

Package ‘restfulSEData’

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Title Example metadata for the “restfulSE” R package

Description Metadata RangedSummarizedExperiment shell for use with restfulSE.

Version 1.2.0

Maintainer Bioconductor Package Maintainer <maintainer@bioconductor.org>

Depends R (>= 3.4), SummarizedExperiment, ExperimentHub

Imports utils, methods

Suggests knitr

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

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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()
```

Value

data object to provide description of datasets

Examples

```
dataResource()
```

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