

# Package: HiContactsData (via r-universe)

October 10, 2026

**Title** HiContacts companion data package

**Version** 1.14.0

**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

**Config/pak/sysreqs** libicu-dev libpng-dev libssl-dev zlib1g-dev

**Repository** Bioconductor 3.23

**Date/Publication** 2026-04-28 12:36:20 UTC

**RemoteUrl** <https://github.com/bioc/HiContactsData>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** 6c18f01adf7c451868435b947c6d8eb865d2f5fc

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### 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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