

Package ‘RTCGA.mRNA’

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Type Package

Title mRNA datasets from The Cancer Genome Atlas Project

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Description Package provides mRNA datasets from The Cancer Genome Atlas Project for all available cohorts types from <http://gdac.broadinstitute.org/>. Data format is explained here <https://wiki.nci.nih.gov/display/TCGA/Gene+expression+data> Data from 2015-11-01 snapshot.

License GPL-2

LazyData TRUE

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

Depends R (>= 3.3.0), RTCGA

Suggests knitr, rmarkdown

biocViews AnnotationData

VignetteBuilder knitr

NeedsCompilation no

RoxygenNote 7.1.1

git_url <https://git.bioconductor.org/packages/RTCGA.mRNA>

git_branch RELEASE_3_21

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mRNA

mRNA datasets from TCGA project

Description

Package provides mRNA 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.data** family can be found here: `browseVignettes("RTCGA")`. mRNA data format is explained here <https://wiki.nci.nih.gov/display/TCGA/Gene+expression+data>. Converting **RTCGA.mRNA** datasets from `data.frames` to Bioconductor classes is explained here [convertTCGA](#).

Usage

`BRCA.mRNA``COAD.mRNA``COADREAD.mRNA``GBMLGG.mRNA``KIPAN.mRNA``KIRC.mRNA``KIRP.mRNA``LGG.mRNA``LUAD.mRNA``LUSC.mRNA``OV.mRNA``READ.mRNA``UCEC.mRNA`

Details

`browseVignettes("RTCGA")`

Value

`Data frames with mRNA data.`

Source

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

Examples

```
## Not run:  
browseVignettes("RTCGA")
```

```
## End(Not run)
```

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