

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: 20260801T190257+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 [RRID](#) .

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).

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.

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

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

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.

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.

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.

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

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.