

# Package ‘sesameData’

November 24, 2021

**Type** Package

**Title** Supporting Data for SeSAmE Package

**Description** Provides supporting annotation and test data for SeSAmE package. This includes chip tango addresses, mapping information, performance annotation, and trained predictor for Infinium array data. This package provides user access to essential annotation data for working with many generations of the Infinium DNA methylation array. Current we support human array (HM27, HM450, EPIC), mouse array (MM285) and the Horvath-MethylChip40 (Mammal40) array.

**Version** 1.12.0

**License** Artistic-2.0

**Depends** R (>= 4.1), ExperimentHub, AnnotationHub, rmarkdown

**Suggests** GenomicRanges, BiocGenerics, sesame, testthat, knitr

**Imports** utils, curl

**biocViews** ExperimentData, MicroarrayData, Genome, ExperimentHub,  
MethylationArrayData

**VignetteBuilder** knitr

**NeedsCompilation** no

**RoxygenNote** 7.1.2

**git\_url** <https://git.bioconductor.org/packages/sesameData>

**git\_branch** RELEASE\_3\_14

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df_master	<i>Master data frame for all object to cache</i>
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### Description

This is an internal object which will be updated on every new release library(ExperimentHub) eh = query(ExperimentHub(localHub=FALSE), c("sesameData", "v1.11.7")) data.frame(name=eh\$title, eh=names(eh))

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sesameDataCache	<i>Cache SeSAmE data for specific platform</i>
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### Description

Cache SeSAmE data for specific platform

### Usage

```
sesameDataCache(platform = NULL, keyword = NULL)
```

### Arguments

platform	EPIC, HM450, MM285, etc.
keyword	keyword used to filter records

### Value

TRUE

### Examples

```
if(FALSE) { sesameDataCache("MM285") }
```

---

sesameDataCacheAll      *Cache all SeSAmE data*

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**Description**

Cache all SeSAmE data

**Usage**

```
sesameDataCacheAll()
```

**Value**

TRUE

**Examples**

```
if(FALSE) { sesameDataCacheAll() }
```

---

sesameDataDownload      *Download auxiliary data for sesame function and documentation*

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**Description**

Download auxiliary data for sesame function and documentation

**Usage**

```
sesameDataDownload(file_name, dest_dir = NULL)
```

**Arguments**

file\_name      name of file to download  
dest\_dir      directory to hold downloaded file. use the temporary directory if not given

**Value**

a list with url, dest\_dir, dest\_file and file\_name

**Examples**

```
if(FALSE) { sesameDataDownload("3999492009_R01C01_Grn.idat") }
```

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sesameDataGet	<i>Get SeSAmE data</i>
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**Description**

Get SeSAmE data

**Usage**

```
sesameDataGet(title, verbose = FALSE)
```

**Arguments**

title	title of the data
verbose	whether to output ExperimentHub message

**Value**

data object

**Examples**

```
sesameDataCache("HM27")
genomeInfo.hg38 <- sesameDataGet('genomeInfo.hg38')
```

---

sesameDataGetAnno	<i>Retrieve manifest file from the supporting website at <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a> and <a href="https://github.com/zhou-lab/InfiniumAnnotation">https://github.com/zhou-lab/InfiniumAnnotation</a></i>
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**Description**

Retrieve manifest file from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation> and <https://github.com/zhou-lab/InfiniumAnnotation>

**Usage**

```
sesameDataGetAnno(title)
```

**Arguments**

title	title of the annotation file
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**Value**

annotation file

**Examples**

```
mft = sesameDataGetAnno("HM27/HM27.hg19.manifest.tsv.gz")
annoS = sesameDataGetAnno("EPIC/EPIC.hg19.typeI_overlap_b151.rds")
```

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sesameDataList	<i>List all SeSAmE data</i>
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**Description**

List all SeSAmE data

**Usage**

```
sesameDataList()
```

**Value**

all titles from SeSAmE Data

**Examples**

```
sesameDataList()
```

---

sesameDataPullVariantAnno_InfiniumI	<i>Retrieve variant annotation file for Infinium-I probes from the supporting website at <a href="http://zwdzwd.github.io/InfiniumAnnotation">http://zwdzwd.github.io/InfiniumAnnotation</a></i>
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**Description**

Retrieve variant annotation file for Infinium-I probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

**Usage**

```
sesameDataPullVariantAnno_InfiniumI(
  platform = c("EPIC"),
  refversion = c("hg19", "hg38"),
  version = "20200704"
)
```

**Arguments**

platform	Infinium platform
refversion	human reference version, irrelevant for mouse array
version	manifest version, default to the latest/current.

**Value**

variant annotation file of infinium I probes

**Examples**

```
annoI = sesameDataPullVariantAnno_InfiniumI('EPIC', 'hg38')
```

---

sesameDataPullVariantAnno\_SNP

*Retrieve variant annotation file for explicit rs probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>*

---

**Description**

Retrieve variant annotation file for explicit rs probes from the supporting website at <http://zwdzwd.github.io/InfiniumAnnotation>

**Usage**

```
sesameDataPullVariantAnno_SNP(  
  platform = c("EPIC"),  
  refversion = c("hg19", "hg38"),  
  version = "20200704"  
)
```

**Arguments**

platform	Infinium platform
refversion	human reference version, irrelevant for mouse array
version	manifest version, default to the latest/current.

**Value**

variant annotation file of explicit rs probes

**Examples**

```
annoS = sesameDataPullVariantAnno_SNP('EPIC', 'hg38')
```

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