

Resource Summary Report

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MCWorkflow

RRID:SCR_027305

Type: Tool

Proper Citation

MCWorkflow (RRID:SCR_027305)

Resource Information

URL: <https://github.com/NikolayOskolkov/MCWorkflow>

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Description: Software application as computational workflow for detecting coordinates of microbial-like or human-like sequences in eukaryotic and procaryotic reference genomes.

Synonyms: Microbial Contamination Workflow

Resource Type: workflow, training material, data or information resource, source code, software resource, narrative resource

Defining Citation: [DOI:10.1101/2025.03.19.644176](https://doi.org/10.1101/2025.03.19.644176)

Keywords: workflow, metagenomics, contamination detection,

Funding: Knut and Alice Wallenberg Foundation ;
Swedish Research Council ;
SciLifeLab

Availability: Free, Available for download, Freely available

Resource Name: MCWorkflow

Resource ID: SCR_027305

Record Creation Time: 20250814T065259+0000

Record Last Update: 20260815T042932+0000

Ratings and Alerts

No rating or validation information has been found for MCWorkflow.

No alerts have been found for MCWorkflow.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Oskolkov N, et al. (2025) Improving taxonomic inference from ancient environmental metagenomes by masking microbial-like regions in reference genomes. GigaScience, 14.