Resource Summary Report

Generated by NIF on Aug 29, 2026

AutoGVP

RRID:SCR_026107
Type: Tool

Proper Citation

AutoGVP (RRID:SCR_026107)

Resource Information

URL: https://github.com/NCI-CGR/PLP_prediction_workflow/tree/autogvp

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Description: Software tool integrates ClinVar variant annotation with modified InterVar classification approach, based on American College of Medical Genetics-Association for Molecular Pathology guidelines, to output germline variant classification. Since AutoGVP input only requires VCF file, it can facilitate large-scale, clinically focused classification of germline sequence variants.

Synonyms: Automated Germline Variant Pathogenicity

Resource Type: software application, software resource, source code

Defining Citation: PMID:38426335

Keywords: germline variant classification, germline sequence variants, germline, sequence variants,

Funding: NCI R01CA237562;
NCI R03CA230366;
NCI R03CA287169

Availability: Free, Available for download, Freely available

Resource Name: AutoGVP

Resource ID: SCR_026107

Record Creation Time: 20241203T053255+0000

Record Last Update: 20260829T183419+0000

Ratings and Alerts

No rating or validation information has been found for AutoGVP.

No alerts have been found for AutoGVP.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 3 mentions in open access literature.

Listed below are recent publications. The full list is available at NIF .

Fiorica PN, et al. (2025) Germline Pathogenic DROSHA Variants Are Linked to Pineoblastoma and Wilms Tumor Predisposition. Clinical cancer research : an official journal of the American Association for Cancer Research, 31(8), 1491.

Kim J, et al. (2024) AutoGVP: a dockerized workflow integrating ClinVar and InterVar germline sequence variant classification. Bioinformatics (Oxford, England), 40(3).

Kim J, et al. (2023) AutoGVP: a dockerized workflow integrating ClinVar and InterVar germline sequence variant classification. bioRxiv : the preprint server for biology.