

Resource Summary Report

Generated by [Kravitz](#) on Sep 14, 2026

VirusHunter

RRID:SCR_001198

Type: Tool

Proper Citation

VirusHunter (RRID:SCR_001198)

Resource Information

URL: <http://pathology.wustl.edu/VirusHunter/>

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Description: A fully automated and modular software package for mining sequence data to identify sequences of microbial origin. The pipeline was optimized for analysis of data generated by the Roche/454 next-generation sequencing platform but can be applied to longer sequences (Sanger sequencing data or assembled contigs) as well. Microbial sequences are identified on the basis of BLAST alignments and the taxonomic classification of the reference sequence(s) to which a read is aligned. Viruses are the focal point of VirusHunter as released, but it can be easily modified to generate parallel outputs for bacterial or parasitic species. To date, VirusHunter has been applied to thousands of specimens, including human, animal and environmental samples, resulting in the detection of many known and novel viruses.

Abbreviations: VirusHunter

Resource Type: software resource

Defining Citation: [PMID:24167629](#)

Keywords: virus, next-generation sequencing, roche, 454, taxonomic classification, alignment, bio.tools

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: VirusHunter

Resource ID: SCR_001198

Alternate IDs: biotools:virushunter, OMICS_02153

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

Record Creation Time: 20220129T080206+0000

Record Last Update: 20260912T195521+0000

Ratings and Alerts

No rating or validation information has been found for VirusHunter.

No alerts have been found for VirusHunter.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We have not found any literature mentions for this resource.