

Resource Summary Report

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Pyani

RRID:SCR_021088

Type: Tool

Proper Citation

Pyani (RRID:SCR_021088)

Resource Information

URL: <https://pypi.org/project/pyani/>

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Description: Software package and script for calculation of genome scale average nucleotide identity. Python3 module that provides support for calculating average nucleotide identity and related measures for whole genome comparisons, and rendering relevant graphical summary output. Where available, it takes advantage of multicore systems, and can integrate with SGE/OGE-type job schedulers for the sequence comparisons.

Resource Type: software application, software resource, data analytics software

Keywords: Genome scale average nucleotide identity calculation, nucleotide identity calculation, nucleotide, identity calculation

Availability: Free, Available for download, Freely available

Resource Name: Pyani

Resource ID: SCR_021088

License: MIT License

Record Creation Time: 20220129T080353+0000

Record Last Update: 20260812T044407+0000

Ratings and Alerts

No rating or validation information has been found for Pyani.

No alerts have been found for Pyani.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 90 mentions in open access literature.

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

Jo J, et al. (2026) Genomic and Phenotypic Evaluation of the Gliadin-Degrading Probiotic *Bacillus amyloliquefaciens* EG025 from Cheonggukjang for Celiac Disease Treatment. *Probiotics and antimicrobial proteins*, 18(3), 4012.

Noecker C, et al. (2026) A widespread gut bacterial lineage distinguished by redox metabolism and phage defense. *bioRxiv : the preprint server for biology*.

Revel-Muroz AZ, et al. (2026) Gut Hi-C metagenomes of severe COVID-19 patients: bacteria and yeast involved in gut-lung axis. *mSphere*, 11(6), e0013926.

Ravi A, et al. (2026) Cattle feces are a reservoir of diverse *Acinetobacter* species with potential to spread antibiotic resistance genes. *Animal microbiome*, 8(1).

Pons I, et al. (2026) Fidelity in co-diversified symbiosis. *Nature communications*, 17(1), 1644.

Zhou H, et al. (2026) Two Novel Thiosulfate-Oxidizing Species from Coastal Sediments Reveal Distinct Ecological Strategies: *Pseudothioclava alba* sp. nov. and *Terasakiella sediminum* sp. nov. *Microorganisms*, 14(2).

Juan DR, et al. (2026) Microbial succession and assembly shaped by sulfur, spatial partitioning, and water flow in a volcanic acidic river of northern Patagonia. *The ISME journal*, 20(1).

Rau J, et al. (2026) Up-to-date MALDI-TOF MS-based identification of the *Corynebacterium diphtheriae* species complex for improved diagnostics. *Journal of clinical microbiology*, 64(6), e0132425.

Islam SI, et al. (2026) Hidden in the Pangenome? Machine Learning-Driven Discovery of Antimicrobial Potential in *Corynebacterium glutamicum*. *Bioinformatics and biology insights*, 20, 11779322261461933.

Kim J, et al. (2026) Complete genome and functional insights into *Microbacterium* sp. strain FBCC-B4120, a novel freshwater isolate with diverse biotechnological traits. *PLoS one*, 21(5), e0347549.

Tao J, et al. (2026) Identification of a novel SXT/R391 integrative and conjugative element harboring bla NDM-1 in a clinical *Providencia huaxiensis* isolate. *Frontiers in microbiology*, 17, 1818759.

Rouxel C, et al. (2026) Exploration of geographical population structure of *Anaplasma phagocytophilum*: Insights from 12 newly sequenced European human and bovine genome assemblies. *Current research in parasitology & vector-borne diseases*, 9, 100393.

Yasuda S, et al. (2026) Potential survival strategies of novel comammox and nitrite-oxidizing *Nitrospira* synthesizing osmoprotectants in a wastewater microbiome treating high-ammonia brackish landfill leachate. *Microbiome*, 14(1).

Xu H, et al. (2026) Plasmid-borne *mcr-4.3* in *Acinetobacter nosocomialis* recovered from imported beef cattle: Genomic characterization and one health implications. *One health* (Amsterdam, Netherlands), 22, 101466.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

Wang Y, et al. (2025) Orthopedic infections associated with distinct *Acinetobacter* strains in rural area of Qingdao, China. *Frontiers in cellular and infection microbiology*, 15, 1601779.

Gonzalez-Reyes M, et al. (2025) A global perspective on the genomics of *Moraxella catarrhalis*. *Microbial genomics*, 11(8).

Liu J, et al. (2025) Genetic diversity and evolutionary adaptation of *Clostridium paraputrificum*, a rare pathogen in humans. *Communications biology*, 8(1), 1769.

Kazarina A, et al. (2025) Recovery of 679 metagenome-assembled genomes from different soil depths along a precipitation gradient. *Scientific data*, 12(1), 521.

Majidian S, et al. (2025) EvANI benchmarking workflow for evolutionary distance estimation. *Briefings in bioinformatics*, 26(3).