

# Package ‘RTCGA.rnaseq’

October 17, 2019

**Title** Rna-seq datasets from The Cancer Genome Atlas Project

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**Description** Package provides rna-seq datasets from The Cancer Genome Atlas Project for all cohorts types from <http://gdac.broadinstitute.org/>. Rna-seq data format is explained here <https://wiki.nci.nih.gov/display/TCGA/RNASeq+Version+2>. Data source is illumina hiseq Level 3 RSEM normalized expression data. Data from 2015-11-01 snapshot.

**License** GPL-2

**LazyData** TRUE

**Repository** Bioconductor

**BugReports** <https://github.com/RTCGA/RTCGA/issues>

**Depends** R (>= 3.2.0), RTCGA

**Suggests** knitr

**biocViews** Annotation Data

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 5.0.1

**git\_url** <https://git.bioconductor.org/packages/RTCGA.rnaseq>

**git\_branch** RELEASE\_3\_9

**git\_last\_commit** 3365f5f

**git\_last\_commit\_date** 2019-05-02

**Date/Publication** 2019-10-17

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`rnaseq`*rnaseq datasets from TCGA project*

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## Description

rnaseq data format is explained here <https://wiki.nci.nih.gov/display/TCGA/RNASeq+Version+2>. Package provides rnaseq datasets from The Cancer Genome Atlas Project for all cohorts types from <http://gdac.broadinstitute.org/>. Data were downloaded using [RTCGA-package](#) and contain snapshots for the date: 2015-11-01. The process is described here: <http://rtcg.github.io/RTCGA/>. Use cases, examples and information about datasets in **RTCGA** family can be found here: `browseVignettes("RTCGA")`. Data source is illumina hiseq Level 3 RSEM normalized expression data. Converting **RTCGA.rnaseq** datasets from `data.frames` to Bioconductor classes is explained here [convertTCGA](#).

## Usage

`ACC.rnaseq``BLCA.rnaseq``BRCA.rnaseq``CESC.rnaseq``CHOL.rnaseq``COAD.rnaseq``COADREAD.rnaseq``DLBC.rnaseq``ESCA.rnaseq``GBM.rnaseq``GBMLGG.rnaseq``HNSC.rnaseq``KICH.rnaseq``KIPAN.rnaseq``KIRC.rnaseq``KIRP.rnaseq``LAML.rnaseq``LGG.rnaseq`

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THYM.rnaseq

UCEC.rnaseq

UCS.rnaseq

UVM.rnaseq

**Details**

`browseVignettes("RTCGA")`

**Value**

Data frames with rnaseq data.

**Source**

<http://gdac.broadinstitute.org/>

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