

Package ‘epimutacionsData’

September 3, 2024

Title Data for epimutacions package

Version 1.9.0

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.

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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 d47f4ab

git_last_commit_date 2024-04-30

Repository Bioconductor 3.20

Date/Publication 2024-09-03

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