

# Resource Summary Report

Generated by [RRID](#) on Apr 28, 2025

## VirusHunter

RRID:SCR\_001198

Type: Tool

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### Proper Citation

VirusHunter (RRID:SCR\_001198)

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### Resource Information

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

**Proper Citation:** VirusHunter (RRID:SCR\_001198)

**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

**Funding:**

**Availability:** GNU General Public License, v3 or later, Acknowledgement requested

**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:** 20250420T014023+0000

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## Ratings and Alerts

No rating or validation information has been found for VirusHunter.

No alerts have been found for VirusHunter.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We have not found any literature mentions for this resource.