# Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 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:** 20260905T133318+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 PRECISE-TBI .

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