

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, software application, software resource, sequence 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: 20260801T190752+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 3102 mentions in open access literature.

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

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.

Bekavac M, et al. (2026) De novo genome assembly of Ansell's mole-rat (*Fukomys anselli*). *G3 (Bethesda, Md.)*, 16(1).

Chen J, et al. (2026) Genomic and transcriptomic analysis of yield enhancement mechanism of lipopeptide iturin W by tryptone supplementation. *Microbiology spectrum*, 14(1), e0324725.

Gao C, et al. (2026) High-Quality Genome Assembly of *Diplocarpon coronariae* Unveils LTR Retrotransposon-Driven Structural Dynamics in Fungi Evolution. *Molecular ecology resources*, 26(1), e70070.

Hu Y, et al. (2026) Novel KPC-2 variants and epidemic ST463 clones underlie ceftazidime/avibactam resistance in carbapenem-resistant *Pseudomonas aeruginosa*. *Microbiology spectrum*, 14(1), e0218725.

Shi M, et al. (2026) Genomic architecture and evolution of heterostyly: new insights from *Cordia subcordata* (Boraginaceae). *Molecular biology and evolution*, 43(1).

Mochales-Riaño G, et al. (2025) Chromosome-level reference genome for the medically important Arabian horned viper (*Cerastes gasperettii*). *GigaScience*, 14.

Liang Y, et al. (2025) The molecular basis of octocoral calcification revealed by genome and skeletal proteome analyses. *GigaScience*, 14.

Liu H, et al. (2025) A telomere-to-telomere gapless genome reveals SIPRR1 control of circadian rhythm and photoperiodic flowering in tomato. *GigaScience*, 14.

Guang X, et al. (2025) Telomere-to-telomere African wild rice (*Oryza longistaminata*) reference genome reveals segmental and structural variation. *GigaScience*, 14.

Paudel R, et al. (2025) Genome assembly and comparative analysis of *Alternaria Linariae* reveal novel genes associated with host colonization and virulence. *BMC genomics*, 26(1), 638.

Kaper D, et al. (2025) Forward genetics in *C. elegans* reveals genetic adaptations to polyunsaturated fatty acid deficiency. *eLife*, 13.

Hernández-García M, et al. (2025) ICU environment as a reservoir of KPC-ST307-*Klebsiella pneumoniae* high-risk clone resistant to ceftazidime-avibactam. *Scientific reports*, 15(1), 29486.

Liu JN, et al. (2025) Pan-genome analyses of 11 *Fraxinus* species provide insights into salt adaptation in ash trees. *Plant communications*, 6(1), 101137.

Whitmire JM, et al. (2025) A unique *Helicobacter pylori* strain to study gastric cancer development. *Microbiology spectrum*, 13(1), e0216324.

Yibar A, et al. (2025) Integrated assessment of mucilage impact on human health using the One Health approach: Prevalence and antimicrobial resistance profiles of *Escherichia coli* and *Clostridium perfringens* in the Marmara Sea, Türkiye. *Heliyon*, 11(3), e42103.

Han Y, et al. (2025) Antibiotic-associated changes in *Akkermansia muciniphila* alter its effects on host metabolic health. *Microbiome*, 13(1), 48.

Antwerpen M, et al. (2025) Archival and Newly Isolated Historical *Bacillus anthracis* Strains Populate the Deeper Phylogeny of the A.Br.075(Sterne) Clade. *Pathogens (Basel, Switzerland)*, 14(1).

Sun Y, et al. (2025) *Bacillus paralicheniformis* SYN-191 isolated from ginger rhizosphere soil and its growth-promoting effects in ginger farming. *BMC microbiology*, 25(1), 75.

Patel J, et al. (2025) Whole genome sequencing, assembly and annotation of the Southern Ground Hornbill - *Bucorvus leadbeateri*. *Scientific data*, 12(1), 58.