

Resource Summary Report

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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: 20260801T190254+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 1711 mentions in open access literature.

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

Buiatte ABG, et al. (2026) Genomic epidemiology reveals statewide dispersal of clinical Shiga toxin-producing *Escherichia coli* and their antimicrobial resistome. *Microbiology spectrum*, 14(1), e0095625.

Visser M, et al. (2026) *Neisseria gonorrhoeae* Sequence Types During an Increase of Gonorrhea Among Young Women in 2022 and 2023 in the Netherlands. *Open forum infectious diseases*, 13(1), ofaf767.

Li Y, et al. (2026) A machine-learning informed circulating microbial DNA signature for early diagnosis of esophageal adenocarcinoma. *Gut microbes*, 18(1), 2604334.

Dockman RL, et al. (2026) Improved chromosome-level genome assembly of the American cockroach, *Periplaneta americana*. *G3 (Bethesda, Md.)*, 16(1).

Sia CM, et al. (2025) Distinct adaptation and epidemiological success of different genotypes within *Salmonella enterica* serovar Dublin. *eLife*, 13.

Durán-Fuentes JA, et al. (2025) Repeatome diversity in sea anemone genomics (Cnidaria: Actiniaria) based on the Actiniaria-REPlib library. *BMC genomics*, 26(1), 473.

Villette R, et al. (2025) Human gut microbiome gene co-expression network reveals a loss in taxonomic and functional diversity in Parkinson's disease. *NPJ biofilms and microbiomes*, 11(1), 142.

Li W, et al. (2025) Benchmarking and optimizing qualitative and quantitative pipelines in environmental metatranscriptomics using mixture controlling experiments. *ISME communications*, 5(1), ycaf090.

Villette R, et al. (2025) Integrated multi-omics highlights alterations of gut microbiome functions in prodromal and idiopathic Parkinson's disease. *Microbiome*, 13(1), 200.

Roush SM, et al. (2025) Shared genomic features of HIV+ diffuse large B-cell lymphoma in two African cohorts. *Scientific reports*, 15(1), 24599.

Nishisaka Y, et al. (2025) Molecular characterization of feline caliciviruses isolated from several adult cats with atypical infection showing severe flu-like symptoms on a remote

island in Ehime, Japan. *Virus research*, 353, 199535.

Dawson RA, et al. (2025) Carbon monoxide-oxidising *Pseudomonadota* on volcanic deposits. *Environmental microbiome*, 20(1), 12.

Tång Hallbäck E, et al. (2025) Evaluation of nationwide analysis surveillance for methicillin-resistant *Staphylococcus aureus* within Genomic Medicine Sweden. *Microbial genomics*, 11(1).

Morey-León G, et al. (2025) Global epidemiology of *Mycobacterium tuberculosis* lineage 4 insights from Ecuadorian genomic data. *Scientific reports*, 15(1), 3823.

Yao H, et al. (2025) Gut Microbiota-Mediated hsa_circ_0126925 Targets BCAA Metabolic Enzyme BCAT2 to Exacerbate Colorectal Cancer Progression. *Molecular cancer research : MCR*, 23(3), 202.

Wang X, et al. (2025) Gut-liver translocation of pathogen *Klebsiella pneumoniae* promotes hepatocellular carcinoma in mice. *Nature microbiology*, 10(1), 169.

Peng Q, et al. (2025) Modeling bacterial interactions uncovers the importance of outliers in the coastal lignin-degrading consortium. *Nature communications*, 16(1), 639.

Zamunér CFC, et al. (2025) Evolution and spread of *Xanthomonas citri* subsp. *citri* in the São Paulo, Brazil, citrus belt inferred from 758 novel genomes. *Microbial genomics*, 11(1).

Soni J, et al. (2025) Protocol for investigating intracellular microbial diversity using single-cell RNA-seq in immune cells of SARS-CoV-2-positive and recovered patients. *STAR protocols*, 6(1), 103546.

Haldorsen BC, et al. (2025) Import of global high-risk clones is the primary driver of carbapenemase-producing *Pseudomonas aeruginosa* in Norway. *Journal of medical microbiology*, 74(1).