

Resource Summary Report

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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: 20260805T044429+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 [dkNET](#).

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.

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.

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*.

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.

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.

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.

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.

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

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).