Resource Summary Report

Generated by dkNET on Apr 29, 2025

HaploClique

RRID:SCR_002353
Type: Tool

Proper Citation

HaploClique (RRID:SCR_002353)

Resource Information

URL: https://github.com/armintoepfer/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

Funding:

Resource Name: HaploClique

Resource ID: SCR_002353

Alternate IDs: OMICS_03442

Record Creation Time: 20220129T080212+0000

Record Last Update: 20250420T014101+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 dkNET.

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

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

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

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

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