

# Package ‘RNAmodR.Data’

April 16, 2024

**Type** Package

**Title** Example data for the RNAmodR package

**Version** 1.16.0

**Date** 2020-02-13

**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>

**git\_url** <https://git.bioconductor.org/packages/RNAmodR.Data>

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**Author** Felix G.M. Ernst [aut, cre],  
Denis L.J. Lafontaine [ctb, fnd]

**Maintainer** Felix G.M. Ernst <[felix.gm.ernst@outlook.com](mailto:felix.gm.ernst@outlook.com)>

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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()
```

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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]

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

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## 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*

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### 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()
```

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RNAmoDR.Data.RMS *RNAmoDR RiboMethSeq example data*

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### 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()
```

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`RNAmodR.Data.snoRNAdb` *snoRNAdb data*

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### **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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