Resource Summary Report

Generated by dkNET on May 19, 2025

Hybrid-denovo

RRID:SCR_015866
Type: Tool

Proper Citation

Hybrid-denovo (RRID:SCR_015866)

Resource Information

URL: http://bioinformaticstools.mayo.edu/research/hybrid-denovo/

Proper Citation: Hybrid-denovo (RRID:SCR_015866)

Description: Software for a de novo OTU-picking pipeline integrating single- and paired-end 16S sequence tags. It is designed to take Illumina paired-end sequencing reads as input and output the OTU BIOM table, together with their representative sequences and a phylogenetic tree of OTUs.

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

Keywords: hybrid-denovo, 16S rRNA, microbiota pipeline, single-end, paired-end, illumina read, de novo, otu-picking pipeline, phylogenetic tree, python, bio.tools

Funding:

Availability: Free, Available for download, Runs on Linux

Resource Name: Hybrid-denovo

Resource ID: SCR_015866

Alternate IDs: biotools:hybrid-denovo

Alternate URLs: https://bio.tools/hybrid-denovo

Record Creation Time: 20220129T080327+0000

Record Last Update: 20250517T060228+0000

Ratings and Alerts

No rating or validation information has been found for Hybrid-denovo.

No alerts have been found for Hybrid-denovo.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Balakrishnan B, et al. (2023) Eggerthella lenta augments preclinical autoantibody production and metabolic shift mimicking senescence in arthritis. Science advances, 9(35), eadg1129.

Hieken TJ, et al. (2022) The breast tissue microbiome, stroma, immune cells and breast cancer. Neoplasia (New York, N.Y.), 27, 100786.

Chen X, et al. (2018) Hybrid-denovo: a de novo OTU-picking pipeline integrating single-end and paired-end 16S sequence tags. GigaScience, 7(3), 1.