

# Package ‘HiContactsData’

April 23, 2026

**Title** HiContacts companion data package

**Version** 1.13.0

**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** devel

**git\_last\_commit** 300b55b

**git\_last\_commit\_date** 2025-10-29

**Repository** Bioconductor 3.24

**Date/Publication** 2026-04-23

**Author** Jacques Serizay [aut, cre]

**Maintainer** Jacques Serizay <jacquesserizay@gmail.com>

## Contents

HiContactsData . . . . .	2
<b>Index</b>	<b>3</b>

---

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](#)