

Resource Summary Report

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SemiBin

RRID:SCR_026896

Type: Tool

Proper Citation

SemiBin (RRID:SCR_026896)

Resource Information

URL: <https://github.com/BigDataBiology/SemiBin/>

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Description: Software command tool for metagenomic binning with deep learning, handles both short and long reads. Used for metagenomic binning at contig level which uses deep contrastive learning.

Synonyms: SemiBin2

Resource Type: software application, software resource, source code

Defining Citation: [PMID:35484115](#), [PMID:37387171](#)

Keywords: command tool, metagenomic binning, contig level, short and long reads,

Funding: National Natural Science Foundation of China ;
Shanghai Municipal Science and Technology Major Project

Availability: Free, Available for download, Freely available

Resource Name: SemiBin

Resource ID: SCR_026896

Record Creation Time: 20250503T055712+0000

Record Last Update: 20260904T001118+0000

Ratings and Alerts

No rating or validation information has been found for SemiBin.

No alerts have been found for SemiBin.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 20 mentions in open access literature.

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

Belay G, et al. (2026) Microorganisms and functional genes in an aerobic-anoxic integrated gold mine wastewater treatment system. World journal of microbiology & biotechnology, 42(4).

Tóth AG, et al. (2026) Protocol for the assessment of the impact of mycotoxins and glyphosate residues on the gut microbiome and resistome of European fallow deer. STAR protocols, 7(2), 104498.

Ricci F, et al. (2026) Chemosynthesis enables microbial communities to flourish in a marine cave ecosystem. The ISME journal, 20(1).

Achudhan AB, et al. (2026) Metagenome Sequencing and Recovery of 52 Microbial Genomes from Plastic-Polluted Coastal Sediment. Scientific data, 13(1).

Zhai Z, et al. (2026) HLRMDB: a comprehensive database of the human microbiome with metagenomic assembly, taxonomic classification, and functional annotation by analysis of long-read and hybrid sequencing data. Nucleic acids research, 54(D1), D763.

Hagenbeek A, et al. (2026) Genome-resolved metagenomics reveals unexpected diversity and host range of Candidatus Lariskella (Rickettsiales: Midichloriaceae). BMC genomics, 27(1).

Chopade A, et al. (2026) Shared biosynthetic architectures generate diverse β -amino polyketide residues in cyanobacterial peptides. bioRxiv : the preprint server for biology.

Park J, et al. (2026) Comparative pangenome analysis of methanogenic archaea from diverse ecosystems reveals potential targets for methane mitigation in rumen microbiome. Journal of animal science and technology, 68(3), 935.

Serrana JM, et al. (2025) Microbial hydrocarbon degradation potential of the Baltic Sea ecosystem. Microbiome, 13(1), 204.

Li L, et al. (2025) Systematic metaproteomics mapping reveals functional and ecological landscapes of Ex vivo human gut microbiota responses to therapeutic drugs. Nature communications, 16(1), 9383.

Pallen MJ, et al. (2025) Faecal metagenomes of great tits and blue tits provide insights into host, diet, pathogens and microbial biodiversity. Access microbiology, 7(4).

He J, et al. (2025) Multi-Habitat Landscape Promotes Microbial Diversity: Insights from the Traditional Agricultural Heritage and the Global Trend. Advanced science (Weinheim,

Baden-Wurttemberg, Germany), 12(46), e06402.

Kiguchi Y, et al. (2025) Giant extrachromosomal element "Inocle" potentially expands the adaptive capacity of the human oral microbiome. *Nature communications*, 16(1), 7397.

Haro-Moreno JM, et al. (2025) The hidden genetic reservoir: structural variants as drivers of marine microbial and viral microdiversity. *Environmental microbiome*, 20(1), 110.

Kohtz AJ, et al. (2025) Cultivation of Methanonezhaarchaeia, the third class of methanogens within the phylum Thermoproteota. *Science advances*, 11(50), eaea0936.

Bloemen B, et al. (2025) Overcoming challenges in metagenomic AMR surveillance with nanopore sequencing: a case study on fluoroquinolone resistance. *Frontiers in microbiology*, 16, 1614301.

Li H, et al. (2025) Reconstruction of 1,979 prokaryotic metagenome-assembled genomes from 37 global cave environments. *Scientific data*, 12(1), 1896.

Pan S, et al. (2023) SemiBin2: self-supervised contrastive learning leads to better MAGs for short- and long-read sequencing. *Bioinformatics (Oxford, England)*, 39(39 Suppl 1), i21.

Pan S, et al. (2022) A deep siamese neural network improves metagenome-assembled genomes in microbiome datasets across different environments. *Nature communications*, 13(1), 2326.

Tadrent N, et al. (2022) SnakeMAGs: a simple, efficient, flexible and scalable workflow to reconstruct prokaryotic genomes from metagenomes. *F1000Research*, 11, 1522.