

Resource Summary Report

Generated by T1D on Sep 20, 2026

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: 20260919T195040+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 96 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#) .

Ali H, et al. (2026) Seasonal shifts in vegetation, soil properties, and microbial communities in Western Himalayan forests. *Environmental microbiome*, 21(1), 22.

Orr RJS, et al. (2026) Spatial and temporal patterns of public transit aerobiomes. *Microbiome*, 14(1), 64.

Stead CE, et al. (2026) Exploring the biotechnological potential of terrestrial hot spring microbiomes for CO₂ utilisation. *Environmental microbiome*, 21(1).

Jackson SA, et al. (2026) New insights into the microbiome of the deep-sea sponge *Inflatella pellicula* and the secondary metabolic potential of metagenome-assembled genomes and the wider microbiome. *Microbial genomics*, 12(1).

Yang K, et al. (2026) Soil antibiotic resistome in farmland exhibits higher diversity and horizontal transfer potential than adjacent pastureland in agro-pastoral ecotone. *Environmental microbiome*, 21(1).

Luo S, et al. (2026) Temperature-driven metabolic adaptation in thermophilic microbial communities of Western Sichuan hot springs. *BMC microbiology*, 26(1).

Haro-Moreno JM, et al. (2026) Effects of marine heatwaves on the dynamics of marine coastal microbial communities. *Environmental microbiome*, 21(1).

Conrad RE, et al. (2026) Metagenome-based vertical profiling of the Gulf of Mexico highlights its uniqueness and far-reaching effects of freshwater input. *Applied and environmental microbiology*, 92(2), e0258925.

St John E, et al. (2026) Global deep-sea hydrothermal deposit metagenomes and metagenome-assembled genomes over time and space. *Scientific data*, 13(1), 283.

Du H, et al. (2026) Virome diversity and zoonotic risks of rodents along ecological gradients in the Northern Tianshan Mountains, China. *Microbiome*, 14(1), 19.

Pantiukh K, et al. (2026) Metagenome-assembled genomes from a population-based cohort uncover novel gut species and within-species diversity, revealing prevalent disease associations. *mSystems*, 11(4), e0011426.

Jeilu O, et al. (2026) CAZyme fold architecture is conserved between disparate environments despite extreme sequence divergence. *mSystems*, 11(6), e0048526.

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.

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

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).

Aminu S, et al. (2025) Genome-resolved surveillance and predictive ecological risk modeling of urban microbiomes. *Microbiome*, 14(1), 45.

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