Resource Summary Report

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CD-HIT-OTU

RRID:SCR_006983
Type: Tool

Proper Citation

CD-HIT-OTU (RRID:SCR_006983)

Resource Information

URL: http://weizhong-lab.ucsd.edu/cd-hit-otu/

Proper Citation: CD-HIT-OTU (RRID:SCR_006983)

Description: Data analysis service and software program that perform Operantional Taxonomic Units (OTUs) finding. It uses a three-step clustering for identifying OTUs. The first-step clustering is raw read filtering and trimming. The second step is error-free reads picking.. At the last step, OTU clustering is done at different distanct cutoffs (0.01, 0.02, 0.03... 0.12).

Abbreviations: CD-HIT-OTU

Resource Type: software resource

Defining Citation: PMID:22772836, PMID:21899761

Keywords: 454, read, illumina, rrna, fasta, metagenome, sequence, clustering, metagenomics, next-generation sequencing, protein

Funding:

Availability: GNU General Public License, v2, Acknowledgement requested

Resource Name: CD-HIT-OTU

Resource ID: SCR_006983

Alternate IDs: OMICS_01441

Record Creation Time: 20220129T080239+0000

Record Last Update: 20250410T065505+0000

Ratings and Alerts

No rating or validation information has been found for CD-HIT-OTU.

No alerts have been found for CD-HIT-OTU.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 88 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

Kim KE, et al. (2024) Ecological Interaction between Bacteriophages and Bacteria in Sub-Arctic Kongsfjorden Bay, Svalbard, Norway. Microorganisms, 12(2).

Kim JW, et al. (2024) Difference of Microbial Community in the Stream Adjacent to the Mixed Antibiotic Effluent Source. Toxics, 12(2).

Im C, et al. (2024) Low electric current in a bioelectrochemical system facilitates ethanol production from CO using CO-enriched mixed culture. Frontiers in microbiology, 15, 1438758.

Jang KB, et al. (2024) Dietary ?-mannanase reduced post-weaning diarrhea of pigs by positively modulating gut microbiota and attenuating systemic immune responses. Animal microbiome, 6(1), 59.

Naghipour S, et al. (2024) Circulating TMAO, the gut microbiome and cardiometabolic disease risk: an exploration in key precursor disorders. Diabetology & metabolic syndrome, 16(1), 133.

Guo Z, et al. (2024) Unveiling the microbiota-metabolite-myocardium axis: a novel perspective on cardiovascular health. Frontiers in microbiology, 15, 1389311.

Perveen N, et al. (2024) Microbiome of Hyalomma dromedarii (Ixodida: Ixodidae) Ticks: Variation in Community Structure with Regard to Sex and Host Habitat. Insects, 16(1).

Zhang M, et al. (2023) Gut microbiota of Suncus murinus, a naturally obesity-resistant animal, improves the ecological diversity of the gut microbiota in high-fat-diet-induced obese

mice. PloS one, 18(11), e0293213.

Yang H, et al. (2023) Dynamics of Functional Genes and Bacterial Community during Bioremediation of Diesel-Contaminated Soil Amended with Compost. Journal of microbiology and biotechnology, 33(4), 471.

Kim HJ, et al. (2023) Marine Bacterioplankton Community Dynamics and Potentially Pathogenic Bacteria in Seawater around Jeju Island, South Korea, via Metabarcoding. International journal of molecular sciences, 24(17).

Kim KE, et al. (2023) Covariance of Marine Nucleocytoplasmic Large DNA Viruses with Eukaryotic Plankton Communities in the Sub-Arctic Kongsfjorden Ecosystem: A Metagenomic Analysis of Marine Microbial Ecosystems. Microorganisms, 11(1).

Santorelli LA, et al. (2023) Beehives possess their own distinct microbiomes. Environmental microbiome, 18(1), 1.

Gil-Serna J, et al. (2022) Searching for the Fusarium spp. Which Are Responsible for Trichothecene Contamination in Oats Using Metataxonomy to Compare the Distribution of Toxigenic Species in Fields from Spain and the UK. Toxins, 14(9).

Lee HB, et al. (2022) The Diversity Patterns of Rare to Abundant Microbial Eukaryotes Across a Broad Range of Salinities in a Solar Saltern. Microbial ecology, 84(4), 1103.

Kim H, et al. (2022) Analysis of Major Bacteria and Diversity of Surface Soil to Discover Biomarkers Related to Soil Health. Toxics, 10(3).

Kameno K, et al. (2022) Loss of body weight in old 5xFAD mice and the alteration of gut microbiota composition. Experimental gerontology, 166, 111885.

Chaudhary DK, et al. (2022) Seasonal trends of mercury bioaccumulation and assessment of toxic effects in Asian clams and microbial community from field study of estuarine sediment. Environmental research, 212(Pt C), 113439.

Kim JW, et al. (2021) Metagenomic Analysis for Evaluating Change in Bacterial Diversity in TPH-Contaminated Soil after Soil Remediation. Toxics, 9(12).

Lee K, et al. (2021) Lactobacillus plantarum HY7715 Ameliorates Sarcopenia by Improving Skeletal Muscle Mass and Function in Aged Balb/c Mice. International journal of molecular sciences, 22(18).

E Silva B, et al. (2021) Microbiota identified from preserved Anopheles. Malaria journal, 20(1), 230.