Package ‘RTCGA.mutations’

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**Type** Package

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

**Version** 20151101.4.0

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**Author** Marcin Kosinski &lt;m.p.kosinski@gmail.com&gt;

**Maintainer** Marcin Kosinski &lt;m.p.kosinski@gmail.com&gt;

**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. Data from 2015-11-01 snapshot.

**License** GPL-2

**LazyData** TRUE

**Repository** Bioconductor

**BugReports** https://github.com/RTCGA/RTCGA/issues

**Depends** R (&gt;= 3.2.0), RTCGA

**Suggests** knitr

**biocViews** Annotation Data

**VignetteBuilder** knitr

**NeedsCompilation** no

**R topics documented:**

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Description


Usage

```
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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
```
```r
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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