

Resource Summary Report

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Bestus Bioinformaticus Duk

RRID:SCR_016969

Type: Tool

Proper Citation

Bestus Bioinformaticus Duk (RRID:SCR_016969)

Resource Information

URL: <https://jgi.doe.gov/data-and-tools/bbtools/bb-tools-user-guide/bbduk-guide/>

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Description: Software tool for trimming and filtering sequencing data. Used to combine data quality related trimming, filtering, and masking operations into a single tool adapter. BBDuk2 allows multiple kmer based operations in a single pass.

Abbreviations: BBDuk

Synonyms: BB Duk, Decontamination Using Kmers, Bestus Bioinformaticus Decontamination using kmers, BBDuk2, BBDUK, BBDuk, BBDuk 2, Bestus Bioinformaticus Decontamination Using kmers

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

Keywords: sequencing, data, quality, trimming, filtering, masking, operation, single, tool, adapter, contaminant, sequence, GC, length, entropy, format, conversion, histogram, kmer, estimation, decontamination

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Bestus Bioinformaticus Duk

Resource ID: SCR_016969

Alternate URLs: <http://seqanswers.com/forums/showthread.php?t=42776>,

<https://www.geneious.com/plugins/bbduk/#links>

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250521T061656+0000

Ratings and Alerts

No rating or validation information has been found for Bestus Bioinformaticus Duk.

No alerts have been found for Bestus Bioinformaticus Duk.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 150 mentions in open access literature.

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

Cheshomi N, et al. (2025) Viral concentration method biases in the detection of viral profiles in wastewater. *Applied and environmental microbiology*, 91(1), e0133924.

Záhonová K, et al. (2025) Comparative Analysis of Protist Communities in Oilsands Tailings Using Amplicon Sequencing and Metagenomics. *Environmental microbiology*, 27(1), e70029.

Heinrich F, et al. (2025) Genomic analysis of three medieval parchments from German monasteries. *Scientific reports*, 15(1), 3156.

Sampson TR, et al. (2025) Alpha synuclein overexpression can drive microbiome dysbiosis in mice. *Scientific reports*, 15(1), 4014.

Smith MF, et al. (2024) Seasonality of respiratory, enteric, and urinary viruses revealed by wastewater genomic surveillance. *mSphere*, 9(5), e0010524.

Porras MÁG, et al. (2024) An intranuclear bacterial parasite of deep-sea mussels expresses apoptosis inhibitors acquired from its host. *Nature microbiology*, 9(11), 2877.

Gagnon MC, et al. (2024) An integrated strategy involving high-throughput sequencing to characterize an unknown GM wheat event in Canada. *Plant biotechnology journal*, 22(4), 904.

Nelson AR, et al. (2024) Soil microbiome feedbacks during disturbance-driven forest ecosystem conversion. *The ISME journal*, 18(1).

Liu P, et al. (2024) PRC2-EZH1 contributes to circadian gene expression by orchestrating chromatin states and RNA polymerase II complex stability. *The EMBO journal*, 43(23), 6052.

Todorov H, et al. (2024) Stage-specific expression patterns and co-targeting relationships among miRNAs in the developing mouse cerebral cortex. *Communications biology*, 7(1), 1366.

Yu S, et al. (2024) Characterization of an *Enterococcus* sp. SMC-9 strain isolated from bile of a patient with cholangitis. *PloS one*, 19(12), e0312953.

Griffiths JA, et al. (2024) Peripheral neuronal activation shapes the microbiome and alters gut physiology. *Cell reports*, 43(4), 113953.

Pastwińska J, et al. (2024) α -Hemolysin from *Staphylococcus aureus* Changes the Epigenetic Landscape of Th17 Cells. *ImmunoHorizons*, 8(9), 606.

Das B, et al. (2024) Exploring the uncharted seas: Metabolite profiling unleashes the anticancer properties of *Oscillatoria salina*. *Heliyon*, 10(16), e36048.

He X, et al. (2024) Pangenome analysis reveals transposon-driven genome evolution in cotton. *BMC biology*, 22(1), 92.

Paz EA, et al. (2024) Revealing the associated microflora hosted by the globally significant parasite *Trichostrongylus colubriformis*. *Scientific reports*, 14(1), 3723.

Hogg CJ, et al. (2024) Extant and extinct bilby genomes combined with Indigenous knowledge improve conservation of a unique Australian marsupial. *Nature ecology & evolution*, 8(7), 1311.

Lee S, et al. (2024) Comprehensive assessment of machine learning methods for diagnosing gastrointestinal diseases through whole metagenome sequencing data. *Gut microbes*, 16(1), 2375679.

Thureborn O, et al. (2024) Plastid phylogenomics and cytonuclear discordance in Rubioideae, Rubiaceae. *PloS one*, 19(5), e0302365.

Bommana S, et al. (2024) Unique microbial diversity, community composition, and networks among Pacific Islander endocervical and vaginal microbiomes with and without *Chlamydia trachomatis* infection in Fiji. *mBio*, 15(1), e0306323.