

# Package ‘RTCGA.mutations’

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**Type** Package

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

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**Author** Marcin Kosinski <m.p.kosinski@gmail.com>

**Maintainer** Marcin Kosinski <m.p.kosinski@gmail.com>

**Description** Package provides mutations datasets from The Cancer Genome Atlas Project for all cohorts types from <http://gdac.broadinstitute.org/>. Mutations data format is explained here [https://wiki.nci.nih.gov/display/TCGA/Mutation+Annotation+Format+\(MAF\)+Specification](https://wiki.nci.nih.gov/display/TCGA/Mutation+Annotation+Format+(MAF)+Specification). There is extra one column with patients' barcodes. 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

**git\_url** <https://git.bioconductor.org/packages/RTCGA.mutations>

**git\_branch** devel

**git\_last\_commit** 0dcb53b

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**Repository** Bioconductor 3.20

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mutations

*Mutations datasets from TCGA project*

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## Description

Package provides mutations 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://rtcg.github.io/RTCGA/>. Use cases, examples and information about datasets in **RTCGA.data** family can be found here: `browseVignettes("RTCGA")` Mutations data format is explained here <https://wiki.nci.nih.gov/display> There is extra one column with patients' barcodes.

## Usage

ACC.mutations

BLCA.mutations

BRCA.mutations

CESC.mutations

CHOL.mutations

COAD.mutations

COADREAD.mutations

DLBC.mutations

ESCA.mutations

GBMLGG.mutations

GBM.mutations

HNSC.mutations

KICH.mutations

KIPAN.mutations

KIRC.mutations

KIRP.mutations

LAML.mutations

LGG.mutations

LIHC.mutations

LUAD.mutations

LUSC.mutations

OV.mutations

PAAD.mutations

PCPG.mutations

PRAD.mutations

READ.mutations

SKCM.mutations

STAD.mutations

STES.mutations

SARC.mutations

TGCT.mutations

THCA.mutations

UCEC.mutations

UCS.mutations

UVM.mutations

**Details**

`browseVignettes("RTCGA")`

**Value**

Data frames with mutations data.

**Source**

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

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