

# Resource Summary Report

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## Virus Variation

RRID:SCR\_013790

Type: Tool

### Proper Citation

Virus Variation (RRID:SCR\_013790)

### Resource Information

**URL:** <http://www.ncbi.nlm.nih.gov/genome/viruses/variation/>

**Proper Citation:** Virus Variation (RRID:SCR\_013790)

**Description:** A repository which supports the search, retrieval, and display of large virus sequence data sets concerning the viruses of Dengue, West Nile, and Influenza. Users can search sequences based on a number of biological and clinical criteria and selected sequences can be downloaded or analyzed using a variety of web-based tools and displays. Virus Variation is an extension of NCBI's Influenza Virus Resource.

**Synonyms:** NCBI Virus Variation

**Resource Type:** data resource

**Keywords:** repository, virus sequence, Dengue, West Nile, Influenza, data set

**Availability:** Free, Public

**Resource Name:** Virus Variation

**Resource ID:** SCR\_013790

**Record Creation Time:** 20220129T080318+0000

**Record Last Update:** 20260801T190454+0000

### Ratings and Alerts

No rating or validation information has been found for Virus Variation.

No alerts have been found for Virus Variation.

### Data and Source Information

## Usage and Citation Metrics

We found 7 mentions in open access literature.

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

Koul M, et al. (2025) VITALdb: to select the best viroinformatics tools for a desired virus or application. Briefings in bioinformatics, 26(2).

Cabral KMDS, et al. (2023) Accuracy of a raw saliva-based COVID-19 RT-LAMP diagnostic assay. The Brazilian journal of infectious diseases : an official publication of the Brazilian Society of Infectious Diseases, 27(4), 102790.

Castells M, et al. (2020) Phylogenetic Analyses of Rotavirus A from Cattle in Uruguay Reveal the Circulation of Common and Uncommon Genotypes and Suggest Interspecies Transmission. Pathogens (Basel, Switzerland), 9(7).

Hatcher EL, et al. (2017) Virus Variation Resource - improved response to emergent viral outbreaks. Nucleic acids research, 45(D1), D482.

O'Leary NA, et al. (2016) Reference sequence (RefSeq) database at NCBI: current status, taxonomic expansion, and functional annotation. Nucleic acids research, 44(D1), D733.

Wada Y, et al. (2016) Directional and reoccurring sequence change in zoonotic RNA virus genomes visualized by time-series word count. Scientific reports, 6, 36197.

Furuse Y, et al. (2015) Conservation of nucleotide sequences for molecular diagnosis of Middle East respiratory syndrome coronavirus, 2015. International journal of infectious diseases : IJID : official publication of the International Society for Infectious Diseases, 40, 25.