

# Package ‘biscuiteerData’

October 28, 2025

**Type** Package

**Title** Data Package for Biscuiteer

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

**Version** 1.23.1

**Date** 2025-05-30

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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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**git\_branch** devel

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|                                              |
|----------------------------------------------|
| biscuiteerData-package                       |
| <i>Supplementary Datasets for Biscuiteer</i> |

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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")
```

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|                        |                                  |
|------------------------|----------------------------------|
| biscuiteerDataCacheAll | <i>Cache all biscuiteer data</i> |
|------------------------|----------------------------------|

---

**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()

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|                   |                                 |
|-------------------|---------------------------------|
| 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> |
|--------------------|---------------------------------|

---

**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> |
|-------------------------|---------------------------------------------|

---

**Description**

List all versions of biscuiteer data

**Usage**

```
biscuiteerDataListDates()
```

**Value**

Sorted unique dates in biscuiteer data

**Examples**

```
biscuiteerDataListDates()
```

---

|           |                  |
|-----------|------------------|
| PMDs.hg19 | <i>PMDs.hg19</i> |
|-----------|------------------|

---

**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

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|           |                  |
|-----------|------------------|
| PMDs.hg38 | <i>PMDs.hg38</i> |
|-----------|------------------|

---

**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 | <i>Zhou_solo_WCGW_inCommonPMDs.hg19</i> |
|----------------------------------|-----------------------------------------|

---

**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*

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**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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