# 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** 2025-10-16

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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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