

Package: RNAmoD.R.Data (via r-universe)

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Type Package

Title Example data for the RNAmoD.R package

Version 1.26.0

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Description RNAmoD.R.Data contains example data, which is used for vignettes and example workflows in the RNAmoD.R and dependent packages.

biocViews ExperimentData, SequencingData, RNASeqData

License Artistic-2.0

Encoding UTF-8

LazyData false

Depends R (>= 3.6), ExperimentHub, ExperimentHubData (>= 1.9.2)

Imports utils

Suggests knitr, rmarkdown, BiocStyle, GenomicRanges, sessioninfo, testthat

Collate 'RNAmoD.R.Data.R' 'zzz.R'

RoxygenNote 7.3.3

VignetteBuilder knitr

BugReports <https://github.com/FelixErnst/RNAmoD.R.Data/issues>

URL <https://github.com/FelixErnst/RNAmoD.R.Data>

Config/pak/sysreqs
make libbz2-dev libicu-dev liblzma-dev libpng-dev libxml2-dev libssl-dev xz-utils zlib1g-dev

Repository Bioconductor 3.23

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example.man.fasta	<i>RNAmodR example data for tests and man pages</i>
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Description

This dataset contains a small data set for tests and man page examples. The individual identifiers are RNAmodR.Data. plus the header from the Datasets section.

Datasets

- example.man.fasta:** sequence of artificial genome for S. cerevisiae containing partial sequences of the 18S rRNA
- example.man.gff3:** annotation of artificial genome for S. cerevisiae containing partial sequences of the 18S rRNA

Examples

```
RNAmodR.Data.example.man.fasta()  
RNAmodR.Data.example.man.gff3()
```

RNAmodR.Data	<i>RNAmodR.Data</i>
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Description

RNAmodR.Data contains example data, which is used for vignettes and example workflows in the RNAmodR and dependent packages.

Author(s)

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See Also

- Useful links:
- <https://github.com/FelixErnst/RNAmodR.Data>
 - Report bugs at <https://github.com/FelixErnst/RNAmodR.Data/issues>

Description

This dataset contains example data for AlkAnilineSeq. The individual identifiers are RNAmodR.Data., plus the header from the Datasets section.

Datasets

example.AAS.fasta: sequence of artificial genome for *S. cerevisiae* containing only the 18S rRNA sequence and 10 tRNA sequences

example.AAS.gff3: annotation of artificial genome for *S. cerevisiae* containing only the 18S rRNA sequence and 10 tRNA sequences

example.bud23.1: sequencing reads mapped to artificial genome from bud23del strain - replicate 1

example.bud23.2: sequencing reads mapped to artificial genome from bud23del strain - replicate 2

example.trm8.1: sequencing reads mapped to artificial genome from trm8del strain - replicate 1

example.trm8.2: sequencing reads mapped to artificial genome from trm8del strain - replicate 2

example.wt.1: sequencing reads mapped to artificial genome from wild type strain - replicate 1

example.wt.2: sequencing reads mapped to artificial genome from wild type strain - replicate 2

example.wt.3: sequencing reads mapped to artificial genome from wild type strain - replicate 3

Examples

```
RNAmodR.Data.example.AAS.fasta()
RNAmodR.Data.example.AAS.gff3()
RNAmodR.Data.example.bud23.1()
RNAmodR.Data.example.bud23.2()
RNAmodR.Data.example.trm8.1()
RNAmodR.Data.example.trm8.2()
RNAmodR.Data.example.wt.1()
RNAmodR.Data.example.wt.2()
RNAmodR.Data.example.wt.3()
```

RNAmodR.Data.example *RNAmodR general example data*

Description

This dataset contains general example data used for different purposes. The individual identifiers are RNAmodR.Data. plus the header from the Datasets section.

Datasets

example.fasta: sequences of artificial genome for *S. cerevisiae* containing only rRNA and tRNA sequences

example.gff3: annotation of artificial genome for *S. cerevisiae* containing only rRNA and tRNA sequences

example.bam.1: sequencing reads mapped to artificial genome - replicate 1

example.bam.2: sequencing reads mapped to artificial genome - replicate 2

example.bam.3: sequencing reads mapped to artificial genome - replicate 3

Examples

```
RNAmodR.Data.example.fasta()
RNAmodR.Data.example.gff3()
RNAmodR.Data.example.bam.1()
RNAmodR.Data.example.bam.2()
RNAmodR.Data.example.bam.3()
```

RNAmodR.Data.RMS *RNAmodR RiboMethSeq example data*

Description

This dataset contains example data for RiboMethSeq. The individual identifiers are RNAmodR.Data. plus the header from the Datasets section.

Datasets

example.RMS.fasta: sequence of artificial genome for *H. sapiens* containing only the 5.8S rRNA sequence

example.RMS.gff3: annotation of artificial genome for *H. sapiens* containing only the 5.8S rRNA sequence

example.RMS.1: sequencing reads mapped to artificial genome - replicate 1

example.RMS.2: sequencing reads mapped to artificial genome - replicate 2

Examples

```
RNAmodR.Data.example.RMS.fasta()  
RNAmodR.Data.example.RMS.gff3()  
RNAmodR.Data.example.RMS.1()  
RNAmodR.Data.example.RMS.2()
```

```
RNAmodR.Data.snoRNAdb  snoRNAdb data
```

Description

The csv files contains a copy of data from the snoRNAdb (<https://www-snorna.biotoul.fr/>) downloaded on the 2019-02-11. The coordinates were updated to current rRNA sequences of hg38.

Examples

```
RNAmodR.Data.snoRNAdb()
```

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