

Package: variants (via r-universe)

October 1, 2026

Title Annotating Genomic Variants

Version 1.37.0

Date 2025-07-18

Description Read and write VCF files. Identify structural location of variants and compute amino acid coding changes for non-synonymous variants. Use SIFT and PolyPhen database packages to predict consequence of amino acid coding changes.

Depends R (>= 3.3.0), GenomeInfoDb, VariantAnnotation, org.Hs.eg.db, TxDb.Hsapiens.UCSC.hg19.knownGene, BSgenome.Hsapiens.UCSC.hg19, PolyPhen.Hsapiens.dbSNP131

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Encoding UTF-8

LazyData true

VignetteBuilder knitr

biocViews ImmunoOncologyWorkflow, AnnotationWorkflow, Workflow

Suggests knitr, rmarkdown, BiocStyle

NeedsCompilation no

URL <https://bioconductor.org/help/workflows/variants/>

Config/pak/sysreqs

make libbz2-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository <https://bioc.r-universe.dev>

Date/Publication 2026-04-28 12:43:22 UTC

RemoteUrl <https://github.com/bioc/variants>

RemoteRef HEAD

RemoteSha 03e91df108131fbd3bcd923bc88ef4e389e71461