Package ‘epimutacionsData’

April 2, 2026

Title Data for epimutacions package

Version 1.15.0

Description This package includes the data necessary to run functions
and examples in epimutacions package.
Collection of DNA methylation data.
The package contains 2 datasets:
(1) Control (GEO: GSE104812), (GEO: GSE97362) case samples; and
(2) reference panel (GEO: GSE127824).
It also contains candidate regions to
be epimutations in 450k methylation arrays.

License MIT + file LICENSE

biocViews ExperimentHub, Homo_sapiens_Data, MethylationArrayData,
MicroarrayData

Suggests rmarkdown, BiocStyle, knitr, ExperimentHub, minfi

VignetteBuilder knitr

Encoding UTF-8

Depends R (>= 4.2.0)

URL `https://github.com/LeireAbarrategui/epimutacionsData`

BugReports `https://github.com/LeireAbarrategui/epimutacionsData/issues`

NeedsCompilation no

RoxygenNote 7.1.2

git_url https://git.bioconductor.org/packages/epimutacionsData

git_branch devel

git_last_commit a9114cc

git_last_commit_date 2025-10-29

Repository Bioconductor 3.23

Date/Publication 2026-04-02

Author Leire Abarrategui [aut, cre],
Juan R. Gonzalez [aut],
Carlos Ruiz-Arenas [aut],
Carles Hernandez-Ferrer [aut]

Maintainer Leire Abarrategui <`abarrategui.leire@gmail.com`>

Contents