

Resource Summary Report

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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: sequence analysis software, software resource, data analysis software, software application, 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: 20260820T054827+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 1 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.