

# Package ‘RTCGA.PANCAN12’

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**Type** Package

**Title** PanCan 12 from Genome Cancer Browser

**Version** 1.0.2

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**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

**biocViews** AnnotationData

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 5.0.1

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pancan12

*PANCAN12 datasets from Cancer Browser project*

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### **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/>

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