

Resource Summary Report

Generated by [RRID](#) on Aug 2, 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: 20260801T190146+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 [RRID](#) .

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.