

Resource Summary Report

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[kraken2](#)

RRID:SCR_026838

Type: Tool

Proper Citation

kraken2 (RRID:SCR_026838)

Resource Information

URL: <https://github.com/DerrickWood/kraken2>

Proper Citation: kraken2 (RRID:SCR_026838)

Description: Software tool as second version of Kraken taxonomic sequence classification system.

Resource Type: software application, software resource, source code

Defining Citation: [PMID:31779668](#)

Keywords: taxonomic sequence classification system, taxonomic, sequence, classification system,

Funding: NSF ;
NIGMS R01 GM118568;
NIGMS R35 GM130151

Availability: Free, Available for download, Freely available

Resource Name: kraken2

Resource ID: SCR_026838

License: MIT license

Record Creation Time: 20250424T064808+0000

Record Last Update: 20260805T044606+0000

Ratings and Alerts

No rating or validation information has been found for kraken2.

No alerts have been found for kraken2.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1107 mentions in open access literature.

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

Ip YCA, et al. (2026) Fast, Flexible, Feasible: A Transparent Framework for Evaluating eDNA Workflow Trade-Offs in Resource-Limited Settings. *Molecular ecology resources*, 26(1), e70091.

Yun Y, et al. (2026) Gut microbiome plasticity explains the altitudinal distribution pattern and adaptability in a small mammal species (*Apodemus draco*). *Microbiology spectrum*, 14(1), e0238825.

Huang C, et al. (2026) The High-Altitude Adaptation Characteristics of Microbiota-Host Cross-Talk in Yak Gastrointestinal Track. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 13(1), e14862.

Zamparo S, et al. (2026) Metabarcoding Reveals a Potentially Undescribed Columnaris-Causing Bacterium in Peracute Skin Disease of Rainbow Trout (*Oncorhynchus mykiss*, Walbaum). *Journal of fish diseases*, 49(1), e70004.

Hodgson RJ, et al. (2026) Contrasting Microbial Taxonomic and Functional Colonisation Patterns in Wild Populations of the Pan-Palaeotropical C4 Grass, *Themeda triandra*. *Plant, cell & environment*, 49(1), 209.

Light-Maka I, et al. (2025) Bronze Age *Yersinia pestis* genome from sheep sheds light on hosts and evolution of a prehistoric plague lineage. *Cell*.

Garsmeur O, et al. (2025) The genomic footprints of wild *Saccharum* species trace domestication, diversification, and modern breeding of sugarcane. *Cell*, 188(25), 7252.

Deézsi-Magyar N, et al. (2025) Evaluating enterovirus diversity among symptomatic patients in Hungary during and after easing the COVID-19 lockdown. *Virology journal*, 22(1), 204.

Mikko A, et al. (2025) Sequencing airborne DNA to monitor crop pathogens and pests. *iScience*, 28(7), 112912.

Vaccaro M, et al. (2025) Pond water microbiome antibiotic resistance genes vary seasonally with environmental pH and tannins. *Microbiology spectrum*, 13(5), e0303424.

Nothdurfter S, et al. (2025) Epidemiology of Tularemia among Humans and Animals, Baden-Wuerttemberg, Germany, 2012-2022. *Emerging infectious diseases*, 31(4), 678.

Haagmans R, et al. (2025) Assessing Bias and Reproducibility of Viral Metagenomics Methods for the Combined Detection of Faecal RNA and DNA Viruses. *Viruses*, 17(2).

Mogashoa T, et al. (2025) Whole genomic analysis uncovers high genetic diversity of rifampicin-resistant *Mycobacterium tuberculosis* strains in Botswana. *Frontiers in microbiology*, 16, 1535160.

Díez López C, et al. (2025) Unravelling the hidden side of laundry: malodour, microbiome and pathogenome. *BMC biology*, 23(1), 40.

Morni MA, et al. (2025) Gut microbiome community profiling of Bornean bats with different feeding guilds. *Animal microbiome*, 7(1), 21.

Yao J, et al. (2025) Chloroplast Genome Sequencing and Comparative Analysis of Six Medicinal Plants of *Polygonatum*. *Ecology and evolution*, 15(1), e70831.

Björnberg A, et al. (2025) Critical Steps in Shotgun Metagenomics-Based Diagnosis of Bloodstream Infections Using Nanopore Sequencing. *APMIS : acta pathologica, microbiologica, et immunologica Scandinavica*, 133(1), e13511.

L'Heureux JE, et al. (2025) Oral microbiome and nitric oxide biomarkers in older people with mild cognitive impairment and APOE4 genotype. *PNAS nexus*, 4(1), pgae543.

Ye GC, et al. (2025) Comprehensive analysis of the interaction microbiome and prostate cancer: an initial exploration from multi-cohort metagenome and GWAS studies. *Journal of translational medicine*, 23(1), 130.

Hauff L, et al. (2025) De Novo Genome Assembly for an Endangered Lemur Using Portable Nanopore Sequencing in Rural Madagascar. *Ecology and evolution*, 15(1), e70734.