

Resource Summary Report

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Bestus Bioinformaticus Merge

RRID:SCR_016970

Type: Tool

Proper Citation

Bestus Bioinformaticus Merge (RRID:SCR_016970)

Resource Information

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

Proper Citation: Bestus Bioinformaticus Merge (RRID:SCR_016970)

Description: Software tool to merge two overlapping paired reads into a single read. Used in amplicon studies and in assembly, where longer reads allow the use of longer kmers or fewer comparisons.

Abbreviations: BBMerge

Synonyms: BB Merge, BestusBioinformaticusMerge, Bestus Bioinformaticus Merge, BBMerge

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

Keywords: merge, overlapping, read, single, amplicon, assembly, kmer, compare

Availability: Freely Available, Open Source

Resource Name: Bestus Bioinformaticus Merge

Resource ID: SCR_016970

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260821T194100+0000

Ratings and Alerts

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

No alerts have been found for Bestus Bioinformaticus Merge.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 38 mentions in open access literature.

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

Stern YE, et al. (2026) Targeting CDK12/13 Drives Mitotic Arrest to Overcome Resistance to KRASG12C Inhibitors. *Cancer research*, 86(2), 485.

Pinder MIM, et al. (2025) Bamboozle: A Bioinformatic Tool for Identification and Quantification of Intraspecific Barcodes. *Molecular ecology resources*, 25(4), e14067.

Knoppersen RS, et al. (2025) Inside the Belly of the Beast: Exploring the Gut Bacterial Diversity of *Gonipterus* sp. n. 2. *Microbial ecology*, 88(1), 27.

Singh N, et al. (2025) Transmission pathways of *Campylobacter jejuni* between humans and livestock in rural Ethiopia are highly complex and interdependent. *Gut pathogens*, 17(1), 26.

Ghiotto G, et al. (2025) Exploring genetic adaptation and microbial dynamics in engineered anaerobic ecosystems via strain-level metagenomics. *Cell genomics*, 5(9), 100949.

Bose T, et al. (2025) Tissue ontogeny and chemical composition influence bacterial biodiversity in the wood and shoot tip of *Populus nigra*. *Plant biology (Stuttgart, Germany)*, 27(5), 913.

Fu P, et al. (2025) A mobile genetic element-derived primase-polymerase harbors multiple activities implicated in DNA replication and repair. *Nucleic acids research*, 53(2).

Thatikonda S, et al. (2025) PV-10 Triggers Immunogenic Cell Death in Head and Neck Squamous Cell Carcinoma via Endoplasmic Reticulum Stress and Apoptosis. *Molecular cancer therapeutics*, 24(11), 1733.

Guinda EFX, et al. (2024) Efficacy of fenbendazole against gastrointestinal nematodes in naturally infected goats in Maputo Province, Mozambique using in vivo, in vitro and molecular assessment. *International journal for parasitology. Drugs and drug resistance*, 27, 100572.

Ghasemian E, et al. (2024) Genomic insights into local-scale evolution of ocular *Chlamydia trachomatis* strains within and between individuals in Gambian trachoma-endemic villages. *Microbial genomics*, 10(3).

Anderson MS, et al. (2024) Molecular Characterization of Noroviruses Causing Acute Gastroenteritis Outbreaks among US Military Recruits, 2013-2023. *Emerging infectious diseases*, 30(14), 71.

Hoffmann A, et al. (2023) Environmental Filtering Drives Fungal Phyllosphere Community in Regional Agricultural Landscapes. *Plants (Basel, Switzerland)*, 12(3).

Loera-Sánchez M, et al. (2022) A multispecies amplicon sequencing approach for genetic diversity assessments in grassland plant species. *Molecular ecology resources*, 22(5), 1725.

Martínez-Pérez C, et al. (2022) Phylogenetically and functionally diverse microorganisms reside under the Ross Ice Shelf. *Nature communications*, 13(1), 117.

Tlais AZA, et al. (2022) How Microbiome Composition Correlates with Biochemical Changes during Sauerkraut Fermentation: a Focus on Neglected Bacterial Players and Functionalities. *Microbiology spectrum*, 10(4), e0016822.

Oberpaul M, et al. (2022) Trichoderma-Derived Pentapeptides from the Infected Nest Mycobiome of the Subterranean Termite *Coptotermes testaceus*. *Chembiochem : a European journal of chemical biology*, 23(10), e202100698.

Curlin JZ, et al. (2022) Evolution of SIVmac239 following serial passaging in humanized mice. *Journal of medical primatology*, 51(5), 284.

Maran MIJ, et al. (2022) Benefits of merging paired-end reads before pre-processing environmental metagenomics data. *Marine genomics*, 61, 100914.

Braun KM, et al. (2021) Acute SARS-CoV-2 infections harbor limited within-host diversity and transmit via tight transmission bottlenecks. *PLoS pathogens*, 17(8), e1009849.

Baczenas JJ, et al. (2021) Propagation of SARS-CoV-2 in Calu-3 Cells to Eliminate Mutations in the Furin Cleavage Site of Spike. *Viruses*, 13(12).