

Resource Summary Report

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Nonpareil

RRID:SCR_004629

Type: Tool

Proper Citation

Nonpareil (RRID:SCR_004629)

Resource Information

URL: <https://github.com/lmrodriguezr/nonpareil>

Proper Citation: Nonpareil (RRID:SCR_004629)

Description: Estimate average coverage and create Nonpareil curves for metagenomic datasets.

Abbreviations: Nonpareil

Resource Type: software resource

Defining Citation: [PMID:24123672](#)

Resource Name: Nonpareil

Resource ID: SCR_004629

Alternate IDs: OMICS_01419

Record Creation Time: 20220129T080225+0000

Record Last Update: 20260725T190552+0000

Ratings and Alerts

No rating or validation information has been found for Nonpareil.

No alerts have been found for Nonpareil.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 83 mentions in open access literature.

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

Zou X, et al. (2025) Accurate Diagnosis of Lower Respiratory Infections Using Host Response and Respiratory Microbiome from a Single Metatranscriptome Test of Bronchoalveolar Lavage Fluid. *Advanced science* (Weinheim, Baden-Wurttemberg, Germany), 12(6), e2405087.

Chen N, et al. (2025) Novel Gene Clusters for Secondary Metabolite Synthesis in Mesophotic Sponge-Associated Bacteria. *Microbial biotechnology*, 18(2), e70107.

Noell SE, et al. (2025) Antarctic Geothermal Soils Exhibit an Absence of Regional Habitat Generalist Microorganisms. *Environmental microbiology*, 27(1), e70032.

Van Goethem MW, et al. (2025) Novel adaptive immune systems in pristine Antarctic soils. *Scientific reports*, 15(1), 2368.

Zhao J, et al. (2025) Quantifying the contribution of the rare biosphere to natural disturbances. *The ISME journal*, 19(1).

Lauritsen JG, et al. (2025) Robust, Open-Source and Automation-Friendly DNA Extraction Protocol for Hologenomic Research. *Molecular ecology resources*, 25(8), e70042.

Rumi MA, et al. (2025) Mapping the underlying drivers of resistome risk across diverse environments. *Research square*.

Haugum K, et al. (2025) Evaluation of shotgun metagenomics as a diagnostic tool for infectious gastroenteritis. *PloS one*, 20(9), e0331288.

Mumcu H, et al. (2025) Exploring extreme environments in Türkiye for novel P450s through metagenomic analysis. *PloS one*, 20(9), e0330523.

Escobar-Prieto JD, et al. (2025) Microbial diversity and functional potential of the *Halobates melleus* (Heteroptera: Gerridae) microbiome from the Red Sea coastline. *Environmental microbiome*, 20(1), 103.

Redgwell TA, et al. (2025) Prophages in the infant gut are pervasively induced and may modulate the functionality of their hosts. *NPJ biofilms and microbiomes*, 11(1), 46.

Midot F, et al. (2025) Temporal dynamics of soil microbial C and N cycles with GHG fluxes in the transition from tropical peatland forest to oil palm plantation. *Applied and environmental microbiology*, 91(1), e0198624.

Lee J, et al. (2025) Longitudinal monitoring of sewershed resistomes in socioeconomically diverse urban neighborhoods. *Communications medicine*, 5(1), 7.

Ba?c? C, et al. (2025) Ultra-deep long-read metagenomics captures diverse taxonomic and biosynthetic potential of soil microbes. *GigaScience*, 14.

Tian C, et al. (2025) Industrialization drives the gut microbiome and resistome of the Chinese populations. *mSystems*, 10(3), e0137224.

Fan Y, et al. (2025) Fecal microbiome profiling of children with *Shigella* diarrhea from low- and middle-income countries. *Microbiology spectrum*, 13(7), e0057325.

Francioli D, et al. (2025) Microbial inoculants modulate the rhizosphere microbiome, alleviate plant stress responses, and enhance maize growth at field scale. *Genome biology*, 26(1), 148.

Zhao J, et al. (2025) Promiscuous and genome-wide recombination underlies the sequence-discrete species of the SAR11 lineage in the deep ocean. *The ISME journal*, 19(1).

Unzueta-Martínez A, et al. (2025) Taxonomic diversity and functional potential of microbial communities in oyster calcifying fluid. *Applied and environmental microbiology*, 91(1), e0109424.

Kifushi M, et al. (2025) Strain-level dissection of complex rhizoplane and soil bacterial communities using single-cell genomics and metagenomics. *DNA research : an international journal for rapid publication of reports on genes and genomes*, 32(6).