

# Package ‘EpipwR.data’

April 24, 2025

**Type** Package

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

**Version** 1.3.0

**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** 081fdd4

**git\_last\_commit\_date** 2025-04-15

**Repository** Bioconductor 3.22

**Date/Publication** 2025-04-24

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

**Maintainer** Jackson Barth <[Jackson\\_Barth@Baylor.edu](mailto:Jackson_Barth@Baylor.edu)>

## Contents

EpipwR.data . . . . .	2
<b>Index</b>	<b>3</b>

---

EpiwR.data

*EpiwR.data: Reference data for EpiwR packages*

---

**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](#)