

# Package: RnaSeqGeneEdgeRQL (via r-universe)

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**Title** Gene-level RNA-seq differential expression and pathway analysis using Rsubread and the edgeR quasi-likelihood pipeline

**Version** 1.36.0

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**Author** Yunshun Chen, Aaron Lun, Gordon Smyth

**Maintainer** Yunshun Chen <yuchen@wehi.edu.au>

**Description** This workflow package provides, through its vignette, a complete case study analysis of an RNA-Seq experiment using the Rsubread and edgeR packages. The workflow starts from read alignment and continues on to data exploration, to differential expression and, finally, to pathway analysis. The analysis includes publication quality plots, GO and KEGG analyses, and the analysis of a expression signature as generated by a prior experiment.

**Depends** R (>= 3.3.0), edgeR (>= 4.3.6), gplots, org.Mm.eg.db, GO.db, BiocStyle

**License** Artistic-2.0

**VignetteBuilder** knitr

**biocViews** Workflow, GeneExpressionWorkflow, ImmunoOncologyWorkflow

**Suggests** knitr, knitcitations, rmarkdown

**NeedsCompilation** no

**URL** <http://f1000research.com/articles/5-1438/v2>

**Config/pak/sysreqs** cmake make libpng-dev libuv1-dev libssl-dev zlib1g-dev

**Repository** Bioconductor 3.23

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

**RemoteRef** RELEASE\_3\_23

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