

Package ‘restfulSEData’

April 11, 2023

Title Example metadata for the ‘restfulSE’ R package

Description Metadata RangedSummarizedExperiment shell for use with restfulSE.

Version 1.20.0

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 RELEASE_3_16

git_last_commit 9f0d3b3

git_last_commit_date 2022-11-01

Date/Publication 2023-04-11

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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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