

# Package ‘restfulSEData’

May 2, 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

**git\_last\_commit** aad0edd

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.19

**Date/Publication** 2024-05-02

**Author** Vincent Carey [aut],  
Shweta Gopaulakrishnan [cre, aut]

## Contents

restfulSEData-package . . . . .	2
dataResource . . . . .	2
<b>Index</b>	<b>3</b>

---

restfulSEData-package *Example metadata for the "restfulSE" R package*

---

**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
```

---

dataResource *Convenience functions to explore the datasets*

---

**Description**

Convenience functions to explore the datasets

**Usage**

```
dataResource()
```

**Examples**

```
dataResource()
```

# Index

`dataResource`, [2](#)

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

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