

Resource Summary Report

Generated by [kravitz2](#) on Sep 4, 2026

Proovread

RRID:SCR_017331

Type: Tool

Proper Citation

Proovread (RRID:SCR_017331)

Resource Information

URL: <https://github.com/BioInf-Wuerzburg/proovread>

Proper Citation: Proovread (RRID:SCR_017331)

Description: Software tool for PacBio hybrid error correction through iterative short read consensus.

Resource Type: data analysis software, data processing software, sequence analysis software, software application, software resource

Defining Citation: [PMID:25015988](#)

Keywords: PacBio, hybrid, error, correction, short, read, consensus, DNA, sequencing, bio.tools

Funding: European Research Council

Availability: Free, Available for download, Freely available

Resource Name: Proovread

Resource ID: SCR_017331

Alternate IDs: biotools:proovread

Alternate URLs: <https://bio.tools/proovread>

License: MIT License

Record Creation Time: 20220129T080334+0000

Record Last Update: 20260903T235429+0000

Ratings and Alerts

No rating or validation information has been found for Proovread.

No alerts have been found for Proovread.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Kong W, et al. (2024) Full-Length Transcriptomes Reconstruction Reveals Intraspecific Diversity in Hairy Vetch (*Vicia villosa* Roth) and Smooth Vetch (*V. villosa* Roth var. *glabrescens*). *Plants* (Basel, Switzerland), 13(23).

Beiki H, et al. (2024) Enhanced bovine genome annotation through integration of transcriptomics and epi-transcriptomics datasets facilitates genomic biology. *GigaScience*, 13.

Shirasawa K, et al. (2023) An improved reference genome for *Trifolium subterraneum* L. provides insight into molecular diversity and intra-specific phylogeny. *Frontiers in plant science*, 14, 1103857.

Li CX, et al. (2022) Three-Dimensional Genome Map of the Filamentous Fungus *Penicillium oxalicum*. *Microbiology spectrum*, 10(3), e0212121.

Yang C, et al. (2021) A review of computational tools for generating metagenome-assembled genomes from metagenomic sequencing data. *Computational and structural biotechnology journal*, 19, 6301.

Jeon JH, et al. (2021) Genetic Characterization of *Clostridium botulinum* Isolated from the First Case of Infant Botulism in Korea. *Annals of laboratory medicine*, 41(5), 489.

Papadopoulos AST, et al. (2021) Rapid Parallel Adaptation to Anthropogenic Heavy Metal Pollution. *Molecular biology and evolution*, 38(9), 3724.

Zhu X, et al. (2020) Genome Sequencing and Analysis of *Thraustochytridae* sp. SZU445 Provides Novel Insights into the Polyunsaturated Fatty Acid Biosynthesis Pathway. *Marine drugs*, 18(2).

Yuan H, et al. (2020) Characterization and analysis of full-length transcriptomes from two grasshoppers, *Gomphocerus licenti* and *Mongolotettix japonicus*. *Scientific reports*, 10(1), 14228.

Warr A, et al. (2020) An improved pig reference genome sequence to enable pig genetics and genomics research. *GigaScience*, 9(6).

Jin Z, et al. (2020) Complete Genome Sequence of *Bifidobacterium adolescentis* ZJ2, Isolated from a Centenarian in Anhui, China. *Microbiology resource announcements*, 9(29).

Fu S, et al. (2019) A comparative evaluation of hybrid error correction methods for error-prone long reads. *Genome biology*, 20(1), 26.

Wang L, et al. (2019) A draft genome assembly of halophyte *Suaeda aralocaspica*, a plant that performs C4 photosynthesis within individual cells. *GigaScience*, 8(9).

Tian Y, et al. (2019) Characterization of Full-Length Transcriptome Sequences and Splice Variants of *Lateolabrax maculatus* by Single-Molecule Long-Read Sequencing and Their Involvement in Salinity Regulation. *Frontiers in genetics*, 10, 1126.