## **Resource Summary Report**

Generated by NIF on Apr 28, 2025

# **ABySS**

RRID:SCR\_010709 Type: Tool

**Proper Citation** 

ABySS (RRID:SCR\_010709)

#### **Resource Information**

URL: http://www.bcgsc.ca/platform/bioinfo/software/abyss

Proper Citation: ABySS (RRID:SCR\_010709)

**Description:** Software providing de novo, parallel, paired-end sequence assembler that is designed for short reads. ABySS 1.0 originally showed that assembling human genome using short 50 bp sequencing reads was possible by aggregating half terabyte of compute memory needed over several computers using standardized message passing system. ABySS 2.0 is Resource Efficient Assembly of Large Genomes using Bloom Filter. ABySS 2.0 departs from MPI and instead implements algorithms that employ Bloom filter, probabilistic data structure, to represent de Bruijn graph and reduce memory requirements.

Abbreviations: ABySS

Synonyms: ABySS 1.0, ABySS 2.0

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

Defining Citation: PMID:19251739, DOI:10.1101/068338, DOI:10.1101/gr.214346.116

**Keywords:** paired-end sequence assembler, short reads, assembling human genome, large genomes, bloom filter,

**Funding:** Genome Canada ; Genome British Columbia ; British Columbia Cancer Foundation ; NHGRI R01HG007182 Availability: Free, Available for download, Freely available

Resource Name: ABySS

Resource ID: SCR\_010709

Alternate IDs: biotools:abyss, OMICS\_00006

Alternate URLs: https://github.com/bcgsc/abyss, https://sources.debian.org/src/abyss/, https://bio.tools/abyss,

Record Creation Time: 20220129T080300+0000

Record Last Update: 20250428T053623+0000

#### **Ratings and Alerts**

No rating or validation information has been found for ABySS.

No alerts have been found for ABySS.

#### Data and Source Information

Source: <u>SciCrunch Registry</u>

### **Usage and Citation Metrics**

We found 717 mentions in open access literature.

Listed below are recent publications. The full list is available at <u>NIF</u>.

Patel J, et al. (2025) Whole genome sequencing, assembly and annotation of the Southern Ground Hornbill - Bucorvus leadbeateri. Scientific data, 12(1), 58.

Almirón C, et al. (2025) Functional and genomic analyses of plant growth promoting traits in Priestia aryabhattai and Paenibacillus sp. isolates from tomato rhizosphere. Scientific reports, 15(1), 3498.

Wang M, et al. (2025) Antimicrobial Resistance Genes in Clinical Escherichia coli Strains from Livestock and Poultry in Shandong Province, China During 2015-2020. Antibiotics (Basel, Switzerland), 14(1).

Wu Y, et al. (2025) Characterization of the Phosphotransferase from Bacillus subtilis 1101 That Is Responsible for the Biotransformation of Zearalenone. Toxins, 17(1).

Ramírez Martínez J, et al. (2024) Deep population structure linked to host vernalization

requirement in the barley net blotch fungal pathogen. Microbial genomics, 10(5).

Hiltunen Thorén M, et al. (2024) Comparative genomics of Ascetosporea gives new insight into the evolutionary basis for animal parasitism in Rhizaria. BMC biology, 22(1), 103.

Han Y, et al. (2024) Longitudinal multi-omics analysis uncovers the altered landscape of gut microbiota and plasma metabolome in response to high altitude. Microbiome, 12(1), 70.

Wu S, et al. (2024) High quality assemblies of four indigenous chicken genomes and related functional data resources. Scientific data, 11(1), 300.

Shang B, et al. (2024) A Novel Transposon Tn7709 Harbors Multidrug Resistance Genes in a Pathogenic Aeromonas media Strain QST31. Microorganisms, 12(3).

Lu S, et al. (2024) A longitudinal transcriptomic analysis of Rhipicephalus microplus midgut upon feeding. Ticks and tick-borne diseases, 15(2), 102304.

Hu X, et al. (2024) Genomic characterization of highly pathogenic avian influenza A H5N1 virus newly emerged in dairy cattle. Emerging microbes & infections, 13(1), 2380421.

Sharma D, et al. (2024) Genomic analysis of acid tolerance genes and deciphering the function of ydaG gene in mitigating acid tolerance in Priestia megaterium. Frontiers in microbiology, 15, 1414777.

Wang Q, et al. (2024) Metagenomic and culture-dependent analysis of Rhinopithecius bieti gut microbiota and characterization of a novel genus of Sphingobacteriaceae. Scientific reports, 14(1), 13819.

de Sousa-Paula LC, et al. (2024) Exploring the transcriptome of immature stages of Ornithodoros hermsi, the soft-tick vector of tick-borne relapsing fever. Scientific reports, 14(1), 12466.

Chen YH, et al. (2024) Two new strains of Streptomyces with metabolic potential for biological control of pear black spot disease. BMC microbiology, 24(1), 550.

Lu C, et al. (2024) Synthesis of Headful Packaging Phages Through Yeast Transformation-Associated Recombination. Viruses, 17(1).

Najer T, et al. (2024) Mitochondrial genome fragmentation is correlated with increased rates of molecular evolution. PLoS genetics, 20(5), e1011266.

Kanippayoor RL, et al. (2024) Identification and genetic analysis of a pervasive 'needle-eye' sperm phenotype in Drosophila sterile hybrid males. Proceedings. Biological sciences, 291(2025), 20240483.

Zheng R, et al. (2024) Physiological and metabolic insights into the first cultured anaerobic representative of deep-sea Planctomycetes bacteria. eLife, 12.

Ángeles-Argáiz RE, et al. (2024) Assembly collapsing versus heterozygosity oversizing: detection of homokaryotic and heterokaryotic Laccaria trichodermophora strains by hybrid

genome assembly. Microbial genomics, 10(3).