Pilon

RRID:SCR_014731
Type: Tool

Proper Citation

Pilon (RRID:SCR_014731)

Resource Information

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

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 Name: Pilon

Proper Citation: Pilon (RRID:SCR_014731)

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

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

Resource ID: SCR_014731

Related resources: shovill

References: DOI:10.1371/journal.pone.0112963

Availability: Available for download, Acknowledgement requested

Website Status: Last checked up

Alternate URLs: https://github.com/broadinstitute/pilon/wiki
Mentions Count: 458

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 458 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](#).


Makke G, et al. (2020) Whole-Genome-Sequence-Based Characterization of Extensively Drug-Resistant Acinetobacter baumannii Hospital Outbreak. mSphere, 5(1).


