

Resource Summary Report

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VirusSeq

RRID:SCR_005206

Type: Tool

Proper Citation

VirusSeq (RRID:SCR_005206)

Resource Information

URL: <http://odin.mdacc.tmc.edu/~xsu1/VirusSeq.html>

Proper Citation: VirusSeq (RRID:SCR_005206)

Description: An algorithmic software tool for detecting known viruses and their integration sites using next-generation sequencing of human cancer tissue. VirusSeq takes FASTQ files (paired-end reads) as input.

Abbreviations: VirusSeq

Resource Type: software resource

Keywords: next-generation sequencing, virus, integration site, cancer tissue, genome, rna-seq, whole genome sequencing, fastq, paired-end read, bio.tools

Related Condition: Cancer

Resource Name: VirusSeq

Resource ID: SCR_005206

Alternate IDs: OMICS_00227, biotools:virusseq

Alternate URLs: <https://bio.tools/virusseq>

Record Creation Time: 20220129T080228+0000

Record Last Update: 20260829T182209+0000

Ratings and Alerts

No rating or validation information has been found for VirusSeq.

No alerts have been found for VirusSeq.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 23 mentions in open access literature.

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

Nowicki M, et al. (2025) HPV-KITE: sequence analysis software for rapid HPV genotype detection. Briefings in bioinformatics, 26(2).

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. Briefings in bioinformatics, 26(2).

Gill EE, et al. (2024) The Canadian VirusSeq Data Portal & Duotang: open resources for SARS-CoV-2 viral sequences and genomic epidemiology. ArXiv.

Ghosh S, et al. (2022) Combined TRIP13 and Aurora Kinase Inhibition Induces Apoptosis in Human Papillomavirus-Driven Cancers. Clinical cancer research : an official journal of the American Association for Cancer Research, 28(20), 4479.

Mohsin H, et al. (2021) Potential role of viral metagenomics as a surveillance tool for the early detection of emerging novel pathogens. Archives of microbiology, 203(3), 865.

L??hmussaar K, et al. (2021) Patient-derived organoids model cervical tissue dynamics and viral oncogenesis in cervical cancer. Cell stem cell, 28(8), 1380.

Lu X, et al. (2020) Epigenetic age acceleration of cervical squamous cell carcinoma converged to human papillomavirus 16/18 expression, immunoactivation, and favourable prognosis. Clinical epigenetics, 12(1), 23.

Song H, et al. (2019) Interpretation of EBV infection in pan-cancer genome considering viral life cycle: LiEB (Life cycle of Epstein-Barr virus). Scientific reports, 9(1), 3465.

Kosugi S, et al. (2019) Comprehensive evaluation of structural variation detection algorithms for whole genome sequencing. Genome biology, 20(1), 117.

Huang C, et al. (2019) Development and validation of radiomic signatures of head and neck squamous cell carcinoma molecular features and subtypes. EBioMedicine, 45, 70.

Locati LD, et al. (2019) Mining of Self-Organizing Map Gene-Expression Portraits Reveals Prognostic Stratification of HPV-Positive Head and Neck Squamous Cell Carcinoma. Cancers, 11(8).

Hu X, et al. (2019) HBV Integration-mediated Cell Apoptosis in HepG2.2.15. Journal of Cancer, 10(17), 4142.

Lu X, et al. (2019) Immune Signature-Based Subtypes of Cervical Squamous Cell Carcinoma Tightly Associated with Human Papillomavirus Type 16 Expression, Molecular

Features, and Clinical Outcome. *Neoplasia* (New York, N.Y.), 21(6), 591.

Nooij S, et al. (2018) Overview of Virus Metagenomic Classification Methods and Their Biological Applications. *Frontiers in microbiology*, 9, 749.

Santander CG, et al. (2017) STEAK: A specific tool for transposable elements and retrovirus detection in high-throughput sequencing data. *Virus evolution*, 3(2), vex023.

Yoo S, et al. (2017) A pilot systematic genomic comparison of recurrence risks of hepatitis B virus-associated hepatocellular carcinoma with low- and high-degree liver fibrosis. *BMC medicine*, 15(1), 214.

Kalu NN, et al. (2017) Genomic characterization of human papillomavirus-positive and -negative human squamous cell cancer cell lines. *Oncotarget*, 8(49), 86369.

Singh R, et al. (2017) Analysis of the whole transcriptome from gingivo-buccal squamous cell carcinoma reveals deregulated immune landscape and suggests targets for immunotherapy. *PloS one*, 12(9), e0183606.

Park KJ, et al. (2016) Adeno-Associated Virus 2-Mediated Hepatocellular Carcinoma is Very Rare in Korean Patients. *Annals of laboratory medicine*, 36(5), 469.

Chitsazzadeh V, et al. (2016) Cross-species identification of genomic drivers of squamous cell carcinoma development across preneoplastic intermediates. *Nature communications*, 7, 12601.