial Communities and Diversities in Mudflat Sediments Analyzed Using a Modified Metatranscriptomic Method. Frontiers in microbiology, 9, 93.

Correa-Galeote D, et al. (2018) Maize Endophytic Bacterial Diversity as Affected by Soil Cultivation History. Frontiers in microbiology, 9, 484.

Lin YT, et al. (2018) Effects of Reforestation on the Structure and Diversity of Bacterial

Communities in Subtropical Low Mountain Forest Soils. Frontiers in microbiology, 9, 1968.

Zhang J, et al. (2017) Characteristics of fecal microbial communities in patients with non-anastomotic biliary strictures after liver transplantation. World journal of gastroenterology, 23(46), 8217.

Chen H, et al. (2017) Methane potentials of wastewater generated from hydrothermal liquefaction of rice straw: focusing on the wastewater characteristics and microbial community compositions. Biotechnology for biofuels, 10, 140.

Xue K, et al. (2016) Annual Removal of Aboveground Plant Biomass Alters Soil Microbial Responses to Warming. mBio, 7(5).

Correa-Galeote D, et al. (2016) Bacterial Communities in the Rhizosphere of Amilaceous Maize (Zea mays L.) as Assessed by Pyrosequencing. Frontiers in plant science, 7, 1016.

Wei S, et al. (2016) The Bacteriomes of Ileal Mucosa and Cecal Content of Broiler Chickens and Turkeys as Revealed by Metagenomic Analysis. International journal of microbiology, 2016, 4320412.

Choi YS, et al. (2016) The presence of bacteria within tissue provides insights into the pathogenesis of oral lichen planus. Scientific reports, 6, 29186.

Kim YJ, et al. (2016) Mucosal and salivary microbiota associated with recurrent aphthous stomatitis. BMC microbiology, 16 Suppl 1, 57.

Jung WY, et al. (2016) Functional Characterization of Bacterial Communities Responsible for Fermentation of Doenjang: A Traditional Korean Fermented Soybean Paste. Frontiers in microbiology, 7, 827.

Kwon MJ, et al. (2016) Impact of Organic Carbon Electron Donors on Microbial Community Development under Iron- and Sulfate-Reducing Conditions. PloS one, 11(1), e0146689.

Su L, et al. (2016) Comparative Gut Microbiomes of Four Species Representing the Higher and the Lower Termites. Journal of insect science (Online), 16(1).

Goordial J, et al. (2016) Nearing the cold-arid limits of microbial life in permafrost of an upper dry valley, Antarctica. The ISME journal, 10(7), 1613.

Jung JY, et al. (2016) Effects of Temperature on Bacterial Communities and Metabolites during Fermentation of Myeolchi-Aekjeot, a Traditional Korean Fermented Anchovy Sauce. PloS one, 11(3), e0151351.