

Resource Summary Report

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Pilon

RRID:SCR_014731

Type: Tool

Proper Citation

Pilon (RRID:SCR_014731)

Resource Information

URL: <https://github.com/broadinstitute/pilon/>

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Description: Software tool to automatically improve draft assemblies and find variation among strains, including large event detection. FASTA files of genome along with one or more BAM files of reads aligned as input. Read alignment analysis is used to identify inconsistencies between input genome and evidence in reads, then attempts to make improvements to genome.

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

Defining Citation: [DOI:10.1371/journal.pone.0112963](https://doi.org/10.1371/journal.pone.0112963),
[DOI:10.1371/journal.pone.0112963](https://doi.org/10.1371/journal.pone.0112963)

Keywords: automatically, improve, draft, assembly, variation, strain, genome, read, alignment, analysis, inconsistency, bio.tools

Availability: Available for download, Acknowledgement requested

Resource Name: Pilon

Resource ID: SCR_014731

Alternate IDs: OMICS_14553, biotools:pilon

Alternate URLs: <https://github.com/broadinstitute/pilon/wiki>, <https://bio.tools/pilon>,
<https://sources.debian.org/src/pilon/>

License: GNU General Public License version 2

Record Creation Time: 20220129T080322+0000

Record Last Update: 20260905T133006+0000

Ratings and Alerts

No rating or validation information has been found for Pilon .

No alerts have been found for Pilon .

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3377 mentions in open access literature.

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

Sevillano E, et al. (2026) Saprophyticin S: A Novel Saposin-like, Leaderless Bacteriocin Produced by *Staphylococcus saprophyticus* P1CEA4 of Porcine Origin. *Probiotics and antimicrobial proteins*, 18(3), 4940.

Zhou Z, et al. (2026) Chromosome-level genome provides novel insights into the starch metabolism regulation and evolutionary history of *Tetraselmis helgolandica*. *Journal of advanced research*, 79, 251.

Silcocks M, et al. (2026) Dormancy regulon reduction was pivotal to the evolution of *Mycobacterium tuberculosis*. *Nature communications*, 17(1).

Hao CL, et al. (2026) Mitochondrial Genome of *Abramis brama orientalis* Reveals Dominant Role of Natural Selection over Mutation Pressure in Shaping Codon Usage Bias in Leuciscinae Fishes. *Animals : an open access journal from MDPI*, 16(7).

Tom?? LMR, et al. (2026) Emergence of *Candida (Candidozyma) auris* in Minas Gerais, Brazil: Genomic Surveillance to Guide Rapid Public Health Responses. *Mycoses*, 69(2), e70146.

Jeong HY, et al. (2026) Hybrid Whole-Genome Sequencing for Genetic Stability Assessment of Infectious Laryngotracheitis Virus Vaccine Strains. *Vaccines*, 14(3).

Xu H, et al. (2026) Isolation and characterization of a novel lytic bacteriophage Ecolivirus Myo-P293 targeting avian pathogenic *Escherichia coli*. *Archives of virology*, 171(5).

Zheng J, et al. (2026) Mitochondrial genome of the invasive weed *Amaranthus palmeri*: structural features, RNA editing, and evolutionary insights. *BMC plant biology*, 26(1).

Li K, et al. (2026) Centromere organization and epigenetic regulation in *Aristolochia fimbriata*. *Genome biology*, 27(1).

Ding J, et al. (2026) Highly Resolved Community Sewage Metagenomics Unveiling Landscape and Transmission Patterns of Antibiotic Resistome in Hong Kong Populations. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(20), e08389.

Jani J, et al. (2026) Atypical El Tor *Vibrio cholerae* from the second major global seventh-pandemic cholera wave is endemic in Sabah, Malaysia. *Microbiology spectrum*, 14(3), e0219125.

Ibrahim MS, et al. (2026) AntiPan: a genome-informed in silico pipeline for advancing subunit vaccine discovery against *Staphylococcus aureus*. *Scientific reports*, 16(1), 5396.

Helekal D, et al. (2026) Quantifying the real-world impact of antibiotic use and genetic determinants of resistance on gonococcal dynamics. *Nature microbiology*, 11(2), 375.

Su L, et al. (2026) Molecular epidemiological and genetic variability of *Salmonella* isolates from the tropical mountainous region of southern China (2017-2024). *Microbiology spectrum*, 14(4), e0267625.

Rizzo G, et al. (2026) *Methanothermococcus jasoni* sp. nov., a novel thermophilic methanogen from subseafloor hydrothermal vent fluids of Axial Seamount, Juan de Fuca Ridge. *International journal of systematic and evolutionary microbiology*, 76(3).

Yu Q, et al. (2026) Diversity and evolution of a phase-variable multi-locus antigen in *Neisseria gonorrhoeae*. *bioRxiv* : the preprint server for biology.

Feng J, et al. (2026) A temperate phage encoding a catalytically active endolysin: characterization of phage P7869 and its Lys7869 against *Pseudomonas aeruginosa*. *BMC microbiology*, 26(1).

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Marin-Carvajal S, et al. (2026) Whole-genome sequencing, phenotypic characterization, and antifungal susceptibility profiles of three *Aspergillus hortae* clinical isolates from Colombia. *PloS one*, 21(2), e0342479.

Lee YH, et al. (2026) Molecular and Phenotypic Characterization of Multidrug-Resistant *Aspergillus fumigatus* Clinical Isolates in Republic of Korea. *Journal of fungi (Basel, Switzerland)*, 12(5).