

Package ‘biscuiteerData’

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Type Package

Title Data Package for Biscuiteer

Description Contains default datasets used by the Bioconductor package biscuiteer.

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Depends R (>= 4.1.0), ExperimentHub

Imports AnnotationHub, utils, curl, GenomicRanges

Suggests knitr, rmarkdown, markdown

biocViews ExperimentHub, ExperimentData, Genome, Homo_sapiens_Data

Encoding UTF-8

RoxygenNote 6.1.1

Roxygen list(markdown = TRUE)

VignetteBuilder knitr

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biscuiteerData-package

Supplementary Datasets for Biscuiteer

Description

A handful of datasets to be used in biscuiteer

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See Also

Useful links:

- <https://github.com/trichelab/biscuiteer>
- Report bugs at <https://github.com/trichelab/biscuiteer/issues>

Examples

```
Zhou_solo_WCGW_inCommonPMDs.hg19 <-
  biscuiteerDataGet("Zhou_solo_WCGW_inCommonPMDs.hg19.rda")
PMDs.hg19 <- biscuiteerDataGet("PMDs.hg19.rda")
```

biscuiteerDataCacheAll

Cache all biscuiteer data

Description

Cache all biscuiteer data

Usage

```
biscuiteerDataCacheAll(dateAdded = "all", showProgress = FALSE)
```

Arguments

| | |
|---------------------------|--|
| <code>dateAdded</code> | Version of the data (given by the date added), if "all" then all dates will be cached (DEFAULT: "all") |
| <code>showProgress</code> | Whether to show progress of download (DEFAULT: FALSE) |

Value

TRUE

Examples

```
biscuiteerDataCacheAll()
```

| | |
|--------------------------------|---------------------------------|
| <code>biscuiteerDataGet</code> | <i>Retrieve biscuiteer data</i> |
|--------------------------------|---------------------------------|

Description

Retrieve biscuiteer data

Usage

```
biscuiteerDataGet(title, dateAdded = "2019-09-25", verbose = FALSE)
```

Arguments

| | |
|------------------------|---|
| <code>title</code> | Title of the data |
| <code>dateAdded</code> | Version of the data (given by the date added) (DEFAULT: "2019-09-25") |
| <code>verbose</code> | Whether to output ExperimentHub message (DEFAULT: FALSE) |

Value

Data object

Examples

```
wcgws <- biscuiteerDataGet("Zhou_solo_WCGW_inCommonPMDs.hg19.rda")
```

biscuiteerDataList *List all biscuiteer data*

Description

List all biscuiteer data

Usage

```
biscuiteerDataList(dateAdded = "all")
```

Arguments

dateAdded Version of the data (given by the date added), if "all" then all dates will be shown (DEFAULT: "all")

Value

All titles from biscuiteer data

Examples

```
biscuiteerDataList()
```

biscuiteerDataListDates
 List all versions of biscuiteer data

Description

List all versions of biscuiteer data

Usage

```
biscuiteerDataListDates()
```

Value

Sorted unique dates in biscuiteer data

Examples

```
biscuiteerDataListDates()
```

PMDs.hg19

PMDs.hg19

Description

Common PMD locations in hg19 genome

Details

Source URL: http://zwdzwd.io/pmd/PMD_coordinates_hg19.bed.gz Source type: BED file Return type: GRanges

PMDs.hg38

PMDs.hg38

Description

Common PMD locations in hg38 genome

Details

Source URL: http://zwdzwd.io/pmd/PMD_coordinates_hg38.bed.gz Source type: BED file Return type: GRanges

Zhou_solo_WCGW_inCommonPMDs.hg19

Zhou_solo_WCGW_inCommonPMDs.hg19

Description

Solo WCGWs living in hg19 common PMDs

Details

Source URL: http://zwdzwd.io/pmd/solo_WCGW_inCommonPMDs_hg19.bed.gz Source type: BED file Return type: GRanges

Zhou_solo_WCGW_inCommonPMDs.hg38

Zhou_solo_WCGW_inCommonPMDs.hg38

Description

Solo WCGWs living in hg38 common PMDs

Details

Source URL: http://zwdzwd.io/pmd/solo_WCGW_inCommonPMDs_hg38.bed.gz Source type: BED file Return type: GRanges

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