

Package: annotation (via r-universe)

October 1, 2026

Title Genomic Annotation Resources

Version 1.37.0

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Encoding UTF-8

Description Annotation resources make up a significant proportion of the Bioconductor project. And there are also a diverse set of online resources available which are accessed using specific packages. This walkthrough will describe the most popular of these resources and give some high level examples on how to use them.

Depends R (>= 3.3.0), GenomeInfoDb, VariantAnnotation, AnnotationHub, TxDb.Hsapiens.UCSC.hg19.knownGene, TxDb.Hsapiens.UCSC.hg38.knownGene, TxDb.Mmusculus.UCSC.mm10.ensGene, org.Hs.eg.db, org.Mm.eg.db, Homo.sapiens, BSgenome.Hsapiens.UCSC.hg19, biomaRt, BSgenome, TxDb.Athaliana.BioMart.plantmart22

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VignetteBuilder knitr

biocViews AnnotationWorkflow, Workflow

Workflow true

Suggests knitr, rmarkdown, BiocStyle

NeedsCompilation no

URL <http://bioconductor.org/packages/annotation>

Config/pak/sysreqs

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

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

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

RemoteRef HEAD

RemoteSha 77a311d7329a0be174a0ae1bb73462fed53287ba