

# Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

## qcat

RRID:SCR\_024195

Type: Tool

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### Proper Citation

qcat (RRID:SCR\_024195)

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### 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:** 20260905T133317+0000

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### Ratings and Alerts

No rating or validation information has been found for qcat.

No alerts have been found for qcat.

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### Data and Source Information

## Usage and Citation Metrics

We found 22 mentions in open access literature.

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

Shin GY, et al. (2026) Comparative genomics of *Pantoea allii* lineages and distribution of ecologically relevant traits. *Microbial genomics*, 12(2).

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.

Tanmoy AM, et al. (2025) Evolution of pneumococcal serotype 19A in children in Bangladesh: insights from genomic analysis. *BMC microbiology*, 25(1), 773.

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.

Hiralal A, et al. (2024) Comparative genomic analysis of nickel homeostasis in cable bacteria. *BMC genomics*, 25(1), 692.

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

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

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

Fang L, et al. (2023) Haplotyping SNPs for allele-specific gene editing of the expanded huntingtin allele using long-read sequencing. *HGG advances*, 4(1), 100146.

Eagle SHC, et al. (2023) Evaluation of five commercial DNA extraction kits using *Salmonella* as a model for implementation of rapid Nanopore sequencing in routine diagnostic laboratories. *Access microbiology*, 5(2).

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.

Alikhan NF, et al. (2022) Dynamics of *Salmonella enterica* and antimicrobial resistance in the Brazilian poultry industry and global impacts on public health. *PLoS genetics*, 18(6), e1010174.

Haverkamp THA, et al. (2022) Closed Genome Sequences of *Providencia alcalifaciens* Isolates from Dogs. *Microbiology resource announcements*, 11(2), e0095521.

Braun KM, et al. (2021) Viral Sequencing to Investigate Sources of SARS-CoV-2 Infection in US Healthcare Personnel. *Clinical infectious diseases : an official publication of the Infectious Diseases Society of America*, 73(6), e1329.