Resource Summary Report

Generated by NIF on May 4, 2025

AbundantOTU+

RRID:SCR_016527
Type: Tool

Proper Citation

AbundantOTU+ (RRID:SCR_016527)

Resource Information

URL: http://omics.informatics.indiana.edu/AbundantOTU/

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Description: Software tool for analysis of large 16S rRNA pyrosequences by using a consensus alignment algorithm, utilizing the sequence redundancy of abundant species in the pyrosequence dataset.

Abbreviations: AbundantOTU

Synonyms: AbundantOTU:Abundant Operational Taxonomic Unit, Abundant OTU, AbundantOTU+

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

Defining Citation: PMID:22102981

Keywords: pyrosequencing, 16S, rRNA, gene, operational, taxonomic, unit, abundant, species, dataset

Funding: NHGRI R01 HG004908;
NHLBI U01 HL09896001

Availability: Free, Available for download, Freely available

Resource Name: AbundantOTU+

Resource ID: SCR_016527

Record Creation Time: 20220129T080331+0000

Record Last Update: 20250503T060639+0000

Ratings and Alerts

No rating or validation information has been found for AbundantOTU+.

No alerts have been found for AbundantOTU+.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Ellermann M, et al. (2020) Dietary iron variably modulates assembly of the intestinal microbiota in colitis-resistant and colitis-susceptible mice. Gut microbes, 11(1), 32.

Gohir W, et al. (2019) High-fat diet intake modulates maternal intestinal adaptations to pregnancy and results in placental hypoxia, as well as altered fetal gut barrier proteins and immune markers. The Journal of physiology, 597(12), 3029.