

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

CompostBin

RRID:SCR_004619

Type: Tool

Proper Citation

CompostBin (RRID:SCR_004619)

Resource Information

URL: <https://sites.google.com/site/souravc/compostbin>

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Description: A DNA-composition-based binning algorithm for classifying metagenomic reads. It has the ability to accurately bin raw sequence reads without need for assembly or training. It applies principal component analysis to project the data into an informative lower-dimensional space, and then uses the normalized cut clustering algorithm on this filtered data set to classify sequences into taxon-specific bins.

Abbreviations: CompostBin

Resource Type: software resource

Keywords: metagenome, classification, read

Resource Name: CompostBin

Resource ID: SCR_004619

Alternate IDs: OMICS_01472

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260725T190555+0000

Ratings and Alerts

No rating or validation information has been found for CompostBin.

No alerts have been found for CompostBin.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Cornet L, et al. (2018) Consensus assessment of the contamination level of publicly available cyanobacterial genomes. PloS one, 13(7), e0200323.

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

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.