

# Package ‘marinerData’

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**Title** ExperimentHub data for the mariner package

**Version** 1.5.0

**Date** 2023-03-30

**Description** Subsampled Hi-C in HEK cells expressing the NHA9 fusion with an F to S mutated IDR (``FS") or without any mutations to the IDR (``Wildtype" or ``WT"). These files are used for testing mariner functions and some examples.

**License** GPL-3

**BugReports** <https://support.bioconductor.org/t/marinerData>

**Imports** utils, ExperimentHub

**Suggests** knitr, rmarkdown, ExperimentHubData, testthat (>= 3.0.0)

**biocViews** ExperimentHub, ExperimentData, SequencingData

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Config/testthat/edition** 3

**VignetteBuilder** knitr

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FS_5kbLoops.txt	<i>Example NHA9 (FS) Loops</i>
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### Description

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from HEK cells expressing an NHA9 fusion with an F to S mutated IDR.

### Value

Downloads and caches a .txt file in BEDPE format.

### Examples

```
bedpeFile <- FS_5kbLoops.txt()
bedpeFile
```

---

LEUK_HEK_PJA27_inter_30.hic	<i>Example NHA9 (FS) Hi-C data</i>
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### Description

Subsampled Hi-C in HEK cells expressing the NHA9 fusion with an F to S mutated IDR.

### Value

Downloads and caches a .hic file.

**Examples**

```
hicFile <- LEUK_HEK_PJA27_inter_30.hic()
hicFile
```

---

```
LEUK_HEK_PJA30_inter_30.hic
```

*Example NHA9 (WT) Hi-C data*

---

**Description**

Subsampled Hi-C in HEK cells expressing the NHA9 fusion with a Wildtype IDR.

**Value**

Downloads and caches a .hic file.

**Examples**

```
hicFile <- LEUK_HEK_PJA30_inter_30.hic()
hicFile
```

---

```
LIMA_0000.bedpe
```

*Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 0 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0000.bedpe()
bedpeFile
```

---

LIMA\_0030.bedpe      *Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 30 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0030.bedpe()
bedpeFile
```

---

LIMA\_0060.bedpe      *Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 60 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0060.bedpe()
bedpeFile
```

---

LIMA\_0090.bedpe      *Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 90 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0090.bedpe()
bedpeFile
```

---

LIMA\_0120.bedpe      *Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 120 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0120.bedpe()
bedpeFile
```

---

LIMA\_0240.bedpe      *Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 240 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0240.bedpe()
bedpeFile
```

---

LIMA\_0360.bedpe      *Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 360 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_0360.bedpe()
bedpeFile
```

---

`LIMA_1440.bedpe`*Example Timecourse Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from THP-1 cells exposed to LPS & IF-G for 1440 minutes.

**Value**

Downloads and caches a .bedpe file in BEDPE format.

**Examples**

```
bedpeFile <- LIMA_1440.bedpe()
bedpeFile
```

---

`marinerData`*ExperimentHub datasets for the mariner package*

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**Description**

Subsampled Hi-C in HEK cells expressing the NHA9 fusion with an F to S mutated IDR ("FS") or without any mutations to the IDR ("Wildtype" or "WT"). Accompanying loop calls identified using SIP (<https://github.com/PouletAxel/SIP>) are also provided. For more information or full datasets, see <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE143465>.

Also included are loop calls identified using SIP (<https://github.com/PouletAxel/SIP>) from a THP-1 activation timecourse after stimulation with LPS & IF-G for 0, 30, 60, 80, 120, 2440, 360, or 1440 minutes. For more information or full datasets, see <https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE201353>.

These files are used for testing mariner functions and some examples.

**Value**

Downloads and caches .hic or BEDPE-formatted .txt files.

**Author(s)**

Eric S. Davis

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WT\_5kbLoops.txt      *Example NHA9 (WT) Loops*

---

**Description**

Loops called with SIP (<https://github.com/PouletAxel/SIP>) using Hi-C data from HEK cells expressing an NHA9 fusion with a Wildtype IDR.

**Value**

Downloads and caches a .txt file in BEDPE format.

**Examples**

```
bedpeFile <- WT_5kbLoops.txt()
bedpeFile
```



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