

Resource Summary Report

Generated by [RRID](#) on Aug 2, 2026

QuasiRecomb

RRID:SCR_008812

Type: Tool

Proper Citation

QuasiRecomb (RRID:SCR_008812)

Resource Information

URL: <https://github.com/armintoeper/QuasiRecomb/releases>

Proper Citation: QuasiRecomb (RRID:SCR_008812)

Description: A jumping hidden Markov model that describes the generation of the viral quasispecies and a method to infer its parameters by analysing next generation sequencing data.

Abbreviations: QuasiRecomb

Synonyms: QuasiRecomb - Probabilistic inference of viral Quasispecies

Resource Type: software resource

Defining Citation: [PMID:23383997](#)

Keywords: haplotype, next-generation sequencing, virus, parameter, bio.tools

Resource Name: QuasiRecomb

Resource ID: SCR_008812

Alternate IDs: OMICS_00229, biotools:quasirecomb

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

Record Creation Time: 20220129T080249+0000

Record Last Update: 20260801T190353+0000

Ratings and Alerts

No rating or validation information has been found for QuasiRecomb.

No alerts have been found for QuasiRecomb.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 32 mentions in open access literature.

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

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

Dong X, et al. (2025) Using minor variant genomes and machine learning to study the genome biology of SARS-CoV-2 over time. *Nucleic acids research*, 53(4).

Tsai YY, et al. (2024) The molecular epidemiology of a dengue virus outbreak in Taiwan: population wide versus infrapopulation mutation analysis. *PLoS neglected tropical diseases*, 18(6), e0012268.

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

Dong X, et al. (2023) Analysis of SARS-CoV-2 Population Genetics from Samples Associated with Huanan Market and Early Cases Identifies Substitutions Associated with Future Variants of Concern. *Viruses*, 15(8).

Dong X, et al. (2023) Linked Mutations in the Ebola Virus Polymerase Are Associated with Organ Specific Phenotypes. *Microbiology spectrum*, 11(2), e0415422.

Caraballo Cortés K, et al. (2023) T-Cell Exhaustion in HIV-1/Hepatitis C Virus Coinfection Is Reduced After Successful Treatment of Chronic Hepatitis C. *Open forum infectious diseases*, 10(11), ofad514.

Richner J, et al. (2023) SARS-CoV-2 Bottlenecks and Tissue-Specific Adaptation in the Central Nervous System. *Research square*.

Samer S, et al. (2022) Blockade of TGF- β signaling reactivates HIV-1/SIV reservoirs and immune responses in vivo. *JCI insight*, 7(21).

Watson RJ, et al. (2021) Dose-Dependent Response to Infection with Ebola Virus in the Ferret Model and Evidence of Viral Evolution in the Eye. *Journal of virology*, 95(24), e0083321.

Bosworth A, et al. (2021) Analysis of an Ebola virus disease survivor whose host and viral markers were predictive of death indicates the effectiveness of medical countermeasures and supportive care. *Genome medicine*, 13(1), 5.

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

Afridi SQ, et al. (2021) Prolonged norovirus infections correlate to quasispecies evolution resulting in structural changes of surface-exposed epitopes. *iScience*, 24(7), 102802.

Scutari R, et al. (2021) Impact of Analytical Treatment Interruption on Burden and Diversification of HIV Peripheral Reservoir: A Pilot Study. *Viruses*, 13(7).

Serrão de Andrade AA, et al. (2021) Testing the genomic stability of the Brazilian yellow fever vaccine strain using next-generation sequencing data. *Interface focus*, 11(4), 20200063.

Al Khatib HA, et al. (2020) Inter- Versus Intra-Host Sequence Diversity of pH1N1 and Associated Clinical Outcomes. *Microorganisms*, 8(1).

Andreu-Moreno I, et al. (2020) Collective Viral Spread Mediated by Virion Aggregates Promotes the Evolution of Defective Interfering Particles. *mBio*, 11(1).

Dong X, et al. (2020) Variation around the dominant viral genome sequence contributes to viral load and outcome in patients with Ebola virus disease. *Genome biology*, 21(1), 238.

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.

Bellocchi MC, et al. (2019) NS5A Gene Analysis by Next Generation Sequencing in HCV Nosocomial Transmission Clusters of HCV Genotype 1b Infected Patients. *Cells*, 8(7).