

Resource Summary Report

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

[pycoqc](#)

RRID:SCR_024185

Type: Tool

Proper Citation

pycoqc (RRID:SCR_024185)

Resource Information

URL: <https://github.com/a-slide/pycoQC>

Proper Citation: pycoqc (RRID:SCR_024185)

Description: Software application to compute metrics and generate interactive QC plots for Oxford Nanopore technologies sequencing data.

Resource Type: software resource, software toolkit

Keywords: compute metrics, generate interactive QC plots, Oxford Nanopore technologies sequencing data,

Availability: Free, Available for download, Freely available,

Resource Name: pycoqc

Resource ID: SCR_024185

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

Record Creation Time: 20230824T050212+0000

Record Last Update: 20260905T133105+0000

Ratings and Alerts

No rating or validation information has been found for pycoqc.

No alerts have been found for pycoqc.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 24 mentions in open access literature.

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

Meyer D, et al. (2026) Unlocking the full potential of nanopore sequencing: tips, tricks, and advanced data analysis techniques. *Nucleic acids research*, 54(3).

Skouroliahou DI, et al. (2026) Unveiling Protist Composition and Diversity Patterns With eDNA Metabarcoding: Comparing Short- and Long-Read Approaches. *Ecology and evolution*, 16(3), e73218.

Ahmad F, et al. (2026) pTJK, a rare *Mammaliicoccus lentus* phage with broad-host-range, antibiofilm, and synergistic interactions with antimicrobials against resistant *Staphylococcaceae*. *Archives of microbiology*, 208(5).

Dunham TJ, et al. (2026) Optimized library preparation, sequencing, and data analysis protocols for the generation of orbivirus consensus sequences. *BMC genomics*, 27(1), 48.

Albarrán-Cuitiño C, et al. (2026) Development of a plant growth-promoting bacterial EcoBiome derived from desert soil isolates. *Applied and environmental microbiology*, 92(5), e0010326.

Sullivan R, et al. (2025) *Vibrio harveyi* plasmids as drivers of virulence in barramundi (*Lates calcarifer*). *PloS one*, 20(5), e0319450.

Schell T, et al. (2025) Establishing genome sequencing and assembly for non-model and emerging model organisms: a brief guide. *Frontiers in zoology*, 22(1), 7.

Di Pilato V, et al. (2025) Next-generation diagnostics of bloodstream infections enabled by rapid whole-genome sequencing of bacterial cells purified from blood cultures. *EBioMedicine*, 114, 105633.

Izzo M, et al. (2025) Muscle-specific gene editing improves molecular and phenotypic defects in a mouse model of myotonic dystrophy type 1. *Clinical and translational medicine*, 15(2), e70227.

Carneiro DG, et al. (2024) Genome sequencing and analysis of *Salmonella enterica* subsp. *enterica* serotype Enteritidis PT4 578: insights into pathogenicity and virulence. *Access microbiology*, 6(11).

De Meulenaere K, et al. (2024) Selective whole-genome sequencing of *Plasmodium* parasites directly from blood samples by nanopore adaptive sampling. *mBio*, 15(1), e0196723.

Kimemia BB, et al. (2024) Detection of pathogenic bacteria in ticks from Isiolo and Kwale counties of Kenya using metagenomics. *PloS one*, 19(4), e0296597.

Charles RA, et al. (2024) Completing the Puzzle: A Cluster of Hunting Dogs with Tick-Borne Illness from a Fishing Community in Tobago, West Indies. *Pathogens (Basel, Switzerland)*, 13(2).

De Clercq G, et al. (2024) Full characterization of unresolved structural variation through long-read sequencing and optical genome mapping. *Scientific reports*, 14(1), 29142.

Li K, et al. (2024) Genetic diagnosis of facioscapulohumeral muscular dystrophy type 1 using rare-variant linkage analysis and long-read genome sequencing. *Genetics in medicine open*, 2, 101817.

Jacob KM, et al. (2024) Mucin-induced surface dispersal of *Staphylococcus aureus* and *Staphylococcus epidermidis* via quorum-sensing dependent and independent mechanisms. *mBio*, 15(8), e0156224.

Choi MK, et al. (2024) Exposure to elevated glucocorticoid during development primes altered transcriptional responses to acute stress in adulthood. *iScience*, 27(7), 110160.

Desideri F, et al. (2024) CyCoNP lncRNA establishes cis and trans RNA-RNA interactions to supervise neuron physiology. *Nucleic acids research*, 52(16), 9936.

Teullet S, et al. (2023) Metagenomics uncovers dietary adaptations for chitin digestion in the gut microbiota of convergent myrmecophagous mammals. *mSystems*, 8(5), e0038823.

Gomes AR, et al. (2022) A transcriptional switch controls sex determination in *Plasmodium falciparum*. *Nature*, 612(7940), 528.