

# Package ‘RTCGA.mRNA’

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**Type** Package

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

**Version** 1.36.0

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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\_21

**git\_last\_commit** 91cd9ce

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.21

**Date/Publication** 2025-09-11

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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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## \* **datasets**

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