# **Resource Summary Report**

Generated by RRID on May 7, 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:** 20250420T014230+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 RRID.

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.