

# 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:** data analysis software, software resource, software application, data processing software, data analytics software

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

**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:** 20260728T043528+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.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 184 mentions in open access literature.

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

Mukiibi R, et al. (2025) Integrated functional genomic analysis identifies regulatory variants underlying a major QTL for disease resistance in European sea bass. *BMC biology*, 23(1), 75.

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

Das D, et al. (2025) Ethylene promotes SMAX1 accumulation to inhibit arbuscular mycorrhiza symbiosis. *Nature communications*, 16(1), 2025.

Záhonová K, et al. (2025) Comparative genomic analysis of trypanosomatid protists illuminates an extensive change in the nuclear genetic code. *mBio*, 16(6), e0088525.

Kim JG, et al. (2025) K-rice: a comprehensive database of Korean rice germplasm variants. *Frontiers in genetics*, 16, 1544652.

Peng X, et al. (2025) Expanded genetic and functional diversity of oceanic fungi. *Microbiome*, 13(1), 179.

Zhang HZ, et al. (2025) Six new bacterial species of Marinilabiales isolated from the marine coastal sediment and reclassified Ancylomarina and Labilibaculum as Marinifilum comb. nov. based on the genome analysis. *Frontiers in microbiology*, 16, 1634775.

Teber S, et al. (2025) Phylogenetic Relationships and Evolutionary History of Goats (Mammalia: Capra) From Türkiye and Iraq, Inferred From Complete Mitochondrial Genomes. *Ecology and evolution*, 15(8), e71985.

Huang X, et al. (2025) Discovery of viruses and bacteria associated with swine respiratory disease on farms at a nationwide scale in China using metatranscriptomic and metagenomic sequencing. *mSystems*, 10(2), e0002525.

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.

Aguilar GM, et al. (2025) *Streptomyces mayonensis* sp. nov., isolated from the volcanic soils of Mt. Mayon, Philippines. *International journal of systematic and evolutionary microbiology*, 75(9).

Lai C-H, et al. (2025) Region-specific genomic variation and functional divergence of *Helicobacter pylori* clinical isolates from the gastric antrum and corpus. *mSystems*, 10(10), e0102925.

Liu L, et al. (2025) Structural and functional characterization of a porcine intestinal microbial ecosystem developed in vitro. *Scientific reports*, 15(1), 24821.

Guitor AK, et al. (2025) Megaplasמידs associate with *Escherichia coli* and other Enterobacteriaceae. *bioRxiv : the preprint server for biology*.

Muratore D, et al. (2025) Diel partitioning in microbial phosphorus acquisition in the Sargasso Sea. *Proceedings of the National Academy of Sciences of the United States of America*, 122(11), e2410268122.

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

Wasik BR, et al. (2025) The evolution and epidemiology of H3N2 canine influenza virus after 20 years in dogs. *Epidemiology and infection*, 153, e47.

Amistadi S, et al. (2025) Dissecting the epigenetic regulation of the fetal hemoglobin genes to unravel a novel therapeutic approach for  $\beta$ -hemoglobinopathies. *Nucleic acids research*, 53(13).

Musick M, et al. (2025) CDH1 loss remodels gene expression and lineage identity in human mammary epithelial cells. *bioRxiv : the preprint server for biology*.