

Resource Summary Report

Generated by [nidm-terms](#) on Aug 22, 2026

vcfanno

RRID:SCR_024372

Type: Tool

Proper Citation

vcfanno (RRID:SCR_024372)

Resource Information

URL: <https://github.com/brentp/vcfanno>

Proper Citation: vcfanno (RRID:SCR_024372)

Description: Software tool for flexible annotation of genetic variants.Extracts and summarizes attributes from multiple annotation files and integrates annotations within INFO column of the original VCF file.

Resource Type: software application, software resource

Defining Citation: [PMID:27250555](#)

Keywords: annotation of genetic variants, extracts and summarizes attributes, multiple annotation files, integrates annotations, VCF file,

Availability: Free, Available for download, Freely available,

Resource Name: vcfanno

Resource ID: SCR_024372

Alternate IDs: OMICS_11863

Alternate URLs: <https://sources.debian.org/src/vcfanno/>

License: MIT License

Record Creation Time: 20230830T050217+0000

Record Last Update: 20260821T043113+0000

Ratings and Alerts

No rating or validation information has been found for vcfanno.

No alerts have been found for vcfanno.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 1 mentions in open access literature.

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

Smolen C, et al. (2026) Protocol for identifying genetic modifiers of phenotypes in individuals with disease-associated variants. STAR protocols, 7(2), 104546.