

# Package ‘biscuiteerData’

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**Type** Package

**Title** Data Package for Biscuiteer

**Description** Contains default datasets used by the Bioconductor package biscuiteer.

**Version** 1.18.0

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**License** GPL-3

**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*

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## 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()
```

---

`biscuiteerDataGet`*Retrieve biscuiteer data*

---

**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](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](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](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](http://zwdzwd.io/pmd/solo_WCGW_inCommonPMDs_hg38.bed.gz) Source type: BED  
file Return type: GRanges

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