

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: NIGMS R01 GM118568;
NIGMS R35 GM130151;
NSF

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: 20260912T200513+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 1421 mentions in open access literature.

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

Zhou Z, et al. (2026) Integrative analysis of the mouse cecal microbiome across diet, age, and weight in the diverse BXD population. *Microbiome*, 14(1).

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.

Rosendal E, et al. (2026) Rapid drug resistance prediction in positive *Mycobacterium tuberculosis* clinical samples using an extensive targeted next-generation sequencing panel. *Emerging microbes & infections*, 15(1), 2627072.

Orr RJS, et al. (2026) Spatial and temporal patterns of public transit aerobiomes. *Microbiome*, 14(1), 64.

Omelchenko O, et al. (2026) Evolved populations of *Listeria monocytogenes* related to biofilm formation and biocide stress in the context of food production environment niches. *Microbial genomics*, 12(1).

Burlandy FM, et al. (2026) Rotavirus Outbreak Traced in Clinical, Environmental, and Food Matrices: Whole Genomic Characterization of an Equine-like G3P[8] Genotype. *Food and environmental virology*, 18(1), 7.

Zhang N, et al. (2026) Microbial characteristics and risk factors in PICU with freshwater drowning-associated pneumonia. *European journal of pediatrics*, 185(2), 127.

Lim FS, et al. (2026) No longer uncertain: the validation of tenebrionid insects as hosts of *Blattambidensovirus incertum*1 isolates by phylogeny and infection studies. *The Journal of general virology*, 107(2).

McCrory K, et al. (2026) Environmental Presence of *Burkholderia pseudomallei* at Military Sites in an Endemic Region: Implications for Future Deployments and Studies. *The American journal of tropical medicine and hygiene*, 114(3), 432.

Daryani NE, et al. (2026) Characterizing the gut virome in ulcerative colitis and crohn's disease: signatures of disease severity. *Virology journal*, 23(1), 46.

Peirson LE, et al. (2026) African carnivore gut bacterial diversity and composition are associated with sample condition but not storage technique. *Animal microbiome*, 8(1).

Consuegra-Asprilla JM, et al. (2026) Characterization of the vaginal microbiome and its metabolic potential in Colombian patients with recurrent vulvovaginal candidiasis. *Medical mycology*, 64(4).

Montes-Carretero LM, et al. (2026) Comparative fecal microbiome analysis of the endangered Volcano rabbit (*Romerolagus diazi*) reveals a microbial core in contrasting habitats of Central Mexico. *PloS one*, 21(3), e0343260.

Alvarado DA, et al. (2026) Effects of Soluble Corn Fiber Consumption on Executive Functions and Gut Microbiota in Middle to Older Age Adults: A Randomized Controlled Crossover Trial. *The Journal of nutrition*, 156(5), 101473.

Chen Q, et al. (2026) Kun-peng enables scalable and accurate pan-domain metagenomic classification. *Briefings in bioinformatics*, 27(2).

Ward B, et al. (2026) Association of nasopharyngeal *Dolosigranulum pigrum* and *Corynebacterium* species with post-acute sequelae of SARS-CoV-2 in a longitudinal cohort. *Microbiology spectrum*, 14(4), e0231325.

Valenzuela-Diaz S, et al. (2026) Impact of phage enrichment on the observed infant gut phageome. *Microbiology spectrum*, 14(5), e0215325.

Muhee A, et al. (2026) Whole genome sequencing reveals environmental pathogen misidentification and potential for cross-phylum antimicrobial resistance gene transfer in bovine mastitis: a pilot genomic study. *BMC veterinary research*, 22(1).

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.

Sun Y, et al. (2026) The impact of the timing of mNGS-guided antibiotic adjustment on clinical outcomes in ICU patients with severe community-acquired pneumonia: a retrospective study. *Annals of clinical microbiology and antimicrobials*, 25(1), 12.