

Resource Summary Report

Generated by [kravitz2](#) on Jul 31, 2026

Kaiju

RRID:SCR_022775

Type: Tool

Proper Citation

Kaiju (RRID:SCR_022775)

Resource Information

URL: <https://kaiju.binf.ku.dk>

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Description: Software tool for sensitive taxonomic classification of high-throughput sequencing reads from metagenomic whole genome sequencing or metatranscriptomics experiments.

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

Defining Citation: [PMID:27071849](#)

Keywords: sensitive taxonomic classification, high-throughput sequencing reads, metagenomic whole genome sequencing, metatranscriptomics experiments

Funding: Novo Nordisk Foundation ;
European Union 7th Framework Programme

Availability: Free, Available for download, Freely available

Resource Name: Kaiju

Resource ID: SCR_022775

Alternate URLs: <https://github.com/bioinformatics-centre/kaiju>

License: GNU GPL v3.0

Record Creation Time: 20220922T050155+0000

Record Last Update: 20260731T043118+0000

Ratings and Alerts

No rating or validation information has been found for Kaiju.

No alerts have been found for Kaiju.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Geraldini DB, et al. (2025) Identification of a putative new virus from the Jingmenvirus group in ticks from wild animals in Brazil. *Virus evolution*, 11(1), veaf045.

Grasso G, et al. (2025) Ancient Microbiomes as Mirrored by DNA Extracted From Century-Old Herbarium Plants and Associated Soil. *Molecular ecology resources*, 25(7), e14122.

Shipelin VA, et al. (2024) Toxicological Characteristics of Bacterial Nanocellulose in an In Vivo Experiment-Part 1: The Systemic Effects. *Nanomaterials (Basel, Switzerland)*, 14(9).

Arikan M, et al. (2024) gNOMO2: a comprehensive and modular pipeline for integrated multi-omics analyses of microbiomes. *GigaScience*, 13.

Wu L, et al. (2024) Construction of high-quality genomes and gene catalogue for culturable microbes of sugarcane (*Saccharum* spp.). *Scientific data*, 11(1), 534.

Wang C, et al. (2023) Bacterial genome size and gene functional diversity negatively correlate with taxonomic diversity along a pH gradient. *Nature communications*, 14(1), 7437.

Quesada-V??zquez S, et al. (2023) Potential therapeutic implications of histidine catabolism by the gut microbiota in NAFLD patients with morbid obesity. *Cell reports. Medicine*, 4(12), 101341.

Zhang Y, et al. (2022) Improved microbial genomes and gene catalog of the chicken gut from metagenomic sequencing of high-fidelity long reads. *GigaScience*, 11.