Resource Summary Report

Generated by NIF on Apr 22, 2025

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

Funding:

Availability: Artistic License, v2

Resource Name: VariantAnnotation

Resource ID: SCR_000074

Alternate IDs: OMICS_02073

Record Creation Time: 20220129T080159+0000

Record Last Update: 20250420T013927+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 4 mentions in open access literature.

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

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.