

# Package ‘RTCGA.PANCAN12’

October 11, 2022

**Type** Package

**Title** PanCan 12 from Genome Cancer Browser

**Version** 1.24.0

**Date** 2015-11-10

**Author** Przemyslaw Biecek <przemyslaw.biecek@gmail.com>

**Maintainer** Marcin Kosinski <m.p.kosinski@gmail.com>

**Description** Package provides clinical, expression, cnv and mutation data from Genome Cancer Browser.

**License** GPL-2

**LazyData** FALSE

**Roxygen** list(wrap = TRUE)

**Repository** Bioconductor

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

**Depends** R (>= 3.3.0), RTCGA

**Suggests** knitr, rmarkdown

**biocViews** AnnotationData

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 5.0.1

**git\_url** <https://git.bioconductor.org/packages/RTCGA.PANCAN12>

**git\_branch** RELEASE\_3\_15

**git\_last\_commit** 8123c86

**git\_last\_commit\_date** 2022-04-26

**Date/Publication** 2022-10-11

## R topics documented:

pancan12 . . . . . 2

**Index** . . . . . 3

---

pancan12

*PANCAN12 datasets from Cancer Browser project*

---

### **Description**

Package provides clinical, expression, cnv and mutation data from Genome Cancer Browser for 12 cohorts types. Converting those datasets from `data.frames` to Bioconductor classes is explained here [convertTCGA](#).

### **Usage**

`clinical.cb`

`cnv.cb`

`mutation.cb`

`expression.cb1`

`expression.cb2`

### **Value**

Data frames PANCAN12 data.

### **Source**

<https://genome-cancer.ucsc.edu/proj/site/hgHeatmap/>

# Index

## \* datasets

pancan12, [2](#)

clinical.cb (pancan12), [2](#)

cnv.cb (pancan12), [2](#)

cnv.cb, (pancan12), [2](#)

convertTCGA, [2](#)

expression.cb, (pancan12), [2](#)

expression.cb1 (pancan12), [2](#)

expression.cb2 (pancan12), [2](#)

mutation.cb (pancan12), [2](#)

mutation.cb, (pancan12), [2](#)

pancan12, [2](#)