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.
There is extra one column with patients' barcodes.

License GPL-2

LazyData TRUE

Repository Bioconductor

BugReports https://github.com/mi2-warsaw/RTCGA.data/issues

Depends R (>= 3.2.0), RTCGA

Suggests knitr

biocViews Annotation Data

VignetteBuilder knitr

NeedsCompilation no

R topics documented:

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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: 2015-08-21. The process is described here: http://mi2-warsaw.github.io/RTCGA.data/. 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/TCGA/Mutation+Annotation+Format+(MAF)+Specification. There is extra one column with patients' barcodes.

Usage

```
ACC.mutations

BLCA.mutations

BRCA.mutations

CESC.mutations

CHOL.mutations

COAD.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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