Package ‘alpineData’

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Title Data for the alpine package vignette
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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, ExperimentHubData
Imports utils, AnnotationHub
Suggests GenomicAlignments, knitr
VignetteBuilder knitr
biocViews SequencingData, RNASEqData, ExpressionData
NeedsCompilation no

R topics documented:
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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


Examples

ERR188297()
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