Resource Summary Report

Generated by dkNET on May 21, 2025

AbundanceBin

RRID:SCR_004648
Type: Tool

Proper Citation

AbundanceBin (RRID:SCR_004648)

Resource Information

URL: http://omics.informatics.indiana.edu/AbundanceBin/

Proper Citation: AbundanceBin (RRID:SCR_004648)

Description: An abundance-based software tool for binning metagenomic sequences, such that the reads classified in a bin belong to species of identical or very similar abundances. AbundanceBin also gives estimations of species abundances and their genome sizes -two important characteristic parameters for a microbial community.

Abbreviations: AbundanceBin

Resource Type: software resource

Defining Citation: PMID:21385052

Keywords: metagenome, sequence

Funding:

Availability: Acknowledgement requested, Free, Public

Resource Name: AbundanceBin

Resource ID: SCR_004648

Alternate IDs: OMICS_01471

Record Creation Time: 20220129T080225+0000

Record Last Update: 20250519T203332+0000

Ratings and Alerts

No rating or validation information has been found for AbundanceBin.

No alerts have been found for AbundanceBin.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Benavides A, et al. (2018) CLAME: a new alignment-based binning algorithm allows the genomic description of a novel Xanthomonadaceae from the Colombian Andes. BMC genomics, 19(Suppl 8), 858.

Sedlar K, et al. (2017) Bioinformatics strategies for taxonomy independent binning and visualization of sequences in shotgun metagenomics. Computational and structural biotechnology journal, 15, 48.

Alaimo S, et al. (2017) Current Knowledge and Computational Techniques for Grapevine Meta-Omics Analysis. Frontiers in plant science, 8, 2241.

Alvarenga DO, et al. (2017) A Metagenomic Approach to Cyanobacterial Genomics. Frontiers in microbiology, 8, 809.

Wang Y, et al. (2015) MBBC: an efficient approach for metagenomic binning based on clustering. BMC bioinformatics, 16, 36.