

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

Keywords: Software, Bioinformatic, Data analysis, sequencing,

Resource Name: Bestus Bioinformaticus Tools

Resource ID: SCR_016968

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260905T132816+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

Usage and Citation Metrics

We found 665 mentions in open access literature.

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

Poulain F, et al. (2026) Clonal origin and early lineage divergence in adenosquamous carcinoma. *Cell reports*, 45(6), 117470.

Cho A, et al. (2026) Aerobic sister lineage of breviate has gene-rich mitochondrial genomes. *Current biology : CB*, 36(6), 1481.

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

Lee C, et al. (2026) Plastid genome variation in the green algal genus *Coelastrum* (Scenedesmaceae). *Frontiers in plant science*, 17, 1736783.

Yang Y, et al. (2026) Chromosomal-level genome assembly of *Ichthyurus bourgeoisi* Gestro using PacBio HiFi and Hi-C sequencing. *Scientific data*, 13(1).

Volk A, et al. (2026) Investigation of cyanobacteria-hosted antibiotic resistance genes in cyanoHAB-impacted drinking water sources. *Environmental science and pollution research international*, 33(13), 6140.

Wu SS, et al. (2026) Longitudinal analysis of viral and host RNA in blood and saliva during controlled human dengue virus 3 infections. *Journal of virology*, 100(6), e0037326.

Spiga L, et al. (2026) An anaerobic pathogen rewires host metabolism to fuel oxidative growth in the inflamed gut. *Cell*, 189(13), 3968.

Steele SE, et al. (2026) Drought-associated genes exhibit high constitutive expression in *Quercus douglasii*, a drought-tolerant California oak. *G3 (Bethesda, Md.)*, 16(2).

Jihnaoui N, et al. (2026) *Bradyrhizobium cedriense* sp. nov., a novel rhizobial species isolated from *Acacia saligna* nodules grown in polluted soils in Tunisia. *International journal of systematic and evolutionary microbiology*, 76(4).

Pike B, et al. (2026) A trio-binning approach for genome assembly reveals extensive structural variation between two *Cannabis* cultivars: Punto Rojo and Cherry Pie. *G3 (Bethesda, Md.)*, 16(2).

Wang J, et al. (2026) Metaviromic Profiling of Genetic Diversity and Prevalence of Suid Herpesviruses Circulating in China. *Viruses*, 18(6).

Khan SM, et al. (2026) *Stenotrophomonas maltophilia* Bloodstream Infection Outbreak in Acute Care Hospital, California, USA, 2022-2023. *Emerging infectious diseases*, 32(3), 315.

Ascandari A, et al. (2026) Cross-cohort resistome and virulome gradients structure the colorectal cancer microbiome. *NPJ biofilms and microbiomes*, 12(1), 40.

Hakim MS, et al. (2026) Reverse vaccinology-based design of a universal multiepitope vaccine against chikungunya virus: Phylogenetic and immunoinformatics approaches. *Scientific reports*, 16(1).

Human ZR, et al. (2026) Seasonality of composition, genomic potential and activity of coniferous forest soil microbiomes. *Scientific data*, 13(1).

Guo J, et al. (2026) Mobile genetic elements shape microbial diversity and functions in thawing permafrost soils. *Nature microbiology*, 11(7), 1800.

Conceição JDS, et al. (2026) Combined effects of incubation temperature and lipopolysaccharide exposure on immune response modulation in the quail gut. *Poultry science*, 105(4), 106418.

Eckmann JB, et al. (2026) Orthogonal chemical genomics approaches reveal genomic targets for increasing anaerobic chemical tolerance in *Zymomonas mobilis*. *mSystems*, 11(1), e0100125.

Ricci F, et al. (2026) Chemosynthesis enables microbial communities to flourish in a marine cave ecosystem. *The ISME journal*, 20(1).