

Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

BBmap

RRID:SCR_016965

Type: Tool

Proper Citation

BBmap (RRID:SCR_016965)

Resource Information

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

Proper Citation: BBmap (RRID:SCR_016965)

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: image analysis software, software resource, software application, data processing software, alignment software, 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

Resource Name: BBmap

Resource ID: SCR_016965

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: 20260728T043523+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 797 mentions in open access literature.

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

Sperschneider J, et al. (2026) The fungal pathogen *Rhizoctonia solani* AG-8 has 2 nuclear haplotypes that differ in abundance. *G3* (Bethesda, Md.), 16(1).

Nakamura M, et al. (2026) Chromatin-associated DEK proteins maintain H3K27me3 balance and coordinate developmental transitions in plants. *The New phytologist*, 249(2), 930.

Du Y, et al. (2025) Multiomics analysis of umbilical cord hematopoietic stem cells from a multiethnic cohort of Hawaii reveals the intergenerational effect of maternal prepregnancy obesity and risks for cancers. *GigaScience*, 14.

Mikko A, et al. (2025) Sequencing airborne DNA to monitor crop pathogens and pests. *iScience*, 28(7), 112912.

Li W, et al. (2025) Benchmarking and optimizing qualitative and quantitative pipelines in environmental metatranscriptomics using mixture controlling experiments. *ISME communications*, 5(1), ycaf090.

Ghasemian E, et al. (2025) Evolutionary dynamics in the genome of ocular *Chlamydia trachomatis* strains from Northern Tanzania following mass drug administration. *Microbial genomics*, 11(7).

Arnedo-Muñoz M, et al. (2025) A New Next-Generation Sequencing Approach in Human Cytomegalovirus for the Identification of Antiviral Resistance Mutations and Genotypic Classification. *Journal of medical virology*, 97(8), e70523.

Wang W, et al. (2025) Characterization of agr-like Loci in *Lactiplantibacillus plantarum* and *L. paraplantarum* and Their Role in Quorum Sensing and Virulence Inhibition of *Staphylococcus aureus*. *Probiotics and antimicrobial proteins*, 17(4), 2332.

Boulton W, et al. (2025) Metagenome-assembled-genomes recovered from the Arctic drift expedition MOSAiC. *Scientific data*, 12(1), 204.

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.

Otani S, et al. (2025) Genomic and functional co-diversification imprint African Hominidae microbiomes to signal dietary and lifestyle adaptations. *Gut microbes*, 17(1), 2484385.

Jensen EEB, et al. (2025) Using genomics to explore the epidemiology of vancomycin resistance in a sewage system. *Microbiology spectrum*, 13(1), e0148924.

Li S, et al. (2025) Influences of fluctuating nutrient loadings on nitrate-reducing microorganisms in rivers. *ISME communications*, 5(1), ycae168.

Custode BM, et al. (2025) Folliculin depletion results in liver cell damage and cholangiocarcinoma through MiT/TFE activation. *Cell death and differentiation*, 32(8), 1460.

Doorenspleet K, et al. (2025) Advancing molecular macrobenthos biodiversity monitoring: a comparison between Oxford Nanopore and Illumina based metabarcoding and metagenomics. *PeerJ*, 13, e19158.

Liu K, et al. (2025) Timp2-modified gelatinhydroxyphenylpropionic acid hydrogels reverse enhanced scleral recovery and suppress myopia development in mice. *Materials today. Bio*, 33, 101942.

Kong L, et al. (2025) Interspecies hydrogen transfer between cyanobacteria and symbiotic bacteria drives nitrogen loss. *Nature communications*, 16(1), 5078.

Denison ER, et al. (2025) Identification of shared viral sequences in peat moss metagenomes reveals elements of a possible Sphagnum core virome. *Environmental microbiome*, 20(1), 62.

Kumawat S, et al. (2025) Monkeyflower (*Mimulus*) uncovers the evolutionary basis of the eukaryote telomere sequence variation. *PLoS genetics*, 21(6), e1011738.

Rahimlou S, et al. (2025) *Malassezia* in environmental studies is derived from human inputs. *mBio*, 16(6), e0114225.