

# Package ‘EpipwR.data’

November 19, 2024

**Type** Package

**Title** EpipwR.data: Reference data for EpipwR

**Version** 1.1.0

**Description** This package provides reference data for EpipwR.

EpipwR is a fast and efficient power analysis for continuous and binary phenotypes of epigenomic-wide association studies. This package is only meant to be used in conjunction with EpipwR.

**License** Artistic-2.0

**Encoding** UTF-8

**LazyData** false

**URL** <https://github.com/jbarth216/EpipwR.data>

**BugReports** <https://github.com/jbarth216/EpipwR.data>

**Imports** ExperimentHub

**Suggests** knitr, rmarkdown, sessioninfo

**biocViews** ExperimentHub, MethylationArrayData, MicroarrayData,  
TissueMicroarrayData, Tissue, ExperimentData

**VignetteBuilder** knitr

**git\_url** <https://git.bioconductor.org/packages/EpipwR.data>

**git\_branch** devel

**git\_last\_commit** e549033

**git\_last\_commit\_date** 2024-10-29

**Repository** Bioconductor 3.21

**Date/Publication** 2024-11-19

**Author** Jackson Barth [aut, cre] (ORCID:  
<<https://orcid.org/0009-0009-6307-9928>>),  
Austin Reynolds [aut]

**Maintainer** Jackson Barth <Jackson\_Barth@Baylor.edu>

## Contents

EpiwR.data . . . . .	2
----------------------	---

<b>Index</b>	<b>3</b>
--------------	----------

---

EpiwR.data	<i>EpiwR.data: Reference data for EpiwR packages</i>
------------	--

---

### Description

This package provides reference data required for the EpiwR package. Additional information about the source of each reference data set can be found in the vignette: `vignette("EpiwR.data")`

### Value

EpiwR.data gives the user access to experiment data needed for the EpiwR R package

# Index

EpipwR.data, [2](#)