

# Resource Summary Report

Generated by NIF on Apr 26, 2025

## MultiQC

RRID:SCR\_014982

Type: Tool

### Proper Citation

MultiQC (RRID:SCR\_014982)

### Resource Information

**URL:** <http://multiqc.info/>

**Proper Citation:** MultiQC (RRID:SCR\_014982)

**Description:** Data aggregate that compiles results from bioinformatics analyses across multiple samples into a single report. It is written in Python.

**Resource Type:** software resource, data access protocol

**Defining Citation:** PMID:27312411, DOI:10.1093/bioinformatics/btw354

**Keywords:** bioinformatics, data aggregate, python, open source, html report, bio.tools

**Funding:** Science for Life Laboratory ;  
National Genomics Infrastructure

**Availability:** Open source, Available for download

**Resource Name:** MultiQC

**Resource ID:** SCR\_014982

**Alternate IDs:** biotools:multiqc, OMICS\_12426

**Alternate URLs:** <https://github.com/ewels/MultiQC> <https://pypi.python.org/pypi/multiqc>,  
<https://bio.tools/multiqc>, <https://sources.debian.org/src/multiqc/>

**License:** GPLv3

**Record Creation Time:** 20220129T080323+0000

**Record Last Update:** 20250425T060038+0000

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## Ratings and Alerts

No rating or validation information has been found for MultiQC.

No alerts have been found for MultiQC.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2283 mentions in open access literature.

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

Wang C, et al. (2025) Transcriptomic profiling of osteoarthritis synovial macrophages reveals a tolerized phenotype compounded by a weak corticosteroid response. *Rheumatology* (Oxford, England), 64(2), 860.

Pimentel MF, et al. (2025) Dual RNA-seq reveals transcriptome changes during *Fusarium virguliforme*-*Trichoderma afroharzianum* interactions. *PLoS one*, 20(1), e0310850.

Stenger PL, et al. (2025) A Multimarker Approach to Identify Microbial Bioindicators for Coral Reef Health Monitoring-Case Study in La Réunion Island. *Microbial ecology*, 87(1), 179.

Mastrantonio V, et al. (2025) De novo transcriptome assembly of the Mediterranean sea-rock pool mosquitoes *Aedes mariae* and *Aedes zammitii*. *Scientific data*, 12(1), 115.

Hruba P, et al. (2025) Transcriptomic Signatures of Antibody-mediated Rejection in Early Biopsies With Negative Histology in HLA-incompatible Kidney Transplantation. *Transplantation direct*, 11(1), e1741.

Beauchemin ET, et al. (2025) Dextran sodium sulfate-induced colitis alters the proportion and composition of replicating gut bacteria. *mSphere*, 10(1), e0082524.

Hrala M, et al. (2025) Whole genome sequences of nine *Taylorella equigenitalis* strains isolated in the Czech Republic between 1982-2021: Molecular dating suggests a common ancestor at the time of Roman Empire. *PLoS one*, 20(1), e0315946.

Burc E, et al. (2025) Life-history adaptation under climate warming magnifies the agricultural footprint of a cosmopolitan insect pest. *Nature communications*, 16(1), 827.

Gupta SK, et al. (2025) Dietary Chia (*Salvia hispanica L.*) seeds oil supplementation

augments growth performance and gut microbial composition in *Labeo rohita* fingerlings. *Scientific reports*, 15(1), 1866.

Khemiri H, et al. (2025) SARS-CoV-2 excretion and genetic evolution in nasopharyngeal and stool samples from primary immunodeficiency and immunocompetent pediatric patients. *Virology journal*, 22(1), 9.

Zhang QS, et al. (2025) SHMT2 regulates CD8+ T cell senescence via the reactive oxygen species axis in HIV-1 infected patients on antiretroviral therapy. *EBioMedicine*, 112, 105533.

Shin H, et al. (2025) Transcriptome profiling of aged-mice ovaries administered with individual ingredients of Samul-tang. *Scientific data*, 12(1), 81.

Wei K, et al. (2025) MYSM1 attenuates osteoarthritis by recruiting PP2A to deubiquitinate and dephosphorylate RIPK2. *Bone research*, 13(1), 3.

Dwi Putra SE, et al. (2025) Genetic variations and clinical significance in young-onset nasopharyngeal cancer: Analysis of EBV interaction with cellular receptor variants and viral glycoproteins. *Heliyon*, 11(1), e41198.

Bastola S, et al. (2025) Endothelial-secreted Endocan activates PDGFRA and regulates vascularity and spatial phenotype in glioblastoma. *Nature communications*, 16(1), 471.

Gannon AD, et al. (2025) Exploring aggregation genes in a *P. aeruginosa* chronic infection model. *Journal of bacteriology*, 207(1), e0042924.

Brown KT, et al. (2025) Extreme Environmental Variability Induces Frontloading of Coral Biomineralisation Genes to Maintain Calcification Under pCO<sub>2</sub> Variability. *Molecular ecology*, 34(2), e17603.

Damodaran AP, et al. (2025) Proteomic study identifies Aurora-A-mediated regulation of alternative splicing through multiple splicing factors. *The Journal of biological chemistry*, 301(1), 108000.

Torang A, et al. (2025) Enterocyte-like differentiation defines metabolic gene signatures of CMS3 colorectal cancers and provides therapeutic vulnerability. *Nature communications*, 16(1), 264.

Coomber AL, et al. (2025) A pangenome analysis reveals the center of origin and evolutionary history of *Phytophthora infestans* and 1c clade species. *PLoS one*, 20(1), e0314509.