Resource Summary Report

Generated by <u>RRID</u> on Apr 19, 2025

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, DOI:10.1186/1471-2105-12-271

Keywords: cluster, dna sequence, gene, 16s rrna 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: 20250410T064744+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 <u>RRID</u>.

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.