

Package ‘biscuiteerData’

September 4, 2025

Type Package

Title Data Package for Biscuiteer

Description Contains default datasets used by the Bioconductor package biscuiteer.

Version 1.22.0

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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
<i>Supplementary Datasets for Biscuiteer</i>

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	<i>Cache all biscuiteer data</i>
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Description

Cache all biscuiteer data

Usage

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

Arguments

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

Value

TRUE

Examples

```
biscuiteerDataCacheAll()
```

biscuiteerDataGet	<i>Retrieve biscuiteer data</i>
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Description

Retrieve biscuiteer data

Usage

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

Arguments

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

Value

Data object

Examples

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

biscuiteerDataList	<i>List all biscuiteer data</i>
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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	<i>List all versions of biscuiteer data</i>
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Description

List all versions of biscuiteer data

Usage

```
biscuiteerDataListDates()
```

Value

Sorted unique dates in biscuiteer data

Examples

```
biscuiteerDataListDates()
```

PMDs.hg19	<i>PMDs.hg19</i>
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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	<i>PMDs.hg38</i>
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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	<i>Zhou_solo_WCGW_inCommonPMDs.hg19</i>
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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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