

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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 analysis software, data processing software, software application, software resource

Defining Citation: [PMID:27071849](#)

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

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

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: 20260905T133016+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 13 mentions in open access literature.

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

Stead CE, et al. (2026) Exploring the biotechnological potential of terrestrial hot spring microbiomes for CO₂ utilisation. *Environmental microbiome*, 21(1).

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.

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.

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

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).

Rosaldo-Benitez V, et al. (2024) Eukaryotic Microalgae Communities from Tropical Karstic Freshwater Lagoons in an Anthropic Disturbance Gradient Microscopic and Metagenomic Analysis. *Microorganisms*, 12(11).

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.

Chen BY, et al. (2023) Integrated Omic Analysis of Human Plasma Metabolites and Microbiota in a Hypertension Cohort. *Nutrients*, 15(9).

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.

Butina TV, et al. (2023) Viral Diversity in Samples of Freshwater Gastropods *Benedictia baicalensis* (Caenogastropoda: Benedictiidae) Revealed by Total RNA-Sequencing. *International journal of molecular sciences*, 24(23).

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.

Xia R, et al. (2022) Metagenomic Sequencing Reveals that the Assembly of Functional Genes and Taxa Varied Highly and Lacked Redundancy in the Earthworm Gut Compared with Soil under Vanadium Stress. *mSystems*, 7(1), e0125321.

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.