

Resource Summary Report

Generated by [dkNET](#) on Aug 31, 2026

Variant Prediction Tools Evaluation

RRID:SCR_023314

Type: Tool

Proper Citation

Variant Prediction Tools Evaluation (RRID:SCR_023314)

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: data analysis software, data processing software, software application, software resource

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

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

License: GNU GPL v3.0

Record Creation Time: 20230303T050211+0000

Record Last Update: 20260829T182757+0000

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.

Data and Source Information

Source: [SciCrunch Registry](#)

Usage and Citation Metrics

We found 2 mentions in open access literature.

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

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.