

# Package ‘restfulSEData’

May 9, 2024

**Title** Example metadata for the ``restfulSE" R package

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

**Version** 1.26.0

**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, BiocStyle, rhdf5client

**License** Artistic-2.0

**LazyLoad** yes

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

**RoxygenNote** 7.2.3

**Collate** dataResource.R zzz.R

**VignetteBuilder** knitr

**PackageStatus** Deprecated

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

**git\_branch** RELEASE\_3\_19

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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()
```

**Examples**

```
dataResource()
```

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