Package: PCAWGmutations (via r-universe)

October 24, 2024

Title Provides easy access to PCAWG datasets

Version 0.0.0.9000

Description R package for loading PCAWG data into R as MAF objects.

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Suggests covr, testthat (>= 3.0.0)

Config/testthat/edition 3

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.1

Imports maftools

Remotes PoisonAlien/maftools@72208f2

Repository https://ccicb.r-universe.dev

RemoteUrl https://github.com/CCICB/PCAWGmutations

RemoteRef HEAD

RemoteSha 803ecdfd1aeb06358c3c5ba98559f79d69d5b83e

Contents

`pcawg_available` *List Available Datasets*

Description

List Available Datasets

Usage

```
pcawg_available()
```

Value

a dataframe listing available datasets

Examples

```
pcawg_available()
```

`pcawg_load` *Load PCAWG mafs*

Description

Load PCAWG maf objects into R. Streams data from PCAWGmutationsDB repo

Usage

```
pcawg_load(cohort, verbose = TRUE)
```

Arguments

`cohort`	abbreviation of PCAWG project. See `pcawg_available()` for valid values (string)
`verbose`	verbose (flag)

Value

MAF object compatible with maftools

Examples

```
pcawg_load("Biliary-AdenoCA")
```

Index