Resource Summary Report

Generated by NIF on Apr 17, 2025

VirusFinder

RRID:SCR_005205
Type: Tool

Proper Citation

VirusFinder (RRID:SCR_005205)

Resource Information

URL: http://bioinfo.mc.vanderbilt.edu/VirusFinder/

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Description: Software tool for efficient and accurate detection of viruses and their integration sites in host genomes through next generation sequencing data. Specifically, it detects virus infection, co-infection with multiple viruses, virus integration sites in host genomes, as well as mutations in the virus genomes. It also facilitates virus discovery by reporting novel contigs, long sequences assembled from short reads that map neither to the host genome nor to the genomes of known viruses. VirusFinder 2 works with both paired-end and single-end data, unlike the previous 1.x versions that accepted only paired-end reads. The types of NGS data that VirusFinder 2 can deal with include whole genome sequencing (WGS), whole transcriptome sequencing (RNA-Seq), targeted sequencing data such as whole exome sequencing (WES) and ultra-deep amplicon sequencing.

Abbreviations: VirusFinder

Resource Type: software resource

Defining Citation: PMID:23717618

Keywords: next-generation sequencing, virus, integration site, genome, mutation, virus genome, contig, paired-end, single-end, whole genome sequencing, whole transcriptome sequencing, rna-seq, targeted sequencing, whole exome sequencing, ultra-deep amplicon sequencing

Related Condition: Viral infection

Funding:

Resource Name: VirusFinder

Resource ID: SCR_005205

Alternate IDs: OMICS_00226

Record Creation Time: 20220129T080228+0000

Record Last Update: 20250410T065235+0000

Ratings and Alerts

No rating or validation information has been found for VirusFinder.

No alerts have been found for VirusFinder.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 14 mentions in open access literature.

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

Watson-Lazowski A, et al. (2022) Loss of PROTEIN TARGETING TO STARCH 2 has variable effects on starch synthesis across organs and species. Journal of experimental botany, 73(18), 6367.

Mwesigwa S, et al. (2021) Unmapped exome reads implicate a role for Anelloviridae in childhood HIV-1 long-term non-progression. NPJ genomic medicine, 6(1), 24.

Patel K, et al. (2021) Whole-Exome Sequencing Analysis of Oral Squamous Cell Carcinoma Delineated by Tobacco Usage Habits. Frontiers in oncology, 11, 660696.

Kawamoto M, et al. (2020) Identification of Characteristic Genomic Markers in Human Hepatoma HuH-7 and Huh7.5.1-8 Cell Lines. Frontiers in genetics, 11, 546106.

Zhang W, et al. (2019) Mutational signatures and the genomic landscape of betel quid chewing-associated tongue carcinoma. Cancer medicine, 8(2), 701.

Heinrich MJ, et al. (2019) Endogenous double-stranded Alu RNA elements stimulate IFN-responses in relapsing remitting multiple sclerosis. Journal of autoimmunity, 100, 40.

Maliogka VI, et al. (2018) Recent Advances on Detection and Characterization of Fruit Tree

Viruses Using High-Throughput Sequencing Technologies. Viruses, 10(8).

Webster P, et al. (2018) Subclonal mutation selection in mouse lymphomagenesis identifies known cancer loci and suggests novel candidates. Nature communications, 9(1), 2649.

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.

Gruber MAM, et al. (2017) Single-stranded RNA viruses infecting the invasive Argentine ant, Linepithema humile. Scientific reports, 7(1), 3304.

Forster M, et al. (2015) Vy-PER: eliminating false positive detection of virus integration events in next generation sequencing data. Scientific reports, 5, 11534.

Wang Q, et al. (2015) VERSE: a novel approach to detect virus integration in host genomes through reference genome customization. Genome medicine, 7(1), 2.

Gannon OM, et al. (2015) No association between HPV positive breast cancer and expression of human papilloma viral transcripts. Scientific reports, 5, 18081.