

# Resource Summary Report

Generated by [T1D](#) on Jul 31, 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 processing software, sequence analysis software, data analysis software, software resource, software application

**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:** 20260731T043019+0000

### Ratings and Alerts

No rating or validation information has been found for Proovread.

No alerts have been found for Proovread.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 12 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [T1D](#).

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

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.

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

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.

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

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.