Resource Summary Report

Generated by dkNET on May 19, 2025

Pychopper

RRID:SCR_018966
Type: Tool

Proper Citation

Pychopper (RRID:SCR_018966)

Resource Information

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

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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, software application, data processing software

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

Funding:

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: 20250513T062029+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 23 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

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.

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 (SlIAA9) using long-reads sequencing oxford nanopore technologies. BMC research notes, 16(1), 40.

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.

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.

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 Difflugia: 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).

Westergren Jakobsson A, et al. (2021) The Human Adenovirus Type 2 Transcriptome: An Amazing Complexity of Alternatively Spliced mRNAs. Journal of virology, 95(4).

Sahlin K, et al. (2021) Error correction enables use of Oxford Nanopore technology for reference-free transcriptome analysis. Nature communications, 12(1), 2.

Treitli SC, et al. (2021) High quality genome assembly of the amitochondriate eukaryote Monocercomonoides exilis. Microbial genomics, 7(12).