

Resource Summary Report

Generated by [Kravitz](#) on Sep 10, 2026

Kraken

RRID:SCR_005484

Type: Tool

Proper Citation

Kraken (RRID:SCR_005484)

Resource Information

URL: <http://www.ebi.ac.uk/research/enright/software/kraken>

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Description: A set of software tools (Reaper, Tally and Sequence Imp) designed to streamline the analysis of next-generation sequencing data. Although designed with small RNA sequence analysis in mind the tools can be used to address issues facing next-generation sequencing in general.

Abbreviations: Kraken

Synonyms: Kraken: A set of tools for quality control and analysis of high-throughput sequence data

Resource Type: software resource

Defining Citation: [PMID:23816787](#)

Keywords: adapter trimming, algorithm, next-generation sequencing, pipeline, rnaseq, sequencing

Availability: Apache License

Resource Name: Kraken

Resource ID: SCR_005484

Alternate IDs: OMICS_01057

Record Creation Time: 20220129T080230+0000

Record Last Update: 20260905T132536+0000

Ratings and Alerts

No rating or validation information has been found for Kraken.

No alerts have been found for Kraken.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1906 mentions in open access literature.

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

Huang KK, et al. (2026) Mutational Signatures and Clonal Hematopoiesis in Intestinal Metaplasia across Countries with Varying Stomach Cancer Incidence. *Cancer discovery*, 16(3), 497.

Cunningham-Oakes E, et al. (2026) Implementing portable, real-time 16S rRNA sequencing in the healthcare sector enhances antimicrobial stewardship. *EBioMedicine*, 129, 106317.

Schmitt AM, et al. (2026) Spatially-resolved subtype progression reveals metabolic vulnerabilities in pancreatic ductal adenocarcinoma. *Molecular cancer*, 25(1).

Boutin S, et al. (2026) Evaluating Seqstant LiveGene Analysis in real-time assessment of metagenomic next-generation sequencing (mNGS) data from respiratory samples. *Infection*, 54(2), 707.

Tamadonfar KO, et al. (2026) The Yeh pilus adhesin is equipped with an α -helical flap motif, which contributes to pectin adherence. *Science advances*, 12(2), eadz1301.

Ajumobi V, et al. (2026) Population structure, antimicrobial resistance, and virulence factors of diabetic foot-associated *Escherichia coli*. *Microbiology spectrum*, 14(2), e0283725.

Camargo M, et al. (2026) Exploring anatomical and geographical drivers of the microbiota in wild capybaras (*Hydrochoerus hydrochaeris*): Baseline Data for zoonotic risk assessment. *PloS one*, 21(3), e0345409.

Jian X, et al. (2026) Large-scale profiling of blood microbial signatures in patients with Parkinson's disease and its association with disease progression: a cross-sectional study. *EBioMedicine*, 126, 106224.

Silva JM, et al. (2026) HYMET: a hybrid metagenomic pipeline for accurate and efficient taxonomic classification. *GigaScience*, 15.

Dong J, et al. (2026) *Lactobacillus rhamnosus* LRA05 mitigates DSS-Induced colitis via boosting beneficial gut microbiota and facilitating CD4⁺Foxp3⁺ Treg differentiation. *BMC microbiology*, 26(1).

Zhang N, et al. (2026) Host and geography shape microbial communities in Kenyan mosquitoes: insights from metatranscriptomics. *mSystems*, 11(2), e0142725.

Marcinkowska K, et al. (2026) Insights Into Sequences of Viral and Bacterial Origin in the Metatranscriptome of *Centaurea cyanus* L. Susceptible and Resistant to Acetolactate Synthase (ALS)-Inhibiting Herbicides. *Environmental microbiology reports*, 18(1), e70287.

Kolenda R, et al. (2026) Copper is an intestinal habitat filter affecting the gut microbiota interactions with *Salmonella Typhimurium*. *Microbiome*, 14(1).

Khodadad CLM, et al. (2026) Microbial community characterization of multi-crop growouts in the XROOTS aeroponic-hydroponic system on the International Space Station. *Frontiers in microbiomes*, 5, 1779816.

Bie??o K, et al. (2026) Exploring the *Tenebrio molitor* gut microbiota response to LDPE and PET: putative genetic indicators and methodological insights. *Frontiers in microbiology*, 17, 1746922.

Neil M, et al. (2026) New isolates from the 1970s to early 2000s provide insights into the evolution of *Acinetobacter baumannii* international clone 2 and its resistome. *Microbial genomics*, 12(7).

?epi? A, et al. (2026) Host genetics shapes the recovery of the gut microbiome after antibiotic treatment: the role of the blood group related B4galnt2 gene. *mSystems*, 11(5), e0164025.

Mahmood S, et al. (2026) Blood feeding triggers the terminal differentiation of precursor cells in tick salivary glands. *Science advances*, 12(13), eaec7620.

Ballard R, et al. (2026) Bloodmeal analysis via COI-targeted DNA capture and enrichment identifies non-cattle hosts of *Amblyomma variegatum* on St. Croix, US Virgin Islands. *Parasites & vectors*, 19(1).

Ndhlovu K, et al. (2026) Elucidating the Functional and Taxonomic Diversity of Soil Microbial Communities From Three Commercial Soybean Farms in South Africa. *Environmental microbiology reports*, 18(3), e70360.