

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

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

Availability: Acknowledgement requested, Free, Public

Resource Name: AbundanceBin

Resource ID: SCR_004648

Alternate IDs: OMICS_01471

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260801T190239+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 6 mentions in open access literature.

Listed below are recent publications. The full list is available at [RRID](#) .

Tomasella F, et al. (2025) MetaComBin: combining abundances and overlaps for binning metagenomics reads. *Frontiers in bioinformatics*, 5, 1504728.

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.

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

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

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