

Resource Summary Report

Generated by [dkNET](#) on Sep 5, 2026

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 analysis software, data processing 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: 20260903T235417+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 23 mentions in open access literature.

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

Meroni G, et al. (2026) Genomic Characterisation of Pyometra-Associated Escherichia coli in a Lombardy Veterinary Clinic: A Nanopore-Based Case Series. Antibiotics (Basel, Switzerland), 15(2).

Carmona-Salido H, et al. (2026) Emergence, climate-driven expansion, and diversification of a European Vibrio vulnificus lineage (L4) with multi-host pathogenic potential. Emerging microbes & infections, 15(1), 2601370.

Kimani MW, et al. (2026) Rapid and recent evolution of fetA phase variability among hyperinvasive MenW:cc11 disease isolates. Microbial genomics, 12(2).

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

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.

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

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).

Ramachandran P, et al. (2025) Population structure analysis of Salmonella serovar Muenchen to redefine geno-serotyping using genome indexing approaches. Frontiers in microbiology, 16, 1681711.

Qin J, et al. (2025) Severe lower limb infection by Kerstersia gyiorum: clinical and genomic insights into an underestimated pathogen. Frontiers in medicine, 12, 1639069.

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

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.

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.

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.

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

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

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