

Package ‘RTCGA.mutations’

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Type Package

Title Mutations datasets from The Cancer Genome Atlas 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/>. 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>

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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://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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