

Package ‘RNAmodR.Data’

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Type Package

Title Example data for the RNAmodR package

Version 1.10.0

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Description RNAmodR.Data contains example data, which is used for vignettes and example workflows in the RNAmodR 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 'RNAmodR.Data.R' 'zzz.R'

RoxygenNote 7.0.2

VignetteBuilder knitr

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

URL <https://github.com/FelixErnst/RNAmodR.Data>

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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)

Felix G.M. Ernst [aut], Denis L.J. Lafontaine [ctb]

`RNAmoDR.Data.AAS`*RNAmoDR AlkAnilineSeq example data*

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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