

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

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: 20260808T190238+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 [SPARC SAWG](#) .

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.

Luo Y, et al. (2026) A chromosome-level genome assembly and multi-omics analyses provide insights into the biosynthesis of piperlongumine in *Piper sarmentosum*. *Communications biology*, 9(1), 170.

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.

Sharma M, et al. (2026) Improved reference assembly and core collection resequencing to facilitate exploration of important agronomical traits for the improvement of oilseed crop, *Carthamus tinctorius* L. *GigaScience*, 15.

Lai Y, et al. (2026) Comparative genomics reveals the molecular basis for divergent algicidal strategies in two *Alteromonas macleodii* strains. *Applied and environmental microbiology*, 92(1), e0196525.

Ruzickova M, et al. (2026) From ecology to evolution: plasmid- and colicin-mediated persistence of antibiotic-resistant *Escherichia coli* in gulls. *mSystems*, 11(2), e0166325.

Shultz RR, et al. (2026) Eye can see clearly now: Identifying the locus associated with a white-eye mutation in honey bees (*Apis mellifera*). *Insect molecular biology*, 35(2), 209.

Lyu Y-Y, et al. (2026) First report of an *Escherichia coli* ST131 clinical isolate co-harboring blaKPC-2 and blaNDM-13 on an IncB/O/K/Z plasmid in China. *Microbiology spectrum*, 14(2), e0052825.

Knibbe E, et al. (2026) Synergistic regulatory mechanisms in glycolysis revealed by pathway transplantation. *mBio*, 17(1), e0021925.

Huang X, et al. (2026) Pangenome Analysis Reveals Structural Variations Associated With Citric Acid Accumulation in *Prunus mume*. *Plant biotechnology journal*, 24(4), 2623.

Gunasekaran D, et al. (2026) Characterizing a Novel *Symbiopectobacterium purcellii* MEX Strain at the Early Stages of Establishing a Symbiotic Relationship. *Genome biology and evolution*, 18(1).

Zhang J, et al. (2026) Cross-kingdom genomic variation in chicken gut microbiomes: insights from China's diverse local breeds. *Microbiome*, 14(1).

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

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.

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.

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.

Fonseca CA, et al. (2026) Analysis of *Aspergillus* spp. Isolates According to Temporal-Spatial, Sociodemographic, and Clinical Variables-Microsatellite Typing of Clinical and Environmental Samples of *Aspergillus fumigatus* in a University Hospital in Sao Paulo, Brazil. *Mycoses*, 69(1), e70126.

Zhao Q, et al. (2026) Multi-omics analyses of *Dracocephalum moldavica* L. reveal two flavonoid glycosyltransferases in tilianin biosynthesis. *BMC genomics*, 27(1), 208.

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.