

# Package: CAGEWorkflow (via r-universe)

October 1, 2026

**Type** Package

**Title** A step-by-step guide to analyzing CAGE data using R/Bioconductor

**Version** 1.29.0

**Description** Workflow for analyzing Cap Analysis of Gene Expression (CAGE) data using R/Bioconductor.

**License** GPL-3

**Encoding** UTF-8

**LazyData** FALSE

**Depends** R (>= 3.6.0), CAGEfightR, nanotubes

**Suggests** knitr, magick, rmarkdown, BiocStyle, BiocWorkflowTools, pheatmap, ggseqlogo, viridis, magrittr, ggforce, ggthemes, tidyverse, dplyr, GenomicRanges, SummarizedExperiment, GenomicFeatures, BiocParallel, InteractionSet, Gviz, DESeq2, limma, edgeR, statmod, BiasedUrn, sva, TFBSTools, motifmatchr, pathview, BSgenome.Mmusculus.UCSC.mm9, TxDb.Mmusculus.UCSC.mm9.knownGene, org.Mm.eg.db, JASPAR2016, png

**VignetteBuilder** knitr

**Workflow** true

**RoxygenNote** 7.1.2

**biocViews** GeneExpressionWorkflow, AnnotationWorkflow

**Config/pak/sysreqs** cmake libglpk-dev make libbz2-dev libicu-dev libjpeg-dev liblzma-dev libpng-dev libuv1-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

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

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**RemoteUrl** <https://github.com/bioc/CAGEWorkflow>

**RemoteRef** HEAD

**RemoteSha** dcacfde7dc04c715a0b0db4e3b1f5d9123048765