

Resource Summary Report

Generated by [RRID](#) on Aug 15, 2026

V-pipe

RRID:SCR_025399

Type: Tool

Proper Citation

V-pipe (RRID:SCR_025399)

Resource Information

URL: <https://cbg-ethz.github.io/V-pipe/>

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Description: Software pipeline for analysis of next-generation sequencing data derived from intra-host and environmental viral populations. Designed for analysing NGS data of short viral genomes. Used for assessing viral genetic diversity from high-throughput data.

Resource Type: data processing software, workflow, software application, data analysis software, training material, data or information resource, software resource, source code, sequence analysis software, narrative resource

Defining Citation: [PMID:33471068](#)

Keywords: viral sequencing data, next-generation sequencing data, viral populations, analysing NGS data, short viral genomes.

Funding: Swiss Institute of Bioinformatics

Availability: Free, Available for download, Freely available

Resource Name: V-pipe

Resource ID: SCR_025399

License: Apache-2.0

Record Creation Time: 20240608T053238+0000

Record Last Update: 20260815T042900+0000

Ratings and Alerts

No rating or validation information has been found for V-pipe.

No alerts have been found for V-pipe.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Fuhrmann L, et al. (2024) V-pipe 3.0: a sustainable pipeline for within-sample viral genetic diversity estimation. GigaScience, 13.