

# Package ‘HiContactsData’

April 25, 2024

**Title** HiContacts companion data package

**Version** 1.5.3

**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** devel

**git\_last\_commit** d5bebe7

**git\_last\_commit\_date** 2024-01-16

**Repository** Bioconductor 3.19

**Date/Publication** 2024-04-25

**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](#)