

Resource Summary Report

Generated by [NIF](#) on Oct 20, 2026

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: 20261017T202607+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 have not found any literature mentions for this resource.