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

Proper Citation: Comparative Metatranscriptomics Workflow (RRID:SCR_017109)

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

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

Record Last Update: 20250519T203947+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 1 mentions in open access literature.

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

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