Resource Summary Report

Generated by FDI Lab - SciCrunch.org on Mar 31, 2025

cd-hit-454

RRID:SCR_005541
Type: Tool

Proper Citation

cd-hit-454 (RRID:SCR_005541)

Resource Information

URL: http://weizhong-lab.ucsd.edu/public/?q=softwares/cd-hit-454

Proper Citation: cd-hit-454 (RRID:SCR_005541)

Description: A software program to identify artificial duplicates from raw 454 sequencing reads, including exact duplicates and near identical duplicates.

Abbreviations: cd-hit-454

Resource Type: software resource

Defining Citation: PMID:20388221

Funding:

Resource Name: cd-hit-454

Resource ID: SCR_005541

Alternate IDs: OMICS_01037

Record Creation Time: 20220129T080230+0000

Record Last Update: 20250214T183029+0000

Ratings and Alerts

No rating or validation information has been found for cd-hit-454.

No alerts have been found for cd-hit-454.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 16 mentions in open access literature.

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

Popgeorgiev N, et al. (2024) A New Inovirus from the Human Blood Encodes Proteins with Nuclear Subcellular Localization. Viruses, 16(3).

Cohen JI, et al. (2023) The Conservation Genetics of Iris lacustris (Dwarf Lake Iris), a Great Lakes Endemic. Plants (Basel, Switzerland), 12(13).

Yoshida K, et al. (2021) Bifidobacterium response to lactulose ingestion in the gut relies on a solute-binding protein-dependent ABC transporter. Communications biology, 4(1), 541.

Schöps R, et al. (2020) Resident and phytometer plants host comparable rhizosphere fungal communities in managed grassland ecosystems. Scientific reports, 10(1), 919.

Redin D, et al. (2019) High throughput barcoding method for genome-scale phasing. Scientific reports, 9(1), 18116.

Fróes AM, et al. (2016) Distribution and Classification of Serine ?-Lactamases in Brazilian Hospital Sewage and Other Environmental Metagenomes Deposited in Public Databases. Frontiers in microbiology, 7, 1790.

Adel M, et al. (2016) Viruses-to-mobile genetic elements skew in the deep Atlantis II brine pool sediments. Scientific reports, 6, 32704.

Quigley KM, et al. (2014) Deep-sequencing method for quantifying background abundances of symbiodinium types: exploring the rare symbiodinium biosphere in reef-building corals. PloS one, 9(4), e94297.

Jennings TN, et al. (2013) Microsatellite primers for the Pacific Northwest conifer Callitropsis nootkatensis (Cupressaceae). Applications in plant sciences, 1(9).

Solonenko SA, et al. (2013) Sequencing platform and library preparation choices impact viral metagenomes. BMC genomics, 14, 320.

Wachholtz M, et al. (2013) Transcriptome analysis of two buffalograss cultivars. BMC genomics, 14, 613.

Jacquiod S, et al. (2013) Soil bacterial community shifts after chitin enrichment: an integrative metagenomic approach. PloS one, 8(11), e79699.

Durban J, et al. (2013) Integrated "omics" profiling indicates that miRNAs are modulators of the ontogenetic venom composition shift in the Central American rattlesnake, Crotalus simus simus. BMC genomics, 14, 234.

Müller T, et al. (2012) A catalogue of putative unique transcripts from Douglas-fir (Pseudotsuga menziesii) based on 454 transcriptome sequencing of genetically diverse, drought stressed seedlings. BMC genomics, 13, 673.

Fouts DE, et al. (2012) Next generation sequencing to define prokaryotic and fungal diversity in the bovine rumen. PloS one, 7(11), e48289.

Schwartz S, et al. (2012) A metagenomic study of diet-dependent interaction between gut microbiota and host in infants reveals differences in immune response. Genome biology, 13(4), r32.