

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Taxonomer

RRID:SCR_014655

Type: Tool

Proper Citation

Taxonomer (RRID:SCR_014655)

Resource Information

URL: https://github.com/Yandell-Lab/taxonomer_0.5

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Description: Genome sequence classification tool based on kmer. The code allows users to build nucleotide databases and protein databases, classify reads, construct binner databases, and create taxonomic relationship files. The website provides information on how to perform these actions with code, though users can access a web-based Taxonomer if they need/want to.

Resource Type: data analysis software, data processing software, software application, software resource, source code, web application

Keywords: metagenomics toolkit, metagenomics analysis, analysis tool, microorganism detection, sequencing, genome sequence classification, kmer, nucleotide database, protein database, read classification, binner database, taxonomic relationship, source code, web application

Availability: Free, Available for download, Written in c and python

Resource Name: Taxonomer

Resource ID: SCR_014655

Alternate URLs: <http://taxonomer.iobio.io>

Record Creation Time: 20220129T080321+0000

Record Last Update: 20260905T132749+0000

Ratings and Alerts

No rating or validation information has been found for Taxonomer.

No alerts have been found for Taxonomer.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 6 mentions in open access literature.

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

Elwan EA, et al. (2023) Exploring virus presence in field-collected potato leaf samples using RNA sequencing. Journal, genetic engineering & biotechnology, 21(1), 106.

Hong NTT, et al. (2020) Performance of Metagenomic Next-Generation Sequencing for the Diagnosis of Viral Meningoencephalitis in a Resource-Limited Setting. Open forum infectious diseases, 7(3), ofaa046.

Schuele L, et al. (2020) Assessment of Viral Targeted Sequence Capture Using Nanopore Sequencing Directly from Clinical Samples. Viruses, 12(12).

Park SJ, et al. (2019) A systematic sequencing-based approach for microbial contaminant detection and functional inference. BMC biology, 17(1), 72.

Schlaberg R, et al. (2018) Fecal Host Transcriptomics for Non-Invasive Human Mucosal Immune Profiling: Proof of Concept in Clostridium Difficile Infection. Pathogens & immunity, 3(2), 164.

Hamilton EP, et al. (2016) Structure of the germline genome of Tetrahymena thermophila and relationship to the massively rearranged somatic genome. eLife, 5.