

Resource Summary Report

Generated by [NIF](#) on Aug 30, 2026

[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

Availability: Free, Available for download, Freely available

Resource Name: pbh5tools

Resource ID: SCR_003027

Alternate IDs: OMICS_05138

Alternate URLs: <http://132.248.34.22:8080/smrtanalysis/doc/bioinformatics-tools/pbh5tools/doc/index.html>

Record Creation Time: 20220129T080216+0000

Record Last Update: 20260829T182120+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

Usage and Citation Metrics

We found 10 mentions in open access literature.

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

Huang Y, et al. (2025) The complete mitochondrial genome sequences of *Phlebopus portentosus* and *Leccinum extremiorientale* (Boletales; Boletinellaceae: *Phlebopus*; *Leccinum*). Mitochondrial DNA. Part B, Resources, 10(7), 606.

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).

B??iveau 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.