

# Package ‘pwrEWAS.data’

December 8, 2021

**Title** pwrEWAS.data: Reference data accompanying pwrEWAS

**Version** 1.8.0

**Description** This package provides reference data required for pwrEWAS.  
pwrEWAS is a user-friendly tool to estimate power in EWAS as a function of sample and effect size for two-group comparisons of DNAm (e.g., case vs control, exposed vs non-exposed, etc.).

**Author** Stefan Graw

**Maintainer** Stefan Graw <shgraw@uams.edu>

**License** Artistic-2.0

**LazyData** FALSE

**Imports** ExperimentHub

**Suggests** knitr, RUnit, BiocGenerics

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

**Encoding** UTF-8

**RoxygenNote** 6.1.1

**VignetteBuilder** knitr

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

**git\_branch** RELEASE\_3\_14

**git\_last\_commit** 560f9f5

**git\_last\_commit\_date** 2021-10-26

**Date/Publication** 2021-12-08

## R topics documented:

pwrEWAS.data . . . . .	2
Index	3

---

pwrEWAS.data

*pwrEWAS.data: Reference data accompanying pwrEWAS*

---

**Description**

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

# Index

- \* **DNAm**

- pwrEWAS.data, [2](#)

- \* **microarray**

- pwrEWAS.data, [2](#)

- \* **tissue**

- pwrEWAS.data, [2](#)

pwrEWAS.data, [2](#)