

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Pychopper

RRID:SCR_018966

Type: Tool

Proper Citation

Pychopper (RRID:SCR_018966)

Resource Information

URL: <https://github.com/nanoporetech/pychopper>

Proper Citation: Pychopper (RRID:SCR_018966)

Description: Software tool to identify, orient and trim full length Nanopore cDNA reads. Able to rescue fused reads.

Synonyms: Pychopper v2

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

Keywords: cDNA reads, Nanopore cDNA reads, identify reads, orient reads, trim full length reads, Nanopore reads, rescue fused reads

Availability: Free, Freely available

Resource Name: Pychopper

Resource ID: SCR_018966

Alternate URLs: <https://sources.debian.org/src/python3-pychopper/>

License: Mozilla Public License

Record Creation Time: 20220129T080342+0000

Record Last Update: 20260905T133056+0000

Ratings and Alerts

No rating or validation information has been found for Pychopper.

No alerts have been found for Pychopper.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 42 mentions in open access literature.

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

Zhou S, et al. (2026) hnRNPM cooperates with BCAS2 to modulate alternative splicing during oocyte development. *Nature communications*, 17(1).

Gooden C, et al. (2026) The gene-like promoter and transcription of LTR retrotransposons. *bioRxiv : the preprint server for biology*.

Levkova M, et al. (2026) A Lightweight Workflow for Targeted Long-Read Transcriptomic Profiling Using Oxford Nanopore Sequencing. *Methods and protocols*, 9(3).

Anderová K, et al. (2026) Discovery of novel murine PML isoforms. *Nucleus (Austin, Tex.)*, 17(1), 2646815.

Takeuchi T, et al. (2026) Forward genetic screening of mutants of the wild diploid ancestor *Nicotiana sylvestris* identifies aspartate oxidase 2 as a key gene for nicotine biosynthesis in cultivated allotetraploid tobacco (*Nicotiana tabacum*). *The Plant journal : for cell and molecular biology*, 126(1), e70818.

Hulsey CD, et al. (2026) Divergence at the IRX gene cluster underlies extreme trophic polymorphism in a cichlid fish (*Herichthys minckleyi*). *Communications biology*, 9(1).

Quinones-Valdez G, et al. (2025) Long-read RNA-seq demarcates cis- and trans-directed alternative RNA splicing. *Nature communications*, 16(1), 9603.

Sheng X, et al. (2025) Chromosome-level genome assembly of *Trichogramma ostrinae* Pang & Chen (Hymenoptera: Trichogrammatidae). *Scientific data*, 13(1), 138.

Deng Y, et al. (2025) Full-length transcriptome of *Camellia perpetua* reveals candidate SCPL1A gene family members involved in galloylated catechins biosynthesis. *Plant biotechnology (Tokyo, Japan)*, 42(4), 389.

Xin H, et al. (2025) Jan and mini-Jan, a model system for potato functional genomics. *Plant biotechnology journal*, 23(4), 1243.

Xu J, et al. (2025) Long-read RNA-sequencing reveals transcript-specific regulation in human-derived cortical neurons. *Open biology*, 15(7), 250200.

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. *Nature communications*, 15(1), 6297.

Guedes JG, et al. (2024) The leaf idioblastome of the medicinal plant *Catharanthus roseus* is associated with stress resistance and alkaloid metabolism. *Journal of experimental*

botany, 75(1), 274.

Shammi T, et al. (2024) Transcriptomics Provide Insights into Early Responses to Sucrose Signaling in *Lupinus albus*, a Model Plant for Adaptations to Phosphorus and Iron Deficiency. *International journal of molecular sciences*, 25(14).

Ulicevic J, et al. (2024) Uncovering the dynamics and consequences of RNA isoform changes during neuronal differentiation. *Molecular systems biology*, 20(7), 767.

Wang C, et al. (2024) Single-cell analysis of isoform switching and transposable element expression during preimplantation embryonic development. *PLoS biology*, 22(2), e3002505.

Xin H, et al. (2024) Jan and mini-Jan, a model system for potato functional genomics. *bioRxiv : the preprint server for biology*.

Li H, et al. (2024) Allelic variation in the autotetraploid potato: genes involved in starch and steroidal glycoalkaloid metabolism as a case study. *BMC genomics*, 25(1), 274.

He Z, et al. (2023) Cross-species comparison illuminates the importance of iron homeostasis for splenic anti-immunosenesence. *Aging cell*, 22(11), e13982.

Zhang Z, et al. (2023) Structure prediction of novel isoforms from uveal melanoma by AlphaFold. *Scientific data*, 10(1), 513.