Resource Summary Report

Generated by PRECISE-TBI on Sep 8, 2026

VariantAnnotation

RRID:SCR_000074
Type: Tool

Proper Citation

VariantAnnotation (RRID:SCR_000074)

Resource Information

URL: http://www.bioconductor.org/packages/2.12/bioc/html/VariantAnnotation.html

Proper Citation: VariantAnnotation (RRID:SCR_000074)

Description: Software package to annotate variants, compute amino acid coding changes, and predict coding outcomes.

Abbreviations: VariantAnnotation

Synonyms: VariantAnnotation - Annotation of Genetic Variants

Resource Type: software resource

Defining Citation: PMID:24681907

Keywords: annotation, genetic variant, data import, genetics, high throughput sequencing, snp, sequencing

Availability: Free, Available for download, Freely available

Resource Name: VariantAnnotation

Resource ID: SCR_000074

Alternate IDs: OMICS_02073

License: Artistic License, v2

Record Creation Time: 20220129T080159+0000

Record Last Update: 20260905T132410+0000

Ratings and Alerts

No rating or validation information has been found for VariantAnnotation.

No alerts have been found for VariantAnnotation.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 9 mentions in open access literature.

Listed below are recent publications. The full list is available at PRECISE-TBI .

Simmons SK, et al. (2026) Experimental and computational methods for allelic imbalance analysis from single-nucleus RNA-seq data. Genome biology, 27(1).

Hu Q, et al. (2025) Circulating tumor DNA monitoring detects minimal residual disease and predicts outcomes in patients with esophageal adenocarcinoma or squamous cell carcinoma after esophagectomy. BJC reports, 3(1), 52.

Simmons SK, et al. (2024) Experimental and Computational Methods for Allelic Imbalance Analysis from Single-Nucleus RNA-seq Data. bioRxiv : the preprint server for biology.

Aribi HB, et al. (2024) NeuroVar: an open-source tool for the visualization of gene expression and variation data for biomarkers of neurological diseases. GigaByte (Hong Kong, China), 2024, gigabyte143.

Han J, et al. (2023) AmpSeqR: an R package for amplicon deep sequencing data analysis. F1000Research, 12, 327.

Dong R, et al. (2022) svaRetro and svaNUMT: modular packages for annotating retrotransposed transcripts and nuclear integration of mitochondrial DNA in genome sequencing data. GigaByte (Hong Kong, China), 2022, gigabyte70.

Chevalier A, et al. (2021) The Mutational Signature Comprehensive Analysis Toolkit (musicatk) for the Discovery, Prediction, and Exploration of Mutational Signatures. Cancer research, 81(23), 5813.

Stokowy T, et al. (2018) Genetic variation in 117 myelination-related genes in schizophrenia: Replication of association to lipid biosynthesis genes. Scientific reports, 8(1), 6915.

Bruna A, et al. (2016) A Biobank of Breast Cancer Explants with Preserved Intra-tumor Heterogeneity to Screen Anticancer Compounds. Cell, 167(1), 260.