

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 Operational 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 distant 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, rna, fasta, metagenome, sequence, clustering, metagenomics, next-generation sequencing, protein

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: 20260815T182331+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 89 mentions in open access literature.

Listed below are recent publications. The full list is available at [NIF](#) .

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

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

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.

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).

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

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.

Zhang M, et al. (2023) Fecal microbiota transplantation from *Suncus murinus*, an obesity-resistant animal, to C57BL/6NCrSlc mice, and the antibiotic effects in the approach. *Frontiers in microbiology*, 14, 1138983.

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.

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

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).

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).

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.

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

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