

Resource Summary Report

Generated by SPARC SAWG on Aug 5, 2026

qcat

RRID:SCR_024195

Type: Tool

Proper Citation

qcat (RRID:SCR_024195)

Resource Information

URL: <https://github.com/nanoporetech/qcat>

Proper Citation: qcat (RRID:SCR_024195)

Description: Software Python command-line tool for demultiplexing Oxford Nanopore reads from FASTQ files.

Resource Type: software application, software resource

Keywords: command-line tool, demultiplexing Oxford Nanopore reads, reads from FASTQ files,

Availability: Free, Available for download, Freely available,

Resource Name: qcat

Resource ID: SCR_024195

Alternate URLs: <https://sources.debian.org/src/qcat/>

License: MPL-2.0 license

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260805T044528+0000

Ratings and Alerts

No rating or validation information has been found for qcat.

No alerts have been found for qcat.

Data and Source Information

Usage and Citation Metrics

We found 12 mentions in open access literature.

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

Björnberg A, et al. (2025) Critical Steps in Shotgun Metagenomics-Based Diagnosis of Bloodstream Infections Using Nanopore Sequencing. *APMIS : acta pathologica, microbiologica, et immunologica Scandinavica*, 133(1), e13511.

Koh V, et al. (2025) Plasmid dynamics driving carbapenemase gene dissemination in healthcare environments: a nationwide analysis of closed Enterobacterales genomes. *Nature communications*, 16(1), 9522.

Gao H, et al. (2025) Whole genome comparisons reveal gut-to-lung translocation of *Escherichia coli* and *Burkholderia cenocepacia* in two cases of ventilator-associated pneumonia in ICU patients. *Respiratory research*, 26(1), 178.

Hasan A, et al. (2025) Concurrent transmission of Zika virus during the 2023 dengue outbreak in Dhaka, Bangladesh. *PLoS neglected tropical diseases*, 19(1), e0012866.

Llarena AK, et al. (2025) DNA extraction protocols for animal fecal material on blood spot cards. *PloS one*, 20(5), e0313808.

Hiralal A, et al. (2024) Closing the genome of unculturable cable bacteria using a combined metagenomic assembly of long and short sequencing reads. *Microbial genomics*, 10(2).

Pop-Vicas AE, et al. (2024) A severe acute respiratory coronavirus virus 2 (SARS-CoV-2) nosocomial cluster with inter-facility spread: Lessons learned. *Infection control and hospital epidemiology*, 45(5), 635.

Sekse C, et al. (2024) Genome sequences of *Clostridium perfringens* isolated from diseased dogs. *Microbiology resource announcements*, 13(9), e0024424.

Baby V, et al. (2023) Comparative genomics of *Mycoplasma feriruminatoris*, a fast-growing pathogen of wild Caprinae. *Microbial genomics*, 9(10).

Vermeulen C, et al. (2023) Ultra-fast deep-learned CNS tumour classification during surgery. *Nature*, 622(7984), 842.

Cummins EA, et al. (2023) Parallel loss of type VI secretion systems in two multi-drug-resistant *Escherichia coli* lineages. *Microbial genomics*, 9(11).

de França Cirilo MV, et al. (2023) Co-circulation of Chikungunya virus, Zika virus, and serotype 1 of Dengue virus in Western Bahia, Brazil. *Frontiers in microbiology*, 14, 1240860.