vcflib
RRID:SCR_001231
Type: Tool

Proper Citation
vcflib (RRID:SCR_001231)

Resource Information

**URL:** [https://github.com/ekg/vcflib](https://github.com/ekg/vcflib)

**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.

**Resource Name:** vcflib

**Proper Citation:** vcflib (RRID:SCR_001231)

**Resource Type:** Resource, software resource, software toolkit, software library

**Keywords:** c++, sequence variation, genomic variation

**Resource ID:** SCR_001231

**Availability:** MIT License

**Website Status:** Last checked up

**Alternate IDs:** OMICS_02112

**Abbreviations:** vcflib

**Mentions Count:** 30

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 30 mentions in open access literature.

**Listed below are recent publications.** The full list is available at [FDI Lab - SciCrunch Infrastructure](#).


Cruz PRS, et al. (2019) Genetic comparison of sickle cell anaemia cohorts from Brazil and the United States reveals high levels of divergence. Scientific reports, 9(1), 10896.

Li F, et al. (2019) Emergence of the Ug99 lineage of the wheat stem rust pathogen through somatic hybridisation. Nature communications, 10(1), 5068.


Simbolo M, et al. (2018) Genetic alterations analysis in prognostic stratified groups identified
TP53 and ARID1A as poor clinical performance markers in intrahepatic cholangiocarcinoma. Scientific reports, 8(1), 7119.


