

Resource Summary Report

Generated by T1D on Sep 4, 2026

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 library, software resource, software toolkit

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

Availability: Free, Available for download, Freely available

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: 20260903T235750+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 129 mentions in open access literature.

Listed below are recent publications. The full list is available at [T1D](#).

Ushtanit A, et al. (2026) A Case of Transmission of Bedaquiline- and Linezolid-Resistant Tuberculosis. *International journal of molecular sciences*, 27(11).

Tensen L, et al. (2026) Reduced Genetic Load and Inbreeding in Reintroduced African Wild Dogs Reflect the Benefits of Admixture. *Molecular ecology*, 35(12), e70424.

Hulsey CD, et al. (2026) Divergence at the IRX gene cluster underlies extreme trophic polymorphism in a cichlid fish (*Herichthys minckleyi*). *Communications biology*, 9(1).

Limia CG, et al. (2026) Sequential, chromosome-specific glutamine synthetase double knockout with Cas-CLOVER establishes enhanced CHO platforms for cell line development. *Biotechnology progress*, 42(2), e70113.

Ghosh S, et al. (2026) Machine learning method for the prediction of Bedaquiline-resistant *Mycobacterium tuberculosis*. *Life science alliance*, 9(7).

Ni A, et al. (2025) Identifying candidate genetic variants for egg number by analyzing over 1,000 fully sequenced layers. *GigaScience*, 14.

Zanconato G, et al. (2025) Refining prognostic stratification of atypical meningiomas: significance of chromosome 1p deletion and brain invasion. *Acta neuropathologica communications*, 13(1), 50.

Li Y, et al. (2025) Biosurveillance of Invasive Southern Corn Rust: Insights Into Recent Migration Patterns and Virulence Variation. *Molecular plant pathology*, 26(10), e70159.

Platt li RN, et al. (2025) Genomic data reveal a north-south split and introgression history of blood fluke populations across Africa. *Nature communications*, 16(1), 3508.

Qiu Y, et al. (2025) Origins, Dispersal, and Impact: Bidirectional Introgression Between Chinese and European Pig Populations. *Advanced science (Weinheim, Baden-Wurttemberg, Germany)*, 12(22), e2416573.

Zimenkov D, et al. (2025) High Prevalence of *atpE* Mutations in Bedaquiline-Resistant *Mycobacterium tuberculosis* Isolates, Russia. *Emerging infectious diseases*, 31(3), 525.

Schiffer AM, et al. (2025) A comparison of short- and long-read whole genome sequencing for microbial pathogen epidemiology. *bioRxiv : the preprint server for biology*.

Liu Y, et al. (2025) Neuronal detection triggers systemic digestive shutdown in response to adverse food sources in *Caenorhabditis elegans*. *eLife*, 14.

Schiffer AM, et al. (2025) A comparison of short- and long-read whole-genome sequencing for microbial pathogen epidemiology. *mSystems*, 10(12), e0142625.

Mekonnen AM, et al. (2025) Variant-aware Cas-OFFinder: web-based in silico variant-aware potential off-target site identification for genome editing applications. *Nucleic acids research*, 53(W1), W118.

Tsushima A, et al. (2025) k-mer-based GWAS reveals a candidate avirulence gene and structural variation in *Puccinia triticina* linked to gain of Lr20 virulence. *BMC genomics*, 26(1), 1076.

Truskey S, et al. (2025) Non-Random Mortality in an Experimental Oyster Restoration. *Evolutionary applications*, 18(7), e70128.

Everitt T, et al. (2025) Unexpectedly low recombination rates and presence of hotspots in termite genomes. *Genome research*, 35(5), 1124.

Stuart OP, et al. (2025) Purging of Highly Deleterious Mutations Through an Extreme Bottleneck. *Molecular biology and evolution*, 42(4).

Berg R, et al. (2025) Peripheral Budding Following Range Expansion Explains Diversity and Distribution of One-Sided Livebearing Fish. *Molecular ecology*, 34(16), e70023.