

Resource Summary Report

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

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: British Columbia Cancer Foundation ;
Genome British Columbia ;
Genome Canada ;
NHGRI R01HG007182

Availability: Free, Available for download, Freely available

Resource Name: ABySS

Resource ID: SCR_010709

Alternate IDs: OMICS_00006, biotools:abyss

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: 20260905T132645+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 808 mentions in open access literature.

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

Schlebusch SA, et al. (2026) Sex chromosome turnover and structural genome divergence shape meiotic outcomes in hybridizing Cobitis. GigaScience, 15.

Liu H, et al. (2026) Long-term outcomes by clinical and molecular risk stratification in patients with medulloblastoma receiving risk-adapted therapy. Med (New York, N.Y.), 7(5), 101076.

Li X, et al. (2026) Characteristics, Whole Genome Analysis of a Virulent Phage from Avian-Derived Enterococcus faecalis and Its Application in Poultry Product Processing Safety. Microorganisms, 14(2).

Wagner M, et al. (2026) The Genomics of Convergent Adaptation to Intertidal Gravel Beaches in Mediterranean Clingfishes. Genome biology and evolution, 18(3).

Lu S, et al. (2026) Further insights into the sialome switch of Amblyomma americanum adult females. BMC genomics, 27(1).

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

Zhang J, et al. (2026) Enhancing the fiber degradation efficiency in dairy cattle rumen through engineered bacterial communities. Microbiome, 14(1).

Ma W, et al. (2026) Type A and D *Clostridium perfringens* with unique genetic evolution characteristics cause mortality in juvenile Bactrian camels. *Frontiers in cellular and infection microbiology*, 16, 1787432.

Yang W, et al. (2026) Therapeutic efficacy of phage vB_SaIP_NW15 and cinnamaldehyde against drug-resistant *Salmonella Enteritidis* in a chicken infection model. *Poultry science*, 105(3), 106327.

Yang L, et al. (2026) *Akkermansia muciniphila* outer membrane protein Amuc_0904 modulates intestinal homeostasis by promoting goblet cell differentiation. *Gut microbes*, 18(1), 2587405.

Salles-Oliveira I, et al. (2026) Structural evolution of the whole mitochondrial genome and phylogenetic inference in snakes (Squamata: Serpentes), including the undescribed mitogenome of the Brazilian endemic and critically endangered pitviper *Bothrops insularis*. *Genetics and molecular biology*, 48(4), e20240196.

Liu S, et al. (2026) Isolation, characterization and biocontrol of a novel bacteriophage against *Ralstonia pseudosolanacearum*. *Applied microbiology and biotechnology*, 110(1).

Mo Y, et al. (2026) Drug resistance mechanisms and molecular epidemiology of carbapenem-resistant *Klebsiella pneumoniae* in pulmonary infections. *BMC infectious diseases*, 26(1).

Aziz T, et al. (2026) Genomic insights into probiotic potential and metabolic adaptability of food derived *Lactiplantibacillus plantarum* and *Pediococcus acidilactici*. *Frontiers in microbiology*, 17, 1847858.

Ofori AD, et al. (2026) Genomic Basis of Lifestyle Divergence in Rice-Associated *Burkholderia*: From Pathogenesis to Plant Growth Promotion. *International journal of molecular sciences*, 27(11).

Oriowo TO, et al. (2026) Different sex determination systems in two closely related Eurasian minnow (*Phoxinus*) species. *Heredity*, 135(4), 259.

Zhang R, et al. (2026) Biological Characteristics and Comparative Genomic Analysis of *Corynebacterium hindlerae* from Bovine Skin Abscess. *Microorganisms*, 14(2).

Lei X, et al. (2026) The gp38 protein inhibits host adsorption of phage vB_EcoM_SD286. *Frontiers in microbiology*, 17, 1751343.

Varga T, et al. (2026) Whole genome sequencing of historical specimens from the world's largest fungal collection yields high-quality assemblies. *The New phytologist*, 251(2), 752.

Xu T, et al. (2026) Isolation and therapeutic potential of phage vB_EcoM_GXW16 against a drug-resistant avian pathogenic *Escherichia coli* strain. *Poultry science*, 105(6), 106701.