

# Package ‘restfulSEData’

August 25, 2022

**Title** Example metadata for the ‘restfulSE’ R package

**Description** Metadata RangedSummarizedExperiment shell for use with restfulSE.

**Version** 1.19.0

**Maintainer** Bioconductor Package Maintainer <maintainer@bioconductor.org>

**Depends** R (>= 3.4), SummarizedExperiment, ExperimentHub, DelayedArray (>= 0.21.2), HDF5Array (>= 1.23.2)

**Imports** utils, methods

**Suggests** knitr, rmarkdown

**License** Artistic-2.0

**LazyLoad** yes

**biocViews** ExperimentData, Mus\_musculus\_Data, Homo\_sapiens\_Data, ExpressionData, SequencingData

**RoxygenNote** 6.0.1

**Collate** dataResource.R

**VignetteBuilder** knitr

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

**git\_branch** master

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## R topics documented:

restfulSEData-package . . . . .	2
dataResource . . . . .	2

<b>Index</b>	<b>3</b>
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restfulSEData-package *Example metadata for the "restfulSE" R package*

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### **Description**

Metadata RangedSummarizedExperiment shell for use with "restfulSE" R package is available in ExperimentHub

### **Examples**

```
library(ExperimentHub)
ehub <- ExperimentHub()
myfiles <- query(ehub, "restfulSEData")
myfiles[[1]] #load the first resource in the list
myfiles[["EH551"]] #load by EH id
```

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dataResource *Convenience functions to explore the datasets*

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### **Description**

Convenience functions to explore the datasets

### **Usage**

```
dataResource()
```

### **Value**

data object to provide description of datasets

### **Examples**

```
dataResource()
```

# Index

`dataResource`, [2](#)

`restfulSEData (restfulSEData-package)`, [2](#)

`restfulSEData-package`, [2](#)