

Resource Summary Report

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[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](#)

Resource Name: cd-hit-454

Resource ID: SCR_005541

Alternate IDs: OMICS_01037

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260808T185835+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 [NIF](#) .

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.

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

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

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.

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.

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

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.