

Resource Summary Report

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BBmap

RRID:SCR_016965

Type: Tool

Proper Citation

BBmap (RRID:SCR_016965)

Resource Information

URL: <http://sourceforge.net/projects/bbmap>

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Description: Software tool as a short read aligner for DNA and RNA seq data. Used for large genomes with millions of scaffolds. Can align reads from Illumina, PacBio, 454, Sanger, Ion Torrent, Nanopore. Fast and accurate, particularly with highly mutated genomes or reads with long indels, even whole gene deletions over 100kbp long. It has no upper limit to genome size or number of contigs. Written in Java, can run on any platform.

Resource Type: alignment software, data processing software, image analysis software, software application, software resource, software toolkit

Keywords: Joint Genome Institute, short, read, aligner, DNA, RNA, sequencing, data, large, genome, scaffold, mutated, long, indel

Availability: Free, Available for download, Freely available

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Alternate URLs: <https://jgi.doe.gov/data-and-tools/bbtools/bb-tools-user-guide/bbmap-guide/>, <https://sources.debian.org/src/bbmap/>

Record Creation Time: 20220129T080332+0000

Record Last Update: 20260919T195331+0000

Ratings and Alerts

No rating or validation information has been found for BBmap.

No alerts have been found for BBmap.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 915 mentions in open access literature.

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

da Silva IB, et al. (2026) Sex-specific division of labor in termites is linked to differential brain architecture and foraging gene expression. *iScience*, 29(4), 115278.

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing *Cobitis*. *GigaScience*, 15.

Kanellos G, et al. (2026) Nucleophosmin supports WNT-driven hyperproliferation and tumor initiation. *Nature genetics*, 58(1), 100.

Passos GS, et al. (2026) Genomic and secondary metabolites of the marine cyanobacterium *Capilliphycus salinus* ALCB114379. *Journal of phycology*, 62(3), 904.

Yang K, et al. (2026) Gut microbiome associations with acute malnutrition relapse in South Sudan. *Microbiology spectrum*, 14(6), e0358725.

Christenson JL, et al. (2026) Metastasis-Associated Wound Repair Promotes Reciprocal Lung Epithelium Activation and Breast Cancer Metastatic Outgrowth. *Cancer research communications*, 6(4), 750.

Rose AE, et al. (2026) Rational engineering of facultative anaerobiosis enables commensal survival in the oxygenated gut. *bioRxiv : the preprint server for biology*.

Sasidharan V, et al. (2026) Extracellular vesicles mediate stem cell signaling and systemic RNAi in planarians. *Science advances*, 12(6), eady1461.

Belay G, et al. (2026) Microorganisms and functional genes in an aerobic-anoxic integrated gold mine wastewater treatment system. *World journal of microbiology & biotechnology*, 42(4).

Sayles NM, et al. (2026) Pregnancy precipitates metabolic imbalance and accelerates death in an animal model of mitochondrial cardiomyopathy. *Molecular metabolism*, 107, 102352.

Hirabayashi K, et al. (2026) A haplotype-phased male genome sequence of the stinging nettle, *Urtica dioica* ssp. *dioica*. *Scientific data*, 13(1).

Klann M, et al. (2026) Cell-cell communication as underlying principle governing color pattern formation in teleost fishes. *Nature communications*, 17(1).

Elmekki NM, et al. (2026) High-throughput analyses of *Phocaeicola vulgatus* reveal fitness determinants for gut colonization and during colitis. *Gut microbes*, 18(1), 2661410.

Peterse IF, et al. (2026) Robust ammonia oxidation by "Candidatus Nitrosacidococcus tergens" across a broad pH range. *mBio*, 17(5), e0297525.

Ries HJ, et al. (2026) Weak selection and stochastic processes limit the emergence of antigenic variants during household transmission of influenza A viruses. *PLoS pathogens*, 22(5), e1013689.

Bell AG, et al. (2026) Assessment of the effectiveness of host depletion techniques for profiling fish skin microbiomes and metagenomic analysis. *Microbiology spectrum*, 14(2), e0183825.

Hamel LP, et al. (2026) Molecular changes in agroinfiltrated leaves of *Nicotiana glauca* expressing suppressor of silencing P19 and coronavirus-like particles. *Plant biotechnology journal*, 24(1), 99.

Li M, et al. (2026) Manipulating root-associated microbiomes to boost drought resistance in dryland winter wheat with *Streptomyces pactum* Act12. *BMC microbiology*, 26(1).

Breman FC, et al. (2026) Comparison of whole genome sequencing approaches for Capripox viruses. *BMC genomics*, 27(1), 174.

Rocha LBA, et al. (2026) Endolithic fungal diversity is present in the unique phosphatized rocks of an environmentally extreme equatorial archipelago revealed by DNA amplicon metagenomics. *Brazilian journal of microbiology* : [publication of the Brazilian Society for Microbiology], 57(1), 46.