

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, data analysis software, software resource, software application, 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: 20260728T043443+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 [nidm-terms](#) .

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 anelli*). *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.

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

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.

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

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

Tu G, et al. (2025) A chromosome-level genome assembly of the mud carp (*Cirrhinus molitorella*). *Scientific data*, 12(1), 285.

Hubert J, et al. (2025) A novel *Erwiniaceae* gut symbiont modulates gene expression of the intracellular bacterium *Cardinium* in the stored product mite *Tyrophagus putrescentiae*. *mSphere*, 10(4), e0087924.

Zan Y, et al. (2025) The genome and GeneBank genomics of allotetraploid *Nicotiana tabacum* provide insights into genome evolution and complex trait regulation. *Nature genetics*, 57(4), 986.

Gaikwad AB, et al. (2025) Chromosome-scale genome assembly of *Trigonella corniculata* (L.)L. (Nagauri pan /Kasuri methi), an important spice. *Scientific data*, 12(1), 509.

Wang Y, et al. (2025) Surfactin: a novel *Aphis gossypii* killing surfactin produced by *Bacillus australimaris* TRM82479 of Taklamakan Desert origin. *Frontiers in microbiology*, 16, 1559495.

Zhang R, et al. (2025) Characterization of FosA13, a novel fosfomycin glutathione transferase identified in a *Morganella morganii* isolate from poultry. *Frontiers in cellular and infection microbiology*, 15, 1534084.

Kim J, et al. (2025) Contributions of interspecific hybrids to genetic variability in *Glycyrrhiza uralensis* and *G. glabra*. *Scientific reports*, 15(1), 8764.

Ghosh S, et al. (2025) Transcriptional diversification in a human-adapting zoonotic pathogen drives niche-specific evolution. *Nature communications*, 16(1), 2067.

Kirbis A, et al. (2025) Comparative analysis using a chromosome-scale genome assembly for *Funaria hygrometrica* suggests greater collinearity in mosses than in seed plants. *Communications biology*, 8(1), 330.

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.