

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, source code, software resource

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: 20260817T040729+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 [dkNET](#) .

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.

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).

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.

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

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.