

Package ‘RTCGA.rnaseq’

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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

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>

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`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`

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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/>

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