Resource Summary Report

Generated by NIF on Sep 19, 2026

V-Phaser 2

RRID:SCR_005212
Type: Tool

Proper Citation

V-Phaser 2 (RRID:SCR_005212)

Resource Information

URL: http://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/v-phaser-2

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Description: A software tool to call variants in genetically heterogeneous populations from ultra-deep sequence data. It combines information regarding the covariation (i.e. phasing) between observed variants to increase sensitivity and an expectation maximization algorithm that iteratively recalibrates base quality scores to increase specificity. V-Phaser can reliably detect rare variants in diverse populations that occur at frequencies of 1%. V-Phaser 2 is a complete rewrite of the original V-Phaser. It contains a new model for length polymorphisms (indels) and incorporates paired end read information in its phasing model. The data access and probability computation sections of the code have also been highly optimized, resulting in substantial improvements in running time and memory usage.

Abbreviations: V-Phaser 2

Resource Type: software resource

Defining Citation: PMID:24088188

Keywords: variant, polymorphism, indel, virus, bio.tools

Funding: NIAID

Availability: Free for academic use, Non-commercial, Http://www.broadinstitute.org/scientific-community/science/projects/viral-genomics/viral-genomics-software-license-v-phaser-2

Resource Name: V-Phaser 2

Resource ID: SCR_005212

Alternate IDs: biotools:v-phaser, OMICS_00232

Alternate URLs: https://bio.tools/v-phaser

Record Creation Time: 20220129T080229+0000

Record Last Update: 20260919T195049+0000

Ratings and Alerts

No rating or validation information has been found for V-Phaser 2.

No alerts have been found for V-Phaser 2.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 2 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Collins DR, et al. (2021) Functional impairment of HIV-specific CD8+ T??cells precedes aborted spontaneous control of viremia. Immunity, 54(10), 2372.

Thomson E, et al. (2016) Comparison of Next-Generation Sequencing Technologies for Comprehensive Assessment of Full-Length Hepatitis C Viral Genomes. Journal of clinical microbiology, 54(10), 2470.