Package ‘alpineData’

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Title Data for the alpine package vignette

Version 1.20.0

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Description A small subset of paired-end RNA-seq reads from four samples of the GEUVADIS project.

License GPL (>=2)

Depends ExperimentHub, GenomicAlignments

Imports utils, AnnotationHub

Suggests GenomicAlignments, knitr, markdown

VignetteBuilder knitr

biocViews SequencingData, RNASeqData, ExpressionData

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R topics documented:

`alpineData` *GAlignmentPairs for four samples from the GEUVADIS project*

Description

FASTQ files for four RNA-seq samples from the GEUVADIS project were downloaded, aligned and constructed as `GAlignmentPairs`, according to the steps presented in `inst/scripts/make-data.R`

Usage

```
ERR188297(metadata=FALSE)
ERR188088(metadata=FALSE)
ERR188204(metadata=FALSE)
ERR188317(metadata=FALSE)
```

Arguments

`metadata`	`logical` value indicating whether metadata only should be returned or if the resource should be loaded. Default behavior(metadata=FALSE) loads the data.

Format

GAlignmentPairs

Value

These accessor functions return GAlignmentPairs objects

Source

FASTQ files for four RNA-seq samples from the GEUVADIS project.

References

Lappalainen, T., et al. Transcriptome and genome sequencing uncovers functional variation in humans. Nature. 501(7468): 506-511 (2013) doi: 10.1038/nature12531

Examples

```
ERR188297()
```

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