

Resource Summary Report

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

ShoRAH

RRID:SCR_005211

Type: Tool

Proper Citation

ShoRAH (RRID:SCR_005211)

Resource Information

URL: <http://www.bsse.ethz.ch/cbg/software/shorah>

Proper Citation: ShoRAH (RRID:SCR_005211)

Description: A software package that allows for inference about the structure of a population from a set of short sequence reads as obtained from ultra-deep sequencing of a mixed sample. The package contains programs that support mapping of reads to a reference genome, correcting sequencing errors by locally clustering reads in small windows of the alignment, reconstructing a minimal set of global haplotypes that explain the reads, and estimating the frequencies of the inferred haplotypes.

Abbreviations: ShoRAH

Synonyms: Short Reads Assembly into Haplotypes, ShoRAH - Short Reads Assembly into Haplotypes

Resource Type: software resource

Defining Citation: [PMID:21521499](#)

Keywords: linux, mac os x, windows, next-generation sequencing, c++, python, perl, structure, population, short sequence read, haplotype, bio.tools

Availability: GNU General Public License, v3

Resource Name: ShoRAH

Resource ID: SCR_005211

Alternate IDs: biotools:shorah, OMICS_00231

Alternate URLs: <https://bio.tools/shorah>

Record Creation Time: 20220129T080229+0000

Ratings and Alerts

No rating or validation information has been found for ShoRAH.

No alerts have been found for ShoRAH.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 35 mentions in open access literature.

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

Walker MR, et al. (2025) Temporal dynamics of viral fitness and the adaptive immune response in HCV infection. *eLife*, 13.

Gabín-García LB, et al. (2025) Functional and evolutionary diversification of luciferase genes in *Metridia lucens*. *Research square*.

Sutcliffe SG, et al. (2024) Tracking SARS-CoV-2 variants of concern in wastewater: an assessment of nine computational tools using simulated genomic data. *Microbial genomics*, 10(5).

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

Fuhrmann L, et al. (2024) VILOCA: sequencing quality-aware viral haplotype reconstruction and mutation calling for short-read and long-read data. *NAR genomics and bioinformatics*, 6(4), lqae152.

Höfler T, et al. (2024) Evolutionary Dynamics of Accelerated Antiviral Resistance Development in Hypermutator Herpesvirus. *Molecular biology and evolution*, 41(7).

Woodford L, et al. (2022) Quantitative and Qualitative Changes in the Deformed Wing Virus Population in Honey Bees Associated with the Introduction or Removal of *Varroa destructor*. *Viruses*, 14(8).

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.

Deng ZL, et al. (2021) Evaluating assembly and variant calling software for strain-resolved analysis of large DNA viruses. *Briefings in bioinformatics*, 22(3).

- Morga B, et al. (2021) Genomic Diversity of the Ostreid Herpesvirus Type 1 Across Time and Location and Among Host Species. *Frontiers in microbiology*, 12, 711377.
- Gaube G, et al. (2020) Characterization of HIV-1 diversity in various compartments at the time of primary infection by ultradeep sequencing. *Scientific reports*, 10(1), 2409.
- Wille M, et al. (2020) Evolutionary genetics of canine respiratory coronavirus and recent introduction into Swedish dogs. *Infection, genetics and evolution : journal of molecular epidemiology and evolutionary genetics in infectious diseases*, 82, 104290.
- Trinks J, et al. (2020) The genetic variability of hepatitis B virus subgenotype F1b precore/core gene is related to the outcome of the acute infection. *Virus research*, 277, 197840.
- Kobayashi K, et al. (2020) Heparan sulfate attachment receptor is a major selection factor for attenuated enterovirus 71 mutants during cell culture adaptation. *PLoS pathogens*, 16(3), e1008428.
- Janiak M, et al. (2019) Hepatitis C virus (HCV) genotype 1b displays higher genetic variability of hypervariable region 1 (HVR1) than genotype 3. *Scientific reports*, 9(1), 12846.
- Walker MR, et al. (2019) Clearance of hepatitis C virus is associated with early and potent but narrowly-directed, Envelope-specific antibodies. *Scientific reports*, 9(1), 13300.
- Henningsson R, et al. (2019) DISSEQT-DISTribution-based modeling of SEQuence space Time dynamics. *Virus evolution*, 5(2), vez028.
- Hathaway NJ, et al. (2018) SeekDeep: single-base resolution de novo clustering for amplicon deep sequencing. *Nucleic acids research*, 46(4), e21.
- Steyer A, et al. (2018) Intrahost Norovirus Evolution in Chronic Infection Over 5 Years of Shedding in a Kidney Transplant Recipient. *Frontiers in microbiology*, 9, 371.
- Caraballo Cortes K, et al. (2018) Next-generation sequencing analysis of a cluster of hepatitis C virus infections in a haematology and oncology center. *PloS one*, 13(3), e0194816.