

# Package ‘biscuiteerData’

April 30, 2026

**Type** Package

**Title** Data Package for Biscuiteer

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

**Version** 1.27.0

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**Author** Tim Triche, Jr. [aut, cre], Wanding Zhou [aut], Ben Johnson [aut], Jacob Morrison [aut], Lyong Heo [aut]

**Maintainer** ``Jacob Morrison" <jacob.morrison@vai.org>

**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

## Author(s)

Timothy J Triche Jr <Tim.Triche@vai.org>,  
 Wanding Zhou <Wanding.Zhou@vai.org>,  
 Ben Johnson <Ben.Johnson@vai.org>,  
 Jacob Morrison <Jacob.Morrison@vai.org>,  
 Lyong Heo <Lyong.Heo@vai.org>

## 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

*Cache all biscuiteer data*

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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()
```

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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     *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()
```

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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

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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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