

Resource Summary Report

Generated by [SPARC SAWG](#) on Sep 19, 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: 20260912T200007+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 [SPARC SAWG](#).

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.