

Resource Summary Report

Generated by [kravitz2](#) on Aug 1, 2026

VIROME

RRID:SCR_004362

Type: Tool

Proper Citation

VIROME (RRID:SCR_004362)

Resource Information

URL: <http://virome.diagcomputing.org/#view=home>

Proper Citation: VIROME (RRID:SCR_004362)

Description: A web-application designed for scientific exploration of metagenome sequence data collected from viral assemblages occurring within a number of different environmental contexts. The VIROME informatics pipeline focuses on the classification of predicted open-reading frames (ORFs) from viral metagenomes. The portal allows you to submit your viral metagenome to be processed through the VIROME analysis pipeline, and enable you to investigate your data via the VIROME user interface., THIS RESOURCE IS NO LONGER IN SERVICE. Documented on September 16,2025.

Abbreviations: VIROME

Synonyms: Viral Informatics Resource for Metagenome Exploration, Viral Informatics Resource for Metagenome Exploration - VIROME

Resource Type: data analysis service, data or information resource, database, service resource, production service resource, analysis service resource

Defining Citation: [PMID:23407591](#)

Keywords: open-reading frame, metagenome, virus, environment, sequence, library, genetic, polymorphism, orfan, environmental sequencing, shotgun metagenomics, viral ecology, function, taxonomy, peptide, blast

Funding: Gordon and Betty Moore Foundation ;
NSF award 0959894

Availability: THIS RESOURCE IS NO LONGER IN SERVICE

Resource Name: VIROME

Resource ID: SCR_004362

Alternate IDs: OMICS_01506

Record Creation Time: 20220129T080224+0000

Record Last Update: 20260801T190240+0000

Ratings and Alerts

No rating or validation information has been found for VIROME.

No alerts have been found for VIROME.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 22 mentions in open access literature.

Listed below are recent publications. The full list is available at [kravitz2](#) .

Norton AM, et al. (2025) Deformed wing virus genotypes A and B do not elicit immunologically different responses in naïve honey bee hosts. *Insect molecular biology*, 34(1), 33.

Verdonckt TW, et al. (2023) Identification and Profiling of a Novel Bombyx mori latent virus Variant Acutely Infecting Helicoverpa armigera and Trichoplusia ni. *Viruses*, 15(5).

Du S, et al. (2023) Highly host-linked viromes in the built environment possess habitat-dependent diversity and functions for potential virus-host coevolution. *Nature communications*, 14(1), 2676.

Kuo YW, et al. (2022) Artificial microRNA guide strand selection from duplexes with no mismatches shows a purine-rich preference for virus- and non-virus-based expression vectors in plants. *Plant biotechnology journal*, 20(6), 1069.

Walsh E, et al. (2022) Culex Mosquito Piwi4 Is Antiviral against Two Negative-Sense RNA Viruses. *Viruses*, 14(12).

Wang X, et al. (2021) Prevalence of a Novel Bunyavirus in Tea Tussock Moth Euproctis pseudoconspersa (Lepidoptera: Lymantriidae). *Journal of insect science (Online)*, 21(4).

Roux S, et al. (2021) Ecology and molecular targets of hypermutation in the global microbiome. *Nature communications*, 12(1), 3076.

McAllister SM, et al. (2021) Aerobic and anaerobic iron oxidizers together drive denitrification and carbon cycling at marine iron-rich hydrothermal vents. *The ISME journal*, 15(5), 1271.

Coffey MJ, et al. (2020) The intestinal virome in children with cystic fibrosis differs from healthy controls. *PloS one*, 15(5), e0233557.

Wang L, et al. (2019) Short-term persistence precedes pathogenic infection: Infection kinetics of cricket paralysis virus in silkworm-derived Bm5 cells. *Journal of insect physiology*, 115, 1.

Santos D, et al. (2019) Generation of Virus- and dsRNA-Derived siRNAs with Species-Dependent Length in Insects. *Viruses*, 11(8).

Nasko DJ, et al. (2019) CRISPR Spacers Indicate Preferential Matching of Specific Virioplankton Genes. *mBio*, 10(2).

Santos D, et al. (2018) Insights into RNAi-based antiviral immunity in Lepidoptera: acute and persistent infections in *Bombyx mori* and *Trichoplusia ni* cell lines. *Scientific reports*, 8(1), 2423.

Segobola J, et al. (2018) Exploring Viral Diversity in a Unique South African Soil Habitat. *Scientific reports*, 8(1), 111.

Woodhouse RM, et al. (2018) Chromatin Modifiers SET-25 and SET-32 Are Required for Establishment but Not Long-Term Maintenance of Transgenerational Epigenetic Inheritance. *Cell reports*, 25(8), 2259.

Dietrich I, et al. (2017) The Antiviral RNAi Response in Vector and Non-vector Cells against Orthobunyaviruses. *PLoS neglected tropical diseases*, 11(1), e0005272.

Remnant EJ, et al. (2017) A Diverse Range of Novel RNA Viruses in Geographically Distinct Honey Bee Populations. *Journal of virology*, 91(16).

Tangherlini M, et al. (2016) Assessing viral taxonomic composition in benthic marine ecosystems: reliability and efficiency of different bioinformatic tools for viral metagenomic analyses. *Scientific reports*, 6, 28428.

Adriaenssens EM, et al. (2016) Metaviromics of Namib Desert Salt Pans: A Novel Lineage of Haloarchaeal Salterproviruses and a Rich Source of ssDNA Viruses. *Viruses*, 8(1).

Kolliopoulou A, et al. (2015) Transcriptome analysis of *Bombyx mori* larval midgut during persistent and pathogenic cytoplasmic polyhedrosis virus infection. *PloS one*, 10(3), e0121447.