

# Package: RNAseq123 (via r-universe)

October 4, 2026

**Title** RNA-seq analysis is easy as 1-2-3 with limma, Glimma and edgeR

**Version** 1.36.0

**Date** 2024-04-26

**Description** R package that supports the F1000Research workflow article on RNA-seq analysis using limma, Glimma and edgeR by Law et al. (2016).

**Depends** R (>= 3.3.0), Glimma (>= 1.1.9), limma, edgeR, gplots, RColorBrewer, Mus.musculus, R.utils, TeachingDemos, statmod, BiocWorkflowTools

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** true

**VignetteBuilder** knitr

**biocViews** Workflow, GeneExpressionWorkflow, ImmunoOncologyWorkflow

**Suggests** knitr, rmarkdown, BiocStyle

**NeedsCompilation** no

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**URL** <https://f1000research.com/articles/5-1408/v3>

**Config/pak/sysreqs** cmake git make libbz2-dev libgit2-dev libicu-dev liblzma-dev libpng-dev libssh2-1-dev libuv1-dev libxml2-dev libssl-dev libx11-dev xz-utils zlib1g-dev

**Repository** Bioconductor 3.23

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**RemoteUrl** <https://github.com/bioc/RNAseq123>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** 09a5145cc779e0e9772311c8420378df63241031