

Resource Summary Report

Generated by PRECISE-TBI on Aug 5, 2026

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

Keywords: Software, Bioinformatic, Data analysis, sequencing,

Resource Name: Bestus Bioinformaticus Tools

Resource ID: SCR_016968

Record Creation Time: 20220129T080333+0000

Record Last Update: 20260805T044402+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 591 mentions in open access literature.

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

Dunn LN, et al. (2026) Altered hepatic metabolism in Down syndrome. Cell reports, 45(1), 116835.

Araya P, et al. (2025) Interferon signaling modulates Down syndrome-associated Alzheimer's disease pathology in a mouse model. iScience, 28(8), 113130.

Gittrich MR, et al. (2025) Isolation and characterization of 24 phages infecting the plant growth-promoting rhizobacterium *Klebsiella* sp. M5al. PloS one, 20(2), e0313947.

Wang C, et al. (2025) A chromosomal-level genome assembly of *Trichogramma chilonis* Ishii, 1941 (Hymenoptera: Trichogrammatidae). Scientific data, 12(1), 457.

Motta BDS, et al. (2025) *Paracoccidioides* Species Circulating in the Endemic Area of Rio de Janeiro, Brazil: Updates into Their Genetic Diversity. Journal of fungi (Basel, Switzerland), 11(2).

Füssy Z, et al. (2025) Genome-resolved biogeography of Phaeocystales, cosmopolitan bloom-forming algae. Nature communications, 16(1), 8559.

Silva JO, et al. (2025) Digestion in the arachnid *Mischonyx squalidus* as a probable source of lipids to synthesize opiliones defense and communication molecules. Scientific reports, 15(1), 32732.

Du C, et al. (2025) A chromosome-level genome assembly of *Myrmica angulata* (Hymenoptera: Formicidae). Scientific data, 12(1), 1685.

Thystrup C, et al. (2025) Using metagenomics and whole-genome sequencing to characterize enteric pathogens across various sources in Africa. Nature communications, 16(1), 11311.

Hanzely P, et al. (2025) Efficacy of oral and rectal administration of human faecal microbiota transplant (FMT) in human microbiota-associated mouse models. Scientific reports, 15(1), 45099.

Ngwese MM, et al. (2025) Infection with gut parasites correlates with gut microbiome diversity across human populations in Africa. Gut microbes, 17(1), 2587966.

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

de León LR, et al. (2025) Polyextremotolerant, opportunistic, and melanin-driven resilient black yeast *Exophiala dermatitidis* in environmental and clinical contexts. Scientific reports, 15(1), 6472.

Molligan J, et al. (2025) De novo assembly and annotation of the *Empoasca fabae* mitochondrial genome. *Mitochondrial DNA. Part B, Resources*, 10(6), 403.

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

Kasmanas JC, et al. (2025) Integrating comparative genomics and risk classification by assessing virulence, antimicrobial resistance, and plasmid spread in microbial communities with gSpreadComp. *GigaScience*, 14.

Melo-Miranda R, et al. (2025) Aging: a possible road toward gut microbiota pathoadaptation. *Gut microbes*, 17(1), 2542375.

Youssef L, et al. (2025) A dynamic biointerface in mussels mediated by a mechanoresponsive intermediate filament-based biopolymer. *Nature communications*, 16(1), 9523.

Hillary LS, et al. (2025) DNA extraction and virome processing methods strongly influence recovered human gut viral community characteristics. *bioRxiv : the preprint server for biology*.

Canus L, et al. (2025) In Vitro and Ex Vivo evidence that pharmacological induction of the hypoxia response pathway efficiently restricts measles and Nipah virus infections. *Emerging microbes & infections*, 14(1), 2563067.