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

Defining Citation: DOI:10.1371/journal.pone.0112963, DOI: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

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Alternate IDs: biotools:pilon, OMICS_14553


Ratings and Alerts
No rating or validation information has been found for Pilon.

No alerts have been found for Pilon.

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**Data and Source Information**

**Source:** SciCrunch Registry

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**Usage and Citation Metrics**

We found 1830 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [RRID](https://rrid.bio/).


Tu GX, et al. (2023) Long-read genome assemblies reveal a cis-regulatory landscape associated with phenotypic divergence in two sister Siniperca fish species. Zoological research, 44(2), 287.

Liu J, et al. (2023) Division of developmental phases of freshwater leech Whitmania pigra and key genes related to neurogenesis revealed by whole genome and transcriptome analysis. BMC genomics, 24(1), 203.


Qi Y, et al. (2023) Chromosome-level genome assembly of Phrynocephalus forsythii using third-generation DNA sequencing and Hi-C analysis. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(2).


Rondeau EB, et al. (2023) Population-size history inferences from the coho salmon (Oncorhynchus kisutch) genome. G3 (Bethesda, Md.), 13(4).

Davis JT, et al. (2023) Whole-genome sequence of synthetically derived Brassica napus inbred cultivar Da-Ae. G3 (Bethesda, Md.), 13(4).

Chang J, et al. (2023) The genome of the king protea, Protea cynaroides. The Plant journal :


Li C, et al. (2023) Efficient CRISPR-Cas9 based cytosine base editors for phytopathogenic bacteria. Communications biology, 6(1), 56.

Ning Y, et al. (2023) The chromosome-scale genome of Kobresia myosuroides sheds light on karyotype evolution and recent diversification of a dominant herb group on the Qinghai-Tibet Plateau. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(1).


Solares E, et al. (2023) Insights into the domestication of avocado and potential genetic contributors to heterodichogamy. G3 (Bethesda, Md.), 13(2).

Palmer W, et al. (2023) Genome assembly and association tests identify interacting loci associated with vigor, precocity, and sex in interspecific pistachio rootstocks. G3 (Bethesda, Md.), 13(2).

Hasegawa Y, et al. (2023) Genome assembly and transcriptomic analyses of the repeatedly rejuvenating jellyfish Turritopsis dohrnii. DNA research : an international journal for rapid publication of reports on genes and genomes, 30(1).