

Resource Summary Report

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Tourmaline

RRID:SCR_022465

Type: Tool

Proper Citation

Tourmaline (RRID:SCR_022465)

Resource Information

URL: <https://github.com/aomlomics/tourmaline>

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Description: Software tool as amplicon sequence processing workflow using QIIME 2 and Snakemake management system. Enables rapid analysis of environmental and biomedical amplicon data, decreasing time from data generation to actionable results.

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

Defining Citation: [DOI:10.1101/2021.09.15.460495](https://doi.org/10.1101/2021.09.15.460495)

Keywords: Amplicon sequence processing workflow, environmental and biomedical amplicon data

Funding: NOAA NA16OAR4320199;
NOAA NA21OAR4320190

Availability: Free, Available for download, Freely available

Resource Name: Tourmaline

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Alternate URLs: <https://hub.docker.com/repository/docker/aomlomics/tourmaline>

License: BSD 3-Clause "New" or "Revised" License

Record Creation Time: 20220607T050155+0000

Record Last Update: 20260803T040825+0000

Ratings and Alerts

No rating or validation information has been found for Tourmaline.

No alerts have been found for Tourmaline.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

D??rr AK, et al. (2024) RiboSnake - a user-friendly, robust, reproducible, multipurpose and documentation-extensive pipeline for 16S rRNA gene microbiome analysis. GigaByte (Hong Kong, China), 2024, gigabyte132.

Thompson LR, et al. (2022) Tourmaline: A containerized workflow for rapid and iterable amplicon sequence analysis using QIIME 2 and Snakemake. GigaScience, 11.