

# Package ‘EpipwR.data’

March 13, 2025

**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

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| EpiwR.data | <i>EpiwR.data: Reference data for EpiwR packages</i> |
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### 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

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