

# Resource Summary Report

Generated by [nidm-terms](#) on Jul 28, 2026

## HaploClique

RRID:SCR\_002353

Type: Tool

### Proper Citation

HaploClique (RRID:SCR\_002353)

### Resource Information

**URL:** <https://github.com/armintoeper/haploclique>

**Proper Citation:** HaploClique (RRID:SCR\_002353)

**Description:** Software providing a computational approach to reconstruct the structure of a viral quasispecies from next-generation sequencing data as obtained from bulk sequencing of mixed virus samples.

**Resource Type:** software resource

**Defining Citation:** [PMID:24675810](#)

**Keywords:** standalone software

**Resource Name:** HaploClique

**Resource ID:** SCR\_002353

**Alternate IDs:** OMICS\_03442

**Record Creation Time:** 20220129T080212+0000

**Record Last Update:** 20260725T190521+0000

### Ratings and Alerts

No rating or validation information has been found for HaploClique.

No alerts have been found for HaploClique.

### Data and Source Information

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

## Usage and Citation Metrics

We found 5 mentions in open access literature.

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

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

Posada-C??spedes S, et al. (2021) V-pipe: a computational pipeline for assessing viral genetic diversity from high-throughput data. Bioinformatics (Oxford, England), 37(12), 1673.

Baaijens JA, et al. (2017) De novo assembly of viral quasispecies using overlap graphs. Genome research, 27(5), 835.

Karagiannis K, et al. (2017) Separation and assembly of deep sequencing data into discrete sub-population genomes. Nucleic acids research, 45(19), 10989.

Seifert D, et al. (2016) A Comprehensive Analysis of Primer IDs to Study Heterogeneous HIV-1 Populations. Journal of molecular biology, 428(1), 238.