

# Package ‘alpineData’

September 11, 2018

**Title** Data for the alpine package vignette

**Version** 1.6.0

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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

**Imports** utils, AnnotationHub

**Suggests** GenomicAlignments, knitr

**VignetteBuilder** knitr

**biocViews** SequencingData, RNASeqData, ExpressionData

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

**git\_branch** RELEASE\_3\_7

**git\_last\_commit** 295f97a

**git\_last\_commit\_date** 2018-04-30

**Date/Publication** 2018-09-11

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alpineData *GAlignmentPairs for four samples from the GEUVADIS project*

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## 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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