

Resource Summary Report

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DNACLUST

RRID:SCR_001771

Type: Tool

Proper Citation

DNACLUST (RRID:SCR_001771)

Resource Information

URL: <http://sourceforge.net/projects/dnaclust/>

Proper Citation: DNACLUST (RRID:SCR_001771)

Description: Software program for clustering large number of short similar DNA sequences. It was originally designed for clustering targeted 16S rRNA pyrosequencing reads.

Synonyms: DNAClust

Resource Type: software resource

Defining Citation: [PMID:21718538](https://pubmed.ncbi.nlm.nih.gov/21718538/), [DOI:10.1186/1471-2105-12-271](https://doi.org/10.1186/1471-2105-12-271)

Keywords: cluster, dna sequence, gene, 16s rna pyrosequencing read, microbiome

Funding:

Availability: Free

Resource Name: DNACLUST

Resource ID: SCR_001771

Alternate IDs: OMICS_01955

Alternate URLs: <https://sources.debian.org/src/dnaclust/>

Record Creation Time: 20220129T080209+0000

Record Last Update: 20250420T014038+0000

Ratings and Alerts

No rating or validation information has been found for DNACLUST.

No alerts have been found for DNACLUST.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Ferraz T, et al. (2023) Genomic history of coastal societies from eastern South America. *Nature ecology & evolution*, 7(8), 1315.

Johnson MS, et al. (2023) Best Practices in Designing, Sequencing, and Identifying Random DNA Barcodes. *Journal of molecular evolution*, 91(3), 263.

Salazar L, et al. (2023) Insights into the genetic histories and lifeways of Machu Picchu's occupants. *Science advances*, 9(30), eadg3377.

Gagnon V, et al. (2020) Vegetation drives the structure of active microbial communities on an acidogenic mine tailings deposit. *PeerJ*, 8, e10109.

Drouin P, et al. (2019) Dynamic Succession of Microbiota during Ensiling of Whole Plant Corn Following Inoculation with *Lactobacillus buchneri* and *Lactobacillus hilgardii* Alone or in Combination. *Microorganisms*, 7(12).

Tremblay J, et al. (2019) Systematic processing of ribosomal RNA gene amplicon sequencing data. *GigaScience*, 8(12).

Yunusova AM, et al. (2017) Deterministic versus stochastic model of reprogramming: new evidence from cellular barcoding technique. *Open biology*, 7(4).

Duniere L, et al. (2017) Bacterial and fungal core microbiomes associated with small grain silages during ensiling and aerobic spoilage. *BMC microbiology*, 17(1), 50.