

Resource Summary Report

Generated by [RRID](#) on Sep 10, 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 [RRID](#) .

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.