

Package ‘RTCGA.mutations’

April 10, 2025

Type Package

Title Mutations datasets from The Cancer Genome Atlas Project

Version 20151101.37.0

Date 2016-04-26

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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 15cec69

git_last_commit_date 2024-10-29

Repository Bioconductor 3.21

Date/Publication 2025-04-10

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mutations

*Mutations datasets from TCGA project***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://rtcga.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/TC> 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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