

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>

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

Resource Type: software resource, software application, 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: 20260731T043221+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 [kravitz2](#) .

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.

Law STS, et al. (2025) Genome of tropical bed bug *Cimex hemipterus* (Cimicidae, Hemiptera) reveals tetraspanin expanded in bed bug ancestor. *Insect science*, 32(1), 42.

Kenney SM, et al. (2025) Genomic evolution of *Salmonella* Dublin in cattle and humans in the United States. *Applied and environmental microbiology*, 91(9), e0068925.

- Lee S, et al. (2025) Functional characterization of a novel plant growth-promoting rhizobacterium enhancing root growth and salt stress tolerance. *Scientific reports*, 15(1), 30405.
- Zhao Y, et al. (2025) Global soil antibiotic resistance genes are associated with increasing risk and connectivity to human resistome. *Nature communications*, 16(1), 7141.
- Periyasamy D, et al. (2025) Targeted syndromic next-generation sequencing panel for simultaneous detection of pathogens associated with bovine reproductive failure. *Journal of clinical microbiology*, 63(1), e0143324.
- Plaza-Diaz J, et al. (2025) Effect of a Novel Food Rich in Miraculin on the Intestinal Microbiome of Malnourished Patients with Cancer and Dysgeusia. *Nutrients*, 17(2).
- Büttner KA, et al. (2025) Evaluating methods for genome sequencing of *Chlamydia trachomatis* and other sexually transmitted bacteria directly from clinical swabs. *Microbial genomics*, 11(2).
- 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.
- 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.
- 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.