

Resource Summary Report

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PIRATE

RRID:SCR_017265

Type: Tool

Proper Citation

PIRATE (RRID:SCR_017265)

Resource Information

URL: <https://github.com/SionBayliss/PIRATE>

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Description: Software pangenomics toolbox for clustering diverged orthologues in bacteria. Used to identify and classify orthologous gene families in bacterial pangenomes over wide range of sequence similarity thresholds.

Synonyms: Pangenome Iterative Refinement And Threshold Evaluation

Resource Type: data processing software, data analysis software, software application, software resource

Defining Citation: [DOI:10.1101/598391](https://doi.org/10.1101/598391)

Keywords: Pangenome, clustering, genomics, bacteria, orthologue, gene, sequence, amino acid, nucleotide, dataset, bio.tools

Availability: Free, Available for download, Freely available

Resource Name: PIRATE

Resource ID: SCR_017265

Alternate IDs: biotools:PIRAtE

Alternate URLs: <https://bio.tools/PIRATE>

License: GNU GPL v3

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260801T190548+0000

Ratings and Alerts

No rating or validation information has been found for PIRATE.

No alerts have been found for PIRATE.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 18 mentions in open access literature.

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

N??pflin N, et al. (2025) Gene-level analysis of core carbohydrate metabolism across the Enterobacteriaceae pan-genome. *Communications biology*, 8(1), 1241.

Newstead L, et al. (2025) Genomic characterization of *Pseudomonas aeruginosa* from canine otitis highlights the need for a One Health approach to this opportunistic pathogen. *Microbial genomics*, 11(5).

Oe F, et al. (2025) Expanding the Eco-collection of Methane-oxidizing Bacteria Inhabiting Rice Roots: Cultivation, Isolation, and Genomic Characterization of Isolates. *Microbes and environments*, 40(4).

Unitt A, et al. (2025) *Neisseria gonorrhoeae* LIN codes provide a robust, multi-resolution lineage nomenclature. *eLife*, 14.

Gao F, et al. (2025) Genomic epidemiology and the evolution of *erm(B)*-mediated macrolide resistance in *Campylobacter*. *Microbial genomics*, 11(10).

Wang J, et al. (2025) DNA gains and losses in gigantic genomes do not track differences in transposable element-host silencing interactions. *Communications biology*, 8(1), 704.

Dewi DAPR, et al. (2024) Detection and genetic characterization of multidrug-resistant staphylococci isolated from public areas in an international airport. *Scientific reports*, 14(1), 27738.

Feng Y, et al. (2024) Population genomics uncovers global distribution, antimicrobial resistance, and virulence genes of the opportunistic pathogen *Klebsiella aerogenes*. *Cell reports*, 43(8), 114602.

Decena-Segarra LP, et al. (2024) Transposable Element Diversity and Activity Patterns in Neotropical Salamanders. *Molecular biology and evolution*, 41(11).

Henning PM, et al. (2023) Annotation of the *Turnera subulata* (Passifloraceae) Draft Genome Reveals the S-Locus Evolved after the Divergence of Turneroideae from Passifloroideae in a Stepwise Manner. *Plants (Basel, Switzerland)*, 12(2).

de Korne-Elenbaas J, et al. (2022) The *Neisseria gonorrhoeae* Accessory Genome and Its Association with the Core Genome and Antimicrobial Resistance. *Microbiology spectrum*, 10(3), e0265421.

White H, et al. (2022) Signatures of selection in core and accessory genomes indicate different ecological drivers of diversification among *Bacillus cereus* clades. *Molecular ecology*, 31(13), 3584.

Liu L, et al. (2021) Genome-Based Taxonomy of *Brevundimonas* with Reporting *Brevundimonas huaxiensis* sp. nov. *Microbiology spectrum*, 9(1), e0011121.

Wang J, et al. (2021) Gigantic Genomes Provide Empirical Tests of Transposable Element Dynamics Models. *Genomics, proteomics & bioinformatics*, 19(1), 123.

Klai K, et al. (2020) Screening of *Helicoverpa armigera* Mobilome Revealed Transposable Element Insertions in Insecticide Resistance Genes. *Insects*, 11(12).

Petit RA, et al. (2020) Bactopia: a Flexible Pipeline for Complete Analysis of Bacterial Genomes. *mSystems*, 5(4).

Zhou Z, et al. (2020) Accurate reconstruction of bacterial pan- and core genomes with PEPPAN. *Genome research*, 30(11), 1667.

Bayliss SC, et al. (2019) PIRATE: A fast and scalable pangenomics toolbox for clustering diverged orthologues in bacteria. *GigaScience*, 8(10).