

Resource Summary Report

Generated by [PRECISE-TBI](#) on Aug 1, 2026

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

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: 20260801T042659+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: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 761 mentions in open access literature.

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

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

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).

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

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

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).

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.

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.

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.

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

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

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.

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.

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.

Ma Y, et al. (2025) Tracing the evolutionary trajectory of the IncP-2 plasmid co-harboring bla IMP-45 and bla VIM-1: an outbreak of Pseudomonas aeruginosa co-producing IMP-45 and VIM-1 carbapenemases in China. Frontiers in cellular and infection microbiology, 15, 1623241.

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

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.

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.

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