Package ‘microRNAome’

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Title SummarizedExperiment for the microRNAome project

Description This package provides a SummarizedExperiment object of read counts for microRNAs across tissues, cell-types, and cancer cell-lines. The read count matrix was prepared and provided by the author of the study: Towards the human cellular microRNAome.

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Depends R (>= 3.4), SummarizedExperiment

Suggests BiocGenerics, RUnit

biocViews ExperimentData, CellCulture, CancerData, SequencingData, RNASeqData, miRNAData

License GPL (>= 2)

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microRNAome

MicroRNAome Data

Description

Read counts per miRNA for the microRNAome collection of RNA-Seq experiments

Usage

```r
data("microRNAome")
```

Format

SummarizedExperiment

Details

Small RNA-seq data on 2406 samples from the Sequence Read Archive (SRA) processed using the miRge3 pipeline.

Source

Read count matrix prepared and provided by authors of the study

References


Examples

```r
data(microRNAome)
## the microRNAome SummarizedExperiment object contains only one matrix
## in the assays field: a matrix of miRNA counts
names(assays(microRNAome))
assays(microRNAome)$counts[1:3,1:3]
```
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