

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 17, 2026

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 rna, pyrosequence

Resource Name: ESPRIT-Tree

Resource ID: SCR_005045

Alternate IDs: OMICS_01445

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260912T195620+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 [SPARC SAWG](#) .

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.