

Resource Summary Report

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Comparative Metatranscriptomics Workflow

RRID:SCR_017109

Type: Tool

Proper Citation

Comparative Metatranscriptomics Workflow (RRID:SCR_017109)

Resource Information

URL: <https://github.com/anwarMZ/CoMW>

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Description: Software tool for standardized and validated workflow to functionally classify quality filtered mRNA reads from metatranscriptomic or total RNA studies generated using NGS short reads. Used for classification of these reads using assembled contigs to reference databases.

Abbreviations: CoMW

Resource Type: data analysis software, data or information resource, data processing software, narrative resource, sequence analysis software, software application, software resource, training material, workflow

Keywords: workflow, functionally, classify, mRNA, metatranscriptomic, RNA, next, generation, sequencing, NGS, short, read, assembly, contig, reference, database, bio.tools

Funding: h2020 EU MicroArctic ITN

Availability: Free, Available for download, Freely available

Resource Name: Comparative Metatranscriptomics Workflow

Resource ID: SCR_017109

Alternate IDs: biotools:comw

Alternate URLs: <https://bio.tools/CoMW>

License: GNU GPL

Record Creation Time: 20220129T080333+0000

Ratings and Alerts

No rating or validation information has been found for Comparative Metatranscriptomics Workflow.

No alerts have been found for Comparative Metatranscriptomics Workflow.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 3 mentions in open access literature.

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

Ellegaard-Jensen L, et al. (2025) Concurrent stimulation of diflufenican biodegradation and changes in the active microbiome in gravel revealed by Total RNA. Microbiology spectrum, 13(10), e0016425.

Thomsen T, et al. (2025) Arctic Soil C and N Cycling Are Linked With Microbial Adaptations During Drought. Global change biology, 31(9), e70502.

Anwar MZ, et al. (2019) To assemble or not to resemble-A validated Comparative Metatranscriptomics Workflow (CoMW). GigaScience, 8(8).