

Resource Summary Report

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Bestus Bioinformaticus Tools

RRID:SCR_016968

Type: Tool

Proper Citation

Bestus Bioinformaticus Tools (RRID:SCR_016968)

Resource Information

URL: <https://jgi.doe.gov/data-and-tools/bbtools/>

Proper Citation: Bestus Bioinformaticus Tools (RRID:SCR_016968)

Description: Software suite of bioinformatics tools for analysis of DNA and RNA sequence data. Used for file formats such as fastq, fasta, sam, scarf, fasta plus qual, compressed or raw, with autodetection of quality encoding and interleaving. Written in Java and works on any platform supporting Java, including Linux, MacOS, and Microsoft Windows.

Abbreviations: BBTools

Synonyms: BB Tools, Bestus Bioinformaticus Tools, BBTools

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

Keywords: Software, Bioinformatic, Data analysis, sequencing,

Funding:

Availability: Free, Available for download, Freely available

Resource Name: Bestus Bioinformaticus Tools

Resource ID: SCR_016968

Record Creation Time: 20220129T080333+0000

Record Last Update: 20250517T060309+0000

Ratings and Alerts

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

No alerts have been found for Bestus Bioinformaticus Tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 523 mentions in open access literature.

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

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.

Solberg T, et al. (2025) Heterochromatin-dependent transcription links the PRC2 complex to small RNA-mediated DNA elimination. *EMBO reports*, 26(1), 273.

Payne PE, et al. (2025) Uncovering novel functions of the enigmatic, abundant, and active Anaerolineae in a salt marsh ecosystem. *mSystems*, 10(1), e0116224.

Konishi CT, et al. (2025) Modeling and correction of protein conformational disease in iPSC-derived neurons through personalized base editing. *Molecular therapy. Nucleic acids*, 36(1), 102441.

Midot F, et al. (2025) Temporal dynamics of soil microbial C and N cycles with GHG fluxes in the transition from tropical peatland forest to oil palm plantation. *Applied and environmental microbiology*, 91(1), e0198624.

Mokshina N, et al. (2025) A Fresh Look at Celery Collenchyma and Parenchyma Cell Walls Through a Combination of Biochemical, Histochemical, and Transcriptomic Analyses. *International journal of molecular sciences*, 26(2).

Rachubinski AL, et al. (2024) JAK inhibition decreases the autoimmune burden in Down syndrome. *eLife*, 13.

Juteršek M, et al. (2024) Transcriptome-informed identification and characterization of *Planococcus citri* cis- and trans-isoprenyl diphosphate synthase genes. *iScience*, 27(4), 109441.

Rafiqullah IM, et al. (2024) Pneumococcal population genomics changes during the early time period of conjugate vaccine uptake in southern India. *Microbial genomics*, 10(2).

Stephenson M, et al. (2024) The mitochondrial genome of the deep-sea pyramid urchin *Echinocrepis rostrata* (Echinoidea: Holasteroidea: Pourtalesiidae). *Mitochondrial DNA. Part B, Resources*, 9(3), 390.

Akbu?a-Schön T, et al. (2024) The keystone gut species *Christensenella minuta* boosts gut microbial biomass and voluntary physical activity in mice. *mBio*, 15(2), e0283623.

Gu Liu C, et al. (2024) Construction and characterization of DNA libraries from cultured phages and environmental viromes. *Applied and environmental microbiology*, 90(10), e0117124.

Seitz VA, et al. (2024) Cover crop root exudates impact soil microbiome functional trajectories in agricultural soils. *Microbiome*, 12(1), 183.

Li R, et al. (2024) Chromosome-level genome assembly of the pygmy grasshopper *Eucriotettix oculatus* (Orthoptera: Tetrigoidea). *Scientific data*, 11(1), 431.

Wu S, et al. (2024) A comprehensive RNA virome identified in the oyster *Magallana gigas* reveals the intricate network of virus sharing between seawater and mollusks. *Microbiome*, 12(1), 263.

Hall BE, et al. (2024) Transcriptome analysis of rheumatoid arthritis uncovers genes linked to inflammation-induced pain. *Scientific reports*, 14(1), 25893.

Nikiforov VV, et al. (2024) The Presence of Two Distinct Lineages of the Foot-And-Mouth Disease Virus Type A in Russia in 2013-2014 Has Significant Implications for the Epidemiology of the Virus in the Region. *Viruses*, 17(1).

Carasso S, et al. (2024) Inflammation and bacteriophages affect DNA inversion states and functionality of the gut microbiota. *Cell host & microbe*, 32(3), 322.

Möller L, et al. (2024) Rich microbial and depolymerising diversity in Antarctic krill gut. *Microbiology spectrum*, 12(4), e0403523.