

# Package ‘RTCGA.mRNA’

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**Type** Package

**Title** mRNA datasets from The Cancer Genome Atlas Project

**Version** 1.32.0

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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\_19

**git\_last\_commit** ebc48c1

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-14

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mRNA

*mRNA datasets from TCGA project*

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### 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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