

Resource Summary Report

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[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: 20260801T042918+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 18 mentions in open access literature.

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

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.

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.

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.

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.

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.

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).

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.

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.

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.

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.

Wang K, et al. (2021) Metagenomic diagnosis of severe psittacosis using multiple sequencing platforms. *BMC genomics*, 22(1), 406.

Waweru JW, et al. (2021) Enrichment approach for unbiased sequencing of respiratory syncytial virus directly from clinical samples. *Wellcome open research*, 6, 99.

Wang K, et al. (2020) Metagenomic Diagnosis for a Culture-Negative Sample From a Patient With Severe Pneumonia by Nanopore and Next-Generation Sequencing. *Frontiers in cellular and infection microbiology*, 10, 182.