Resource Summary Report

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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

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: 20260905T132531+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 66 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Silver NL, et al. (2026) Intratumoral bacteria are immunosuppressive and promote immunotherapy resistance in head and neck squamous cell carcinoma. Nature cancer, 7(1), 80.

Piotrowski SL, et al. (2026) Herpesvirus genome integration in whole-genome sequences of dementia and control cohorts. Alzheimer's & dementia : the journal of the Alzheimer's Association, 22(3), e71047.

Deneuve S, et al. (2026) Mutational signature-based classification uncovers emerging oral cancer subtypes with distinct molecular patterns. International journal of oral science, 18(1).

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.

Sheehan DH, et al. (2025) Altered Bacteria Abundance Is Associated With Outcomes in Head and Neck Squamous Cell Carcinoma. Otolaryngology--head and neck surgery : official journal of American Academy of Otolaryngology-Head and Neck Surgery, 173(2), 420.

Hajjar J, et al. (2025) Gut dysbiosis patterns in CVID patients with noninfectious complications observed in a germ-free mouse model through fecal microbiota transplantation. Journal of human immunity, 1(1).

Shitara K, et al. (2025) Nivolumab plus chemotherapy or ipilimumab in gastroesophageal cancer: exploratory biomarker analyses of a randomized phase 3 trial. Nature medicine, 31(5), 1519.

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.

Karta J, et al. (2025) Fusobacterium nucleatum interacts with cancer-associated fibroblasts to promote colorectal cancer. The EMBO journal, 44(19), 5375.

Booth ME, et al. (2025) The relationship between the gastric cancer microbiome and clinicopathological factors: a metagenomic investigation from the 100,000 genomes project and The Cancer Genome Atlas. Gastric cancer : official journal of the International Gastric Cancer Association and the Japanese Gastric Cancer Association, 28(3), 358.

Hyeon DY, et al. (2025) Proteogenomic characterization of molecular and cellular targets for treatment-resistant subtypes in locally advanced cervical cancers. Molecular cancer, 24(1), 77.

Kerr TD, et al. (2025) HPV status impacts oncobacteria abundance and prognostic relevance in head and neck squamous cell carcinoma. Oncogene, 44(26), 2217.

Choi I, et al. (2025) Secretory IgA dysfunction underlies poor prognosis in Fusobacterium-infected colorectal cancer. Gut microbes, 17(1), 2528428.

Kumar R, et al. (2025) Race-related host and microbe transcriptomic signatures in triple-negative breast cancer. NPJ breast cancer, 11(1), 87.

Lin Y, et al. (2025) Dissecting the role of gut microbiota heterogeneity in the onset of chronic lung diseases. AMB Express, 15(1), 119.

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).

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

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.

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).

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