Package ‘HiContactsData’

May 7, 2026

Title HiContacts companion data package

Version 1.15.0

Date 2022-08-16

Description Provides a collection of Hi-C files (pairs, (m)cool and fastq). These datasets can be read into R and further investigated and visualized with the HiContacts package. Data includes yeast Hi-C data generated by the Koszul lab from the Pasteur Institute.

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URL `https://github.com/js2264/HiContactsData`

BugReports `https://github.com/js2264/HiContactsData/issues`

Depends ExperimentHub

Imports BiocFileCache, AnnotationHub

Suggests testthat, methods, BiocStyle, knitr, rmarkdown

biocViews ExperimentHub, ExperimentData, SequencingData

Encoding UTF-8

VignetteBuilder knitr

LazyData false

Roxygen list(markdown = TRUE)

RoxygenNote 7.2.3

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

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`HiContactsData` *HiContactsData*

Description

Downloads different types of Hi-C processed files (cool, mcool, pairs.gz, fastq) and returns the path of the cached file.

Usage

```
HiContactsData(sample = NULL, format = NULL)
```

Arguments

`sample`	sample
`format`	format

Value

Local path of the queried file cached with BiocFileCache.

Examples

```
HiContactsData(sample = 'yeast_wt', format = 'cool')
```

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