Resource Summary Report

Generated by dkNET on Aug 15, 2026

miQC

RRID:SCR_022697
Type: Tool

Proper Citation

miQC (RRID:SCR_022697)

Resource Information

URL: https://github.com/greenelab/miQC

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Description: Software tool as flexible, probablistic metrics for quality control of scRNA-seq data. Adaptive probabilistic framework for quality control of single-cell RNA-sequencing data. Data driven QC metric that jointly models proportion of reads mapping to mtDNA and number of detected genes with mixture models in probabilistic framework to predict which cells are low quality in given dataset.

Resource Type: data processing software, software application, data analysis software, software resource

Defining Citation: PMID:34428202

Keywords: scRNA-seq data quality control, QC metric, low quality data prediction, single cell RNA-sequencing data

Funding: NCI CA237170;
NHGRI HG009007;
European Union Horizon 2020 research and innovation program ;
Academy of Finland ;
Cancer Foundation Finland

Availability: Free, Available for download, Freely available

Resource Name: miQC

Resource ID: SCR_022697

License: BSD-3-Clause

Record Creation Time: 20220824T050146+0000

Record Last Update: 20260815T182725+0000

Ratings and Alerts

No rating or validation information has been found for miQC.

No alerts have been found for miQC.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 4 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET .

Sakrepatna Nagaraj A, et al. (2026) Ex Vivo Immuno-Oncology Platform Reveals Spatial T-cell Infiltration Patterns Linked to ATR Inhibition Responses in High-Grade Serous Ovarian Cancer. Cancer immunology research, 14(4), 625.

Leu JS, et al. (2026) Combined inhibition of S100A4 and TIGIT suppresses late-stage breast cancer metastasis. Cancer letters, 649, 218491.

Celik C, et al. (2024) Decoding the complexity of delayed wound healing following Enterococcus faecalis infection. eLife, 13.

Millet A, et al. (2024) An exhausted-like microglial population accumulates in aged and APOE4 genotype Alzheimer's brains. Immunity, 57(1), 153.