

# Resource Summary Report

Generated by [SPARC SAWG](#) on Aug 9, 2026

## Variant Prediction Tools Evaluation

RRID:SCR\_023314

Type: Tool

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### Proper Citation

Variant Prediction Tools Evaluation (RRID:SCR\_023314)

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### Resource Information

**URL:** <https://github.com/PedroBarbosa/VETA>

**Proper Citation:** Variant Prediction Tools Evaluation (RRID:SCR\_023314)

**Description:** Software tool that analyses performance of several variant prediction methods at different levels. Used to benchmark variant effect predictors from VCF files.

**Abbreviations:** VETA

**Synonyms:** Variant prEdiction Tools evAluation

**Resource Type:** software resource, software application, data analysis software, data processing software

**Defining Citation:** [DOI:10.3389/fcvm.2022.975478](https://doi.org/10.3389/fcvm.2022.975478)

**Keywords:** variant prediction, benchmark variant effect predictors, VCF files

**Availability:** Free, Available for download, Freely available

**Resource Name:** Variant Prediction Tools Evaluation

**Resource ID:** SCR\_023314

**Alternate URLs:** <https://samtools.github.io/hts-specs/VCFv4.2.pdf>

**License:** GNU GPL v3.0

**Record Creation Time:** 20230303T050211+0000

**Record Last Update:** 20260808T190251+0000

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### Ratings and Alerts

No rating or validation information has been found for Variant Prediction Tools Evaluation.

No alerts have been found for Variant Prediction Tools Evaluation.

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## Data and Source Information

**Source:** [SciCrunch Registry](#)

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## Usage and Citation Metrics

We found 2 mentions in open access literature.

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

Barbosa P, et al. (2022) Clinical significance of genetic variation in hypertrophic cardiomyopathy: comparison of computational tools to prioritize missense variants. Frontiers in cardiovascular medicine, 9, 975478.

Barbosa P, et al. (2022) Computational prediction of human deep intronic variation. GigaScience, 12.