

Resource Summary Report

Generated by [dkNET](#) on Sep 19, 2026

IDseq

RRID:SCR_019038

Type: Tool

Proper Citation

IDseq (RRID:SCR_019038)

Resource Information

URL: <https://idseq.net/>

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Description: Open source cloud based pipeline and analysis service for metagenomic pathogen detection and monitoring. Hypothesis free global software platform that helps scientists identify pathogens in metagenomic sequencing data. IDseq Portal accepts raw mNGS data, performs host and quality filtration steps, then executes assembly based alignment pipeline which results in assignment of reads and contigs to taxonomic categories.

Synonyms: Infectious Disease Sequencing Platform, IDseq Portal

Resource Type: analysis service resource, data or information resource, organism-related portal, portal, production service resource, service resource, topical portal

Defining Citation: [DOI:10.1101/2020.04.07.030551](https://doi.org/10.1101/2020.04.07.030551)

Keywords: Metagenomic pathogen detection, metagenomic pathogen monitoring, identify pathogens, metagenomic sequencing data, data analysis

Funding: Chan Zuckerberg Initiative

Availability: Free, Freely available

Resource Name: IDseq

Resource ID: SCR_019038

Alternate URLs: <https://github.com/chanzuckerberg/idseq-workflows/wiki>

License: MIT License

Record Creation Time: 20220129T080343+0000

Ratings and Alerts

No rating or validation information has been found for IDseq.

No alerts have been found for IDseq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 30 mentions in open access literature.

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

Kincer LP, et al. (2026) Neurosymptomatic Cerebrospinal Fluid Escape Is a Central Nervous System-Focused Form of Antiretroviral Therapy Treatment Failure. Open forum infectious diseases, 13(1), ofaf659.

Nelson A, et al. (2026) Spatiotemporal distribution and diversity of pathogenic Vibrio species in estuarine recreational waters of southeast Louisiana. Applied and environmental microbiology, 92(3), e0194425.

Beuker C, et al. (2026) Spontaneous cervical artery dissection is associated with a distinct peripheral immune cell signature. PloS one, 21(1), e0340592.

Allana R, et al. (2025) Validation of polyester nasal swabs for post-mortem SARS-CoV-2 diagnosis in Karachi, Pakistan: a prospective surveillance analysis. Journal of global health, 15, 04288.

Pomari E, et al. (2025) Unexpected Pediatric Cluster of Enterovirus C105, Verona, Italy. Viruses, 17(2).

Kabir F, et al. (2025) Evaluating the burden of respiratory tract infections among mortality cases in Karachi, Pakistan: a post-pandemic surveillance analysis. Journal of global health, 15, 04198.

Shamim U, et al. (2024) Functional metagenomics highlights varied infection states with dynamics of pathogens and antibiotic resistance in lower respiratory tract infections. Heliyon, 10(19), e38380.

Kebabonye K, et al. (2023) Determining Potential Link between Environmental and Clinical Isolates of Cryptococcus neoformans/Cryptococcus gattii Species Complexes Using Phenotypic and Genotypic Characterisation. Mycobiology, 51(6), 452.

Khan M, et al. (2023) Significance of wastewater surveillance in detecting the prevalence of SARS-CoV-2 variants and other respiratory viruses in the community - A multi-site

evaluation. One health (Amsterdam, Netherlands), 16, 100536.

Ergunay K, et al. (2022) Metagenomic Investigation of Ticks From Kenyan Wildlife Reveals Diverse Microbial Pathogens and New Country Pathogen Records. *Frontiers in microbiology*, 13, 932224.

Ghosh A, et al. (2022) Classification of COVID19 Patients Using Robust Logistic Regression. *Journal of statistical theory and practice*, 16(4), 67.

Tsitsiklis A, et al. (2022) Lower respiratory tract infections in children requiring mechanical ventilation: a multicentre prospective surveillance study incorporating airway metagenomics. *The Lancet. Microbe*, 3(4), e284.

Acharya CB, et al. (2022) Viral Load Among Vaccinated and Unvaccinated, Asymptomatic and Symptomatic Persons Infected With the SARS-CoV-2 Delta Variant. *Open forum infectious diseases*, 9(5), ofac135.

McCauley KE, et al. (2022) Heritable vaginal bacteria influence immune tolerance and relate to early-life markers of allergic sensitization in infancy. *Cell reports. Medicine*, 3(8), 100713.

Kalantar KL, et al. (2022) Integrated host-microbe plasma metagenomics for sepsis diagnosis in a prospective cohort of critically ill adults. *Nature microbiology*, 7(11), 1805.

Tana MM, et al. (2022) Transcriptomic profiling of blood from autoimmune hepatitis patients reveals potential mechanisms with implications for management. *PloS one*, 17(3), e0264307.

Tsitsiklis A, et al. (2021) Impaired immune signaling and changes in the lung microbiome precede secondary bacterial pneumonia in COVID-19. *Research square*.

Lawley B, et al. (2021) Rapid Response to SARS-CoV-2 in Aotearoa New Zealand: Implementation of a Diagnostic Test and Characterization of the First COVID-19 Cases in the South Island. *Viruses*, 13(11).

Nessler JN, et al. (2021) Canine Meningoencephalitis of Unknown Origin-The Search for Infectious Agents in the Cerebrospinal Fluid via Deep Sequencing. *Frontiers in veterinary science*, 8, 645517.

Kim KW, et al. (2021) Respiratory viral co-infections among SARS-CoV-2 cases confirmed by virome capture sequencing. *Scientific reports*, 11(1), 3934.