

# Package ‘RTCGA.rnaseq’

January 30, 2025

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

**Version** 20151101.36.0

**Date** 2016-04-26

**Author** Marcin Kosinski <m.p.kosinski@gmail.com>

**Maintainer** Marcin Kosinski <m.p.kosinski@gmail.com>

**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

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

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

**Suggests** knitr, rmarkdown

**biocViews** Annotation Data

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 7.1.1

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

**git\_branch** RELEASE\_3\_20

**git\_last\_commit** 1922914

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.20

**Date/Publication** 2025-01-30

## Contents

rnaseq . . . . .	2
<b>Index</b>	<b>4</b>

---

rnaseq

*rnaseq datasets from TCGA project*

---

## 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** to Bioconductor datasets' format is explained here [convertTCGA](#).

## Usage

ACC.rnaseq

BLCA.rnaseq

BRCA.rnaseq

CESC.rnaseq

CHOL.rnaseq

COAD.rnaseq

COADREAD.rnaseq

DLBC.rnaseq

ESCA.rnaseq

GBMLGG.rnaseq

GBM.rnaseq

HNSC.rnaseq

KICH.rnaseq

KIPAN.rnaseq

KIRC.rnaseq

KIRP.rnaseq

LAML.rnaseq

LGG.rnaseq

LIHC.rnaseq

LUAD.rnaseq

LUSC.rnaseq

OV.rnaseq

PAAD.rnaseq

PCPG.rnaseq

PRAD.rnaseq

READ.rnaseq

SARC.rnaseq

SKCM.rnaseq

STAD.rnaseq

STES.rnaseq

TGCT.rnaseq

THCA.rnaseq

THYM.rnaseq

UCEC.rnaseq

UCS.rnaseq

UVM.rnaseq

**Details**

`browseVignettes("RTCGA")`

**Value**

Data frames with rnaseq data.

**Source**

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

# Index

## \* datasets

rnaseq, [2](#)

ACC.rnaseq (rnaseq), [2](#)

ACC.rnaseq, BLCA.rnaseq, BRCA.rnaseq, CESC.rnaseq, COAD.rnaseq, COADREAD.rnaseq, DLBC.rnaseq, ESCA.rnaseq, GBMLGG.rnaseq, HNSC.rnaseq, KICH.rnaseq, KIPAN.rnaseq, KIRC.rnaseq, KIRP.rnaseq, LAML.rnaseq, LGG.rnaseq, LIHC.rnaseq, LUAD.rnaseq, LUSC.rnaseq, OV.rnaseq, PAAD.rnaseq, PCPG.rnaseq, PRAD.rnaseq, READ.rnaseq, SARC.rnaseq, SKCM.rnaseq, STES.rnaseq, TGCT.rnaseq, THCA.rnaseq, THYM.rnaseq, UCEC.rnaseq, UCS.rnaseq, UVM.rnaseq, RTCGA-package, [2](#)

BLCA.rnaseq (rnaseq), [2](#)

BRCA.rnaseq (rnaseq), [2](#)

CESC.rnaseq (rnaseq), [2](#)

CHOL.rnaseq (rnaseq), [2](#)

COAD.rnaseq (rnaseq), [2](#)

COADREAD.rnaseq (rnaseq), [2](#)

convertTCGA, [2](#)

DLBC.rnaseq (rnaseq), [2](#)

ESCA.rnaseq (rnaseq), [2](#)

GBM.rnaseq (rnaseq), [2](#)

GBM.rnaseq, HNSC.rnaseq, KICH.rnaseq, KIPAN.rnaseq, KIRC.rnaseq, KIRP.rnaseq, LAML.rnaseq, LGG.rnaseq, LIHC.rnaseq, LUAD.rnaseq, LUSC.rnaseq, OV.rnaseq, PAAD.rnaseq, PCPG.rnaseq, PRAD.rnaseq, READ.rnaseq, SARC.rnaseq, SKCM.rnaseq, STES.rnaseq, TGCT.rnaseq, THCA.rnaseq, THYM.rnaseq, UCEC.rnaseq, UCS.rnaseq, UVM.rnaseq, RTCGA-package, [2](#)

GBMLGG.rnaseq (rnaseq), [2](#)

HNSC.rnaseq (rnaseq), [2](#)

KICH.rnaseq (rnaseq), [2](#)

KIPAN.rnaseq (rnaseq), [2](#)

KIRC.rnaseq (rnaseq), [2](#)

KIRP.rnaseq (rnaseq), [2](#)

LAML.rnaseq (rnaseq), [2](#)

LGG.rnaseq (rnaseq), [2](#)

LIHC.rnaseq (rnaseq), [2](#)

LUAD.rnaseq (rnaseq), [2](#)

LUSC.rnaseq (rnaseq), [2](#)

OV.rnaseq (rnaseq), [2](#)

PAAD.rnaseq (rnaseq), [2](#)

PCPG.rnaseq (rnaseq), [2](#)

PRAD.rnaseq (rnaseq), [2](#)

READ.rnaseq (rnaseq), [2](#)

rnaseq, [2](#)