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/

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

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: 20250521T061656+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 dkNET.

Heinrich F, et al. (2025) Genomic analysis of three medieval parchments from German monasteries. Scientific reports, 15(1), 3156.

Záhonová K, et al. (2025) Comparative Analysis of Protist Communities in Oilsands Tailings Using Amplicon Sequencing and Metagenomics. Environmental microbiology, 27(1), e70029.

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.

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.

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

Gray J, et al. (2024) Transposon mutagenesis screen in Klebsiella pneumoniae identifies genetic determinants required for growth in human urine and serum. eLife, 12.

Hogg CJ, et al. (2024) Extant and extinct bilby genomes combined with Indigenous knowledge improve conservation of a unique Australian marsupial. Nature ecology & evolution, 8(7), 1311.

Scheithauer TPM, et al. (2024) Bacteriophages from treatment-naïve type 2 diabetes individuals drive an inflammatory response in human co-cultures of dendritic cells and T cells. Gut microbes, 16(1), 2380747.

Estevam GO, et al. (2024) Mapping kinase domain resistance mechanisms for the MET receptor tyrosine kinase via deep mutational scanning. bioRxiv : the preprint server for biology.

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).

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

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

Swindell WR, et al. (2024) Meta-analysis of differential gene expression in lower motor neurons isolated by laser capture microdissection from post-mortem ALS spinal cords. Frontiers in genetics, 15, 1385114.

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