

# Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

## ABySS

RRID:SCR\_010709

Type: Tool

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### Proper Citation

ABySS (RRID:SCR\_010709)

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### 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, data analysis software, software resource, 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:** 20260731T042836+0000

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## Ratings and Alerts

No rating or validation information has been found for ABySS.

No alerts have been found for ABySS.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 761 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [kravitz2](#) .

Fogg LG, et al. (2026) The visual system of the longest-living vertebrate, the Greenland shark. Nature communications, 17(1), 39.

Dai Y, et al. (2025) Adaptive attenuation of virulence mediated by Wzc mutation in ST11-KL47 Carbapenem-resistant Klebsiella pneumonia. Frontiers in cellular and infection microbiology, 15, 1561631.

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

Dubin A, et al. (2025) Sexual Antagonism and Sex Determination in Three Syngnathid Species Alongside a Male Pregnancy Gradient. Genome biology and evolution, 17(7).

Bowman JL, et al. (2025) Evolutionary history of sex and accessory chromosomes in hornworts. The New phytologist, 248(1), 24.

Liao CH, et al. (2025) Genomic and Phenotypic Insights Into Antibiotic Resistance and Virulence of Klebsiella pneumoniae From the Environment in Southern Taiwan. The Journal of infectious diseases, 232(5), e721.

Zhang M, et al. (2025) Widespread distribution of BpfA-mediated bisphenol F degradation among members of the Pseudomonadota and Actinomycetota. The ISME journal, 19(1).

Steck MR, et al. (2025) Hiding in plain sight: Genomic and phenotypic characterization of mosquito-borne Bussuquara virus. PLoS neglected tropical diseases, 19(12), e0013774.

Ma T, et al. (2025) Familial Reclassification Within Order Lysobacterales and Proposal of Four Novel Species. Microorganisms, 13(6).

Barnabas GD, et al. (2025) Proteomics and personalized PDX models identify treatment for a progressive malignancy within an actionable timeframe. EMBO molecular medicine, 17(4), 625.

McMullan M, et al. (2025) Developing a crop- wild-reservoir pathogen system to understand pathogen evolution and emergence. eLife, 14.

González-Serrano F, et al. (2025) Amphibian skin bacteria contain a wide repertoire of genes linked to their antifungal capacities. World journal of microbiology & biotechnology, 41(3), 78.

León-Lemus A, et al. (2025) Draft genome sequence and comparative genomic analysis of Halomonas salifodinae strain A2 isolated from the Zapotitlán Salinas Valley, Puebla, Mexico. Extremophiles : life under extreme conditions, 29(2), 28.

Claro IM, et al. (2025) Genomic characterization of arboviruses discovered between the 1950s and 1980s. Journal of virology, 99(10), e0121425.

Bangs MR, et al. (2025) Phylogenomics of sigmodontine rodents (Cricetidae: Sigmodontinae): Cloud forests and Pliocene extinction explain the timing and spread of an iconic South American radiation. PloS one, 20(11), e0317165.

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.

Akusobi C, et al. (2025) Transposon-sequencing across multiple Mycobacterium abscessus isolates reveals significant functional genomic diversity among strains. mBio, 16(2), e0337624.

Yang J, et al. (2025) The development of ideal insertion and deletion (InDel) markers and initial indel map variation in cucumber using re-sequenced data. BMC genomics, 26(1), 391.

Bland DM, et al. (2025) An insight into the salivary gland content of the human body louse, Pediculus humanus. Scientific reports, 15(1), 18322.

Liu Q, et al. (2025) Genomic epidemiology and characterization of Staphylococcus aureus isolates from raw milk in Jilin, China: evidence of contamination with optrA-positive, cfrA-positive, and poxtA-positive strains and human-livestock transmission. Frontiers in microbiology, 16, 1547283.