# Resource Summary Report

Generated by dkNET on May 12, 2025

## PathSeq

RRID:SCR_005203
Type: Tool

### Proper Citation

PathSeq (RRID:SCR_005203)

### Resource Information

**URL:** http://www.broadinstitute.org/software/pathseq/

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**Description:** A computational tool for the identification and analysis of microbial sequences in high-throughput human sequencing data that is designed to work with large numbers of sequencing reads in a scalable manner. This process is composed of a subtractive phase in which input reads are subtracted by alignment to human reference sequences, and an analytic phase in which the remaining reads are aligned to microbial reference sequences (viral, fungal, bacterial, archaeal) and de novo assembled. PathSeq is currently available in a cloud computing environment via Amazon Web Services The typical approach one would take to pathogen discovery with PathSeq: RNA or DNA is extracted from the tissue of interest and sequencing libraries are constructed to be run on the next-generation DNA sequencing platform of choice. The resulting sequence data is run through the PathSeq pipeline in a cloud computing environment. PathSeq reports potential microbes in the sequence data as well as the complete set of reads that could not be identified as human or microbial sequences.

**Abbreviations:** PathSeq

**Synonyms:** PathSeq: Pathogen Discovery

**Resource Type:** software resource

**Defining Citation:** PMID:21552235

**Keywords:** virus, microbe, pathogen, dna, rna, next-generation sequencing

**Funding:**

**Availability:** Acknowledgement requested, Account required, (for Amazon Web Services and you will need to pay for the AWS resource time)

**Resource Name:** PathSeq

**Resource ID:** SCR_005203

**Alternate IDs:** OMICS_00221

**Record Creation Time:** 20220129T080228+0000

**Record Last Update:** 20250420T014246+0000

## Ratings and Alerts

No rating or validation information has been found for PathSeq.

No alerts have been found for PathSeq.

## Data and Source Information

**Source:** SciCrunch Registry

## Usage and Citation Metrics

We found 52 mentions in open access literature.

**Listed below are recent publications.** The full list is available at dkNET.

Aggarwal N, et al. (2025) Insights into expression and localization of HPV16 LCR-associated transcription factors and association with LCR activity in HNSCC. Molecular therapy. Oncology, 33(1), 200926.

Ou L, et al. (2024) Helicobacter pylori infection facilitates cell migration and potentially impact clinical outcomes in gastric cancer. Heliyon, 10(17), e37046.

Nikitina A, et al. (2024) Viral Transcript and Tumor Immune Microenvironment-Based Transcriptomic Profiling of HPV-Associated Head and Neck Squamous Cell Carcinoma Identifies Subtypes Associated with Prognosis. Viruses, 17(1).

Kim JH, et al. (2024) Hemangiosarcoma Cells Promote Conserved Host-derived Hematopoietic Expansion. Cancer research communications, 4(6), 1467.

Robinson W, et al. (2024) Identification of intracellular bacteria from multiple single-cell RNA-seq platforms using CSI-Microbes. Science advances, 10(27), eadj7402.

Xu W, et al. (2024) Elucidating the genotoxicity of Fusobacterium nucleatum-secreted mutagens in colorectal cancer carcinogenesis. Gut pathogens, 16(1), 50.

Taylor KD, et al. (2024) Metagenomic Study of the MESA: Detection of Gemella Morbillorum and Association With Coronary Heart Disease. Journal of the American Heart Association, 13(19), e035693.

Cornish AJ, et al. (2024) The genomic landscape of 2,023 colorectal cancers. Nature, 633(8028), 127.

Tian Q, et al. (2024) Application and Comparison of Machine Learning and Database-Based Methods in Taxonomic Classification of High-Throughput Sequencing Data. Genome biology and evolution, 16(5).

Phumiphanjarphak W, et al. (2024) Entourage: all-in-one sequence analysis software for genome assembly, virus detection, virus discovery, and intrasample variation profiling. BMC bioinformatics, 25(1), 222.

Younginger BS, et al. (2023) Enrichment of oral-derived bacteria in inflamed colorectal tumors and distinct associations of Fusobacterium in the mesenchymal subtype. Cell reports. Medicine, 4(2), 100920.

Zhou P, et al. (2023) The pan-cancer landscape of abnormal DNA methylation and intratumor microorganisms. Neoplasia (New York, N.Y.), 37, 100882.

Duggan WP, et al. (2023) Increased Fusobacterium tumoural abundance affects immunogenicity in mucinous colorectal cancer and may be associated with improved clinical outcome. Journal of molecular medicine (Berlin, Germany), 101(7), 829.

Sambruni G, et al. (2023) Location and condition based reconstruction of colon cancer microbiome from human RNA sequencing data. Genome medicine, 15(1), 32.

Huang KK, et al. (2023) Spatiotemporal genomic profiling of intestinal metaplasia reveals clonal dynamics of gastric cancer progression. Cancer cell, 41(12), 2019.

Galeano Niño JL, et al. (2023) INVADEseq to identify cell-adherent or invasive bacteria and the associated host transcriptome at single-cell-level resolution. Nature protocols, 18(11), 3355.

Tran TDB, et al. (2023) The microbial community dynamics of cocaine sensitization in two behaviorally divergent strains of collaborative cross mice. Genes, brain, and behavior, e12845.

Wu X, et al. (2023) Taxonomic and functional profiling of fecal metagenomes for the early detection of colorectal cancer. Frontiers in oncology, 13, 1218056.

Binh Tran TD, et al. (2023) Microbial glutamate metabolism predicts intravenous cocaine self-administration in diversity outbred mice. Neuropharmacology, 226, 109409.

Morrow JD, et al. (2023) Hepatitis C and HIV detection by blood RNA-sequencing in cohort of smokers. Scientific reports, 13(1), 1357.