

Package ‘HiContactsData’

November 12, 2024

Title HiContacts companion data package

Version 1.8.0

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.

License MIT + file LICENSE

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>

git_branch RELEASE_3_20

git_last_commit e8beefb

git_last_commit_date 2024-10-29

Repository Bioconductor 3.20

Date/Publication 2024-11-12

Author Jacques Serizay [aut, cre]

Maintainer Jacques Serizay <jacquesserizay@gmail.com>

Contents

HiContactsData	2
Index	3

HiContactsData	<i>HiContactsData</i>
----------------	-----------------------

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')
```

Index

HiContactsData, [2](#)