

Resource Summary Report

Generated by T1D on Aug 3, 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: software resource, data processing software, software application

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: 20260803T040803+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 26 mentions in open access literature.

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

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

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.

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.

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

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.

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.

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

He Z, et al. (2023) Cross-species comparison illuminates the importance of iron homeostasis for splenic anti-immunosenescence. *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.

Jayakody TB, et al. (2023) Genome Report: Genome sequence of 1S1, a transformable and highly regenerable diploid potato for use as a model for gene editing and genetic engineering. *G3 (Bethesda, Md.)*, 13(4).

Peng L, et al. (2023) New insights into transcriptome variation during cattle adipocyte adipogenesis by direct RNA sequencing. *iScience*, 26(10), 107753.

Pei T, et al. (2023) Gap-free genome assembly and CYP450 gene family analysis reveal the biosynthesis of anthocyanins in *Scutellaria baicalensis*. *Horticulture research*, 10(12), uhad235.

Petri AJ, et al. (2023) isONform: reference-free transcriptome reconstruction from Oxford Nanopore data. *Bioinformatics (Oxford, England)*, 39(39 Suppl 1), i222.

Liu H, et al. (2023) Cochlear transcript diversity and its role in auditory functions implied by an otoferlin short isoform. *Nature communications*, 14(1), 3085.

Lubis WMY, et al. (2023) Transcriptome dataset from *Solanum lycopersicum* L. cv. Micro-Tom; wild type and two mutants of INDOLE-ACETIC-ACID (SIIAA9) using long-reads sequencing oxford nanopore technologies. *BMC research notes*, 16(1), 40.

Raad S, et al. (2022) iPSCs derived from esophageal atresia patients reveal SOX2 dysregulation at the anterior foregut stage. *Disease models & mechanisms*, 15(11).

González-Miguéns R, et al. (2022) Deconstructing *Diffugia*: The tangled evolution of lobose testate amoebae shells (Amoebozoa: Arcellinida) illustrates the importance of convergent evolution in protist phylogeny. *Molecular phylogenetics and evolution*, 175, 107557.

Ward Z, et al. (2021) Novel and Annotated Long Noncoding RNAs Associated with Ischemia in the Human Heart. *International journal of molecular sciences*, 22(21).