

Package ‘restfulSEData’

May 16, 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 2024-05-16

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

Contents

restfulSEData-package	2
dataResource	2

Index	3
--------------	----------

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](#)