

# Resource Summary Report

Generated by [dkNET](#) on Aug 26, 2026

## Taxonomer

RRID:SCR\_014655

Type: Tool

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### Proper Citation

Taxonomer (RRID:SCR\_014655)

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### Resource Information

**URL:** [https://github.com/Yandell-Lab/taxonomer\\_0.5](https://github.com/Yandell-Lab/taxonomer_0.5)

**Proper Citation:** Taxonomer (RRID:SCR\_014655)

**Description:** Genome sequence classification tool based on kmer. The code allows users to build nucleotide databases and protein databases, classify reads, construct biner 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, biner 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:** 20260821T194006+0000

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### Ratings and Alerts

No rating or validation information has been found for Taxonomer.

No alerts have been found for Taxonomer.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 6 mentions in open access literature.

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

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.