

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

Pore-c Workflow

RRID:SCR_027517

Type: Tool

Proper Citation

Pore-c Workflow (RRID:SCR_027517)

Resource Information

URL: <https://github.com/epi2me-labs/wf-pore-c>

Proper Citation: Pore-c Workflow (RRID:SCR_027517)

Description: Software workflow for analysing Pore-c data for chromatin conformation capture.

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

Keywords: analysing Pore-c data, chromatin conformation capture,

Availability: Free, Available for download, Freely available

Resource Name: Pore-c Workflow

Resource ID: SCR_027517

License URLs: <https://github.com/epi2me-labs/wf-pore-c?tab=License-1-ov-file#readme>

Record Creation Time: 20251010T055859+0000

Record Last Update: 20260815T183302+0000

Ratings and Alerts

No rating or validation information has been found for Pore-c Workflow.

No alerts have been found for Pore-c Workflow.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Abuelanin M, et al. (2026) Single-library chromosome-scale diploid assemblies of vole genomes resolve a species-specific duplication implicated in pair bonding. bioRxiv : the preprint server for biology.

Lee M, et al. (2026) LINE-1 Locus Transcription Nucleates Oncogenic Chromatin Architecture. Cancer discovery, 16(4), 800.

Choi J, et al. (2024) A Chromosome-Scale and Annotated Reference Genome Assembly of *Plecia longiforceps* Duda, 1934 (Diptera: Bibionidae). Genome biology and evolution, 16(10).