

Resource Summary Report

Generated by [kravitz2](#) on Aug 24, 2026

C3Poa

RRID:SCR_025484

Type: Tool

Proper Citation

C3Poa (RRID:SCR_025484)

Resource Information

URL: <https://github.com/christopher-vollmers/C3POa>

Proper Citation: C3Poa (RRID:SCR_025484)

Description: Software to detect DNA splint sequence raw reads. Computational pipeline for calling consensi on R2C2 nanopore data.

Abbreviations: C3Poa

Synonyms: Concatemeric Consensus Caller with Partial Order alignments.

Resource Type: data analysis software, data processing software, software application, software resource, source code

Defining Citation: [PMID:30201725](#)

Keywords: Concatemeric Consensus Caller, Partial Order alignments, detect DNA splint sequence raw reads, calling consensi on R2C2 nanopore data,

Funding: NHGRI 1T32HG008345

Availability: Free, Available for download, Freely available,

Resource Name: C3Poa

Resource ID: SCR_025484

License: GNU GPL v2

Record Creation Time: 20240716T053232+0000

Record Last Update: 20260821T194310+0000

Ratings and Alerts

No rating or validation information has been found for C3Poa.

No alerts have been found for C3Poa.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 5 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. Genome biology, 27(1).

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.

Tang AD, et al. (2023) Detecting haplotype-specific transcript variation in long reads with FLAIR2. bioRxiv : the preprint server for biology.

Naqvi MM, et al. (2022) CRISPR-Cas12a-mediated DNA clamping triggers target-strand cleavage. Nature chemical biology, 18(9), 1014.

Torres Montaguth OE, et al. (2021) ENDO-Pore: high-throughput linked-end mapping of single DNA cleavage events using nanopore sequencing. Nucleic acids research, 49(20), e118.