

Resource Summary Report

Generated by T1D on Aug 7, 2026

RD Pipeline

RRID:SCR_001192

Type: Tool

Proper Citation

RD Pipeline (RRID:SCR_001192)

Resource Information

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

Proper Citation: RD Pipeline (RRID:SCR_001192)

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: RD Pipeline

Synonyms: RDP Pipeline, RDP Amplicon Sequence Pipeline

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

Defining Citation: [PMID:24288368](#)

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

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: RD Pipeline

Resource ID: SCR_001192

Alternate IDs: OMICS_02158

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260807T042520+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 [T1D](#).

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.

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

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

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

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.

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.

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

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.

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

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

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.

Yergeau E, et al. (2016) Comparison of Methods to Identify Pathogens and Associated Virulence Functional Genes in Biosolids from Two Different Wastewater Treatment Facilities in Canada. *PloS one*, 11(4), e0153554.