Resource Summary Report

Generated by NIF on May 15, 2025

vcflib

RRID:SCR_001231
Type: Tool

Proper Citation

vcflib (RRID:SCR_001231)

Resource Information

URL: https://github.com/ekg/vcflib

Proper Citation: vcflib (RRID:SCR_001231)

Description: A C++ library for parsing and manipulating Variant Call Format (VCF) files, and many command-line utilities. The API provides a quick and extremely permissive method to read and write VCF files. Extensions and applications of the library provided in the included utilities (*.cpp) comprise the vast bulk of the library's utility for most users.

Abbreviations: vcflib

Resource Type: software resource, software toolkit, software library

Keywords: c++, sequence variation, genomic variation, bio.tools

Funding:

Availability: MIT License

Resource Name: vcflib

Resource ID: SCR_001231

Alternate IDs: biotools:vcflib, OMICS_02112

Alternate URLs: https://bio.tools/vcflib, https://sources.debian.org/src/libvcflib-dev/

Old URLs: https://sources.debian.org/src/libvcflib-dev/

Record Creation Time: 20220129T080206+0000

Record Last Update: 20250514T061200+0000

Ratings and Alerts

No rating or validation information has been found for vcflib.

No alerts have been found for vcflib.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 104 mentions in open access literature.

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

Jayaprasad S, et al. (2024) Orthopteran Neo-Sex Chromosomes Reveal Dynamics of Recombination Suppression and Evolution of Supergenes. Molecular ecology, 33(23), e17567.

Henningsen EC, et al. (2024) A high-resolution haplotype collection uncovers somatic hybridization, recombination and intercontinental movement in oat crown rust. PLoS genetics, 20(11), e1011493.

Bernos TA, et al. (2024) Widespread admixture blurs population structure and confounds Lake Trout (Salvelinus namaycush) conservation even in the genomic era. Scientific reports, 14(1), 30838.

Yang H, et al. (2024) Characterization of the sex determining region and development of a molecular sex identification method in a Salangid fish. BMC genomics, 25(1), 1120.

Chen J, et al. (2024) From sub-Saharan Africa to China: Evolutionary history and adaptation of Drosophila melanogaster revealed by population genomics. Science advances, 10(16), eadh3425.

Sigeman H, et al. (2024) The rate of W chromosome degeneration across multiple avian neo-sex chromosomes. Scientific reports, 14(1), 16548.

Blom MPK, et al. (2024) Hybridization in birds-of-paradise: Widespread ancestral gene flow despite strong sexual selection in a lek-mating system. iScience, 27(7), 110300.

Al-Yazeedi T, et al. (2024) Overexpression and nonsynonymous mutations of UDP-glycosyltransferases are potentially associated with pyrethroid resistance in Anopheles funestus. Genomics, 116(2), 110798.

Unneberg P, et al. (2024) Ecological genomics in the Northern krill uncovers loci for local adaptation across ocean basins. Nature communications, 15(1), 6297.

Platt RN, et al. (2024) Genomic data reveal a north-south split and introgression history of blood fluke (Schistosoma haematobium) populations from across Africa. bioRxiv : the preprint server for biology.

Durak MR, et al. (2023) Genome-Wide Discovery of Structural Variants Reveals Distinct Variant Dynamics for Two Closely Related Monilinia Species. Genome biology and evolution, 15(6).

Alkemade JA, et al. (2023) Attack of the clones: Population genetics reveals clonality of Colletotrichum lupini, the causal agent of lupin anthracnose. Molecular plant pathology, 24(6), 616.

Whitney JL, et al. (2023) Genomic evidence indicates small island-resident populations and sex-biased behaviors of Hawaiian reef Manta Rays. BMC ecology and evolution, 23(1), 31.

Sperschneider J, et al. (2023) Nuclear exchange generates population diversity in the wheat leaf rust pathogen Puccinia triticina. Nature microbiology, 8(11), 2130.

Bassano I, et al. (2023) Evaluation of variant calling algorithms for wastewater-based epidemiology using mixed populations of SARS-CoV-2 variants in synthetic and wastewater samples. Microbial genomics, 9(4).

Maclary ET, et al. (2023) An allelic series at the EDNRB2 locus controls diverse piebalding patterns in the domestic pigeon. PLoS genetics, 19(10), e1010880.

Lundberg M, et al. (2023) Inversions maintain differences between migratory phenotypes of a songbird. Nature communications, 14(1), 452.

Heaven T, et al. (2023) Dose-Dependent Genetic Resistance to Azole Fungicides Found in the Apple Scab Pathogen. Journal of fungi (Basel, Switzerland), 9(12).

Kloch A, et al. (2023) Cytokine gene polymorphism and parasite susceptibility in free-living rodents: Importance of non-coding variants. PloS one, 18(1), e0258009.

Kant S, et al. (2023) Gre factors help Salmonella adapt to oxidative stress by improving transcription elongation and fidelity of metabolic genes. PLoS biology, 21(4), e3002051.