

Package ‘epimutacionsData’

August 16, 2022

Title Data for epimutacions package

Version 1.0.0

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>

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R topics documented:

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