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, software resource, image analysis software, software application, data processing software, software toolkit

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

Funding:

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/

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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 680 mentions in open access literature.

Listed below are recent publications. The full list is available at FDI Lab - SciCrunch.org.

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.

Yang J, et al. (2025) MARTRE family proteins negatively regulate CCR4-NOT activity to protect poly(A) tail length and promote translation of maternal mRNA. Nature communications, 16(1), 248.

Banerjee S, et al. (2025) Evaluation of MALDI-TOF for identification of Vibrio cholerae and Vibrio parahaemolyticus from growth on agar media. Applied microbiology and biotechnology, 109(1), 5.

Alam Y, et al. (2025) Variation in human gut microbiota impacts tamoxifen pharmacokinetics. mBio, 16(1), e0167924.

Kosch TA, et al. (2025) Comparative analysis of amphibian genomes: An emerging resource for basic and applied research. Molecular ecology resources, 25(1), e14025.

Ji X, et al. (2025) Esketamine alleviates depressive-like behavior in neuropathic pain mice through the METTL3-GluA1 pathway. Cell biology and toxicology, 41(1), 38.

Low SJ, et al. (2025) PathoGD: an integrative genomics approach to primer and guide RNA design for CRISPR-based diagnostics. Communications biology, 8(1), 147.

Valdes P, et al. (2025) Integrative multiomics reveals common endotypes across PSEN1, PSEN2, and APP mutations in familial Alzheimer's disease. Alzheimer's research & therapy, 17(1), 5.

Xu M, et al. (2025) BASAL: a universal mapping algorithm for nucleotide base-conversion

sequencing. Nucleic acids research, 53(2).

Qi YL, et al. (2025) Recovery of nearly 3,000 archaeal genomes from 152 terrestrial geothermal spring metagenomes. Scientific data, 12(1), 151.

Weissensteiner MH, et al. (2025) Combining Individual-Based Radio-Tracking With Whole-Genome Sequencing Data Reveals Candidate for Genetic Basis of Partial Migration in a Songbird. Ecology and evolution, 15(1), e70800.

Stutzman AV, et al. (2024) Heterochromatic 3D genome organization is directed by HP1a- and H3K9-dependent and independent mechanisms. Molecular cell, 84(11), 2017.

Georgeson J, et al. (2024) No evidence for ac4C within human mRNA upon data reassessment. Molecular cell, 84(8), 1601.

Barros KO, et al. (2024) Oxygenation influences xylose fermentation and gene expression in the yeast genera Spathaspora and Scheffersomyces. Biotechnology for biofuels and bioproducts, 17(1), 20.

Zhao R, et al. (2024) An abundant bacterial phylum with nitrite-oxidizing potential in oligotrophic marine sediments. Communications biology, 7(1), 449.

Southwell N, et al. (2024) High fat diet ameliorates mitochondrial cardiomyopathy in CHCHD10 mutant mice. EMBO molecular medicine, 16(6), 1352.

Pilgrim J, et al. (2024) Comparative genomics of a novel Erwinia species associated with the Highland midge (Culicoides impunctatus). Microbial genomics, 10(4).

Montserrat-Malagarriga M, et al. (2024) The Impact of Fiber Source on Digestive Function, Fecal Microbiota, and Immune Response in Adult Dogs. Animals : an open access journal from MDPI, 14(2).

Raymond BB, et al. (2024) Snow alga Sanguina aurantia as revealed through de novo genome assembly and annotation. G3 (Bethesda, Md.), 14(10).