

Package: RTCGA.mutations (via r-universe)

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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

Config/pak/sysreqs cmake make libicu-dev libjpeg-dev libpng-dev libuv1-dev libxml2-dev libssl-dev

Repository Bioconductor 3.23

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RemoteUrl <https://github.com/bioc/RTCGA.mutations>

RemoteRef RELEASE_3_23

RemoteSha d096de7911210160e3594a94d03a94f981adae40

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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://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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