

Package ‘RTCGA.rnaseq’

December 4, 2025

Title Rna-seq datasets from The Cancer Genome Atlas Project

Version 20151101.40.0

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_22

git_last_commit 5188267

git_last_commit_date 2025-10-29

Repository Bioconductor 3.22

Date/Publication 2025-12-04

Contents

rnaseq	2
Index	4

`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://rtcga.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, THCA.rnaseq, THYM.rnaseq, UCEC.rnaseq, UCS.rnaseq, UVM.rnaseq, [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, THCA.rnaseq, THYM.rnaseq, UCEC.rnaseq, UCS.rnaseq, UVM.rnaseq, [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](#)

RTCGA-package, [2](#)

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

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

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

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

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

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

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

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