Resource Summary Report

Generated by RRID on Apr 9, 2025

ESPRIT-Tree

RRID:SCR_005045
Type: Tool

Proper Citation

ESPRIT-Tree (RRID:SCR_005045)

Resource Information

URL: http://plaza.ufl.edu/sunyijun/ES-Tree.htm

Proper Citation: ESPRIT-Tree (RRID:SCR_005045)

Description: Software for hierarchical Clustering Analysis of Millions of 16S rRNA Pyrosequences in Quasi-linear Time.

Abbreviations: ESPRIT-Tree

Synonyms: ESPRIT-Tree: Hierarchical Clustering Analysis of Millions of 16S rRNA Pyrosequences in Quasi-linear Time

Resource Type: software resource

Defining Citation: PMID:21596775

Keywords: clustering, 16s rrna, pyrosequence

Funding:

Resource Name: ESPRIT-Tree

Resource ID: SCR_005045

Alternate IDs: OMICS_01445

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250214T183116+0000

Ratings and Alerts

No rating or validation information has been found for ESPRIT-Tree.

No alerts have been found for ESPRIT-Tree.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

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

Audebert C, et al. (2016) Colonization with the enteric protozoa Blastocystis is associated with increased diversity of human gut bacterial microbiota. Scientific reports, 6, 25255.

Nguyen LD, et al. (2016) Effects of Propidium Monoazide (PMA) Treatment on Mycobiome and Bacteriome Analysis of Cystic Fibrosis Airways during Exacerbation. PloS one, 11(12), e0168860.

Praveckova M, et al. (2016) Indirect Evidence Link PCB Dehalogenation with Geobacteraceae in Anaerobic Sediment-Free Microcosms. Frontiers in microbiology, 7, 933.

Zheng W, et al. (2015) An accurate and efficient experimental approach for characterization of the complex oral microbiota. Microbiome, 3, 48.

Xu Y, et al. (2014) Escherichia coli O157:H7 super-shedder and non-shedder feedlot steers harbour distinct fecal bacterial communities. PloS one, 9(5), e98115.

Bowen JL, et al. (2013) Functional gene pyrosequencing and network analysis: an approach to examine the response of denitrifying bacteria to increased nitrogen supply in salt marsh sediments. Frontiers in microbiology, 4, 342.

Yang I, et al. (2013) Intestinal microbiota composition of interleukin-10 deficient C57BL/6J mice and susceptibility to Helicobacter hepaticus-induced colitis. PloS one, 8(8), e70783.

Jami E, et al. (2012) Composition and similarity of bovine rumen microbiota across individual animals. PloS one, 7(3), e33306.

Sergeant MJ, et al. (2012) High-throughput sequencing of 16S rRNA gene amplicons: effects of extraction procedure, primer length and annealing temperature. PloS one, 7(5), e38094.