

Resource Summary Report

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[pbh5tools](#)

RRID:SCR_003027

Type: Tool

Proper Citation

pbh5tools (RRID:SCR_003027)

Resource Information

URL: <https://github.com/PacificBiosciences/pbh5tools>

Proper Citation: pbh5tools (RRID:SCR_003027)

Description: Software tools for manipulating HDF5 files produced by Pacific Biosciences. Specifically, this package provides functionality for manipulating and extracting data from cmp.h5 and bas.h5 files.

Resource Type: software resource

Keywords: standalone software

Funding:

Resource Name: pbh5tools

Resource ID: SCR_003027

Alternate IDs: OMICS_05138

Record Creation Time: 20220129T080216+0000

Record Last Update: 20250410T064937+0000

Ratings and Alerts

No rating or validation information has been found for pbh5tools.

No alerts have been found for pbh5tools.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at [FDI Lab - SciCrunch.org](#).

Yuan N, et al. (2024) Comprehensive assessment of long-read sequencing platforms and calling algorithms for detection of copy number variation. *Briefings in bioinformatics*, 25(5).

Béliveau C, et al. (2022) The Spruce Budworm Genome: Reconstructing the Evolutionary History of Antifreeze Proteins. *Genome biology and evolution*, 14(6).

Balachandran P, et al. (2022) Transposable element-mediated rearrangements are prevalent in human genomes. *Nature communications*, 13(1), 7115.

Urban JM, et al. (2021) High contiguity de novo genome assembly and DNA modification analyses for the fungus fly, *Sciara coprophila*, using single-molecule sequencing. *BMC genomics*, 22(1), 643.

Mhuantong W, et al. (2020) High Quality *Aspergillus aculeatus* Genomes and Transcriptomes: A Platform for Cellulase Activity Optimization Toward Industrial Applications. *Frontiers in bioengineering and biotechnology*, 8, 607176.

Burkhardt AK, et al. (2019) Assembly, annotation, and comparison of *Macrophomina phaseolina* isolates from strawberry and other hosts. *BMC genomics*, 20(1), 802.

Zhang SJ, et al. (2017) Isoform Evolution in Primates through Independent Combination of Alternative RNA Processing Events. *Molecular biology and evolution*, 34(10), 2453.

Kamada M, et al. (2014) Whole genome complete resequencing of *Bacillus subtilis natto* by combining long reads with high-quality short reads. *PloS one*, 9(10), e109999.

Larsen PA, et al. (2014) The utility of PacBio circular consensus sequencing for characterizing complex gene families in non-model organisms. *BMC genomics*, 15(1), 720.