

# Package ‘raerdata’

December 26, 2024

**Title** A collection of datasets for use with raer package

**Version** 1.5.0

**Description** raerdata is an ExperimentHub package that provides a collection of files useful for demonstrating functionality in the raer package. Datasets include 10x genomics scRNA-seq, bulk RNA-seq, and paired whole-genome and RNA-seq data. Additionally databases of human and mouse RNA editing sites are provided.

**License** MIT + file LICENSE

**Imports** ExperimentHub, Rsamtools, BiocGenerics, rtracklayer, SingleCellExperiment

**Suggests** rmarkdown, knitr, BiocStyle, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.2.3

**Encoding** UTF-8

**biocViews** SingleCellData, SequencingData, RNASeqData, ExperimentHub, PackageTypeData, ExpressionData

**BugReports** <https://github.com/rnabioco/raerdata/issues>

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**Config/testthat/edition** 3

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GSE99249

*RNA sequencing data from study GSE99249*

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## Description

Study [GSE99249](#) examined RNA editing in WT, ADAR1KO, and ADAR1-p150 HEK293T cells treated with and without interferon beta.

## Usage

GSE99249()

## Details

GSE99249() will download BAM and BAM index files from 6 RNA-seq libraries. 3 libraries are ADAR1 knockout cells treated with interferon beta and 3 libraries are wild type cells treated with interferon beta. The BAM files contain alignments from chromosome 18.

## Value

A list containing:

- bams A [BamFileList](#) object, indicating the BAM file paths and BAI indexes.
- fasta A path to a fasta file from chr18 of hg38
- snps a GRanges object containing known SNPs from the REDportal database (hg38)

## Examples

GSE99249()

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`NA12878`*Whole genome and RNA sequencing data from NA12878 cell line*

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**Description**

Whole genome and RNA sequencing data from NA12878 cell line

**Usage**`NA12878()`**Details**

Will download BAM and BAM index files from whole genome and RNA sequencing of the NA12878 cell line, The data is from the first megabase of chromosome 4. Additionally a fasta file and a database of known SNPs will be downloaded.

**Value**

A list containing:

- `bams` A [BamFileList](#) object, indicating the BAM file paths and BAI indexes.
- `fasta` A path to a fasta file containing the genome sequence of the first megabase of chr4 (hg38)
- `snps` a `GRanges` object containing SNPs from the first megabase of chr4

**Examples**`NA12878()`

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`pbmc_10x`*single cell RNA sequencing data from human PBMCs*

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**Description**

A 10x Genomics 3' single cell RNA-seq library from 10k PBMCs. The BAM file contains alignments from chr16. A [SingleCellExperiment](#) is also provided with pre-processed gene expression data, a UMAP projection and cell type annotations.

**Usage**`pbmc_10x()`

**Details**

`pbmc_10x()` will download a BAM, BAM index file, REDIPortal RNA editing sites, and a Single-CellExperiment object from the [ExperimentHub](#).

**Value**

A list containing:

- bam a [BamFile](#) object indicating the BAM and BAI file paths. Contains alignments from only chr16 (hg38).
- sites a GRanges object containing known RNA editing sites from the REDIPortal database (hg38).
- sce a [SingleCellExperiment](#) object containing gene expression data, a UMAP projection and cell type annotations.

**See Also**

<https://www.10xgenomics.com/resources/datasets/10k-human-pbmcs-3-v3-1-chromium-x-with-intronic-reads>

**Examples**

```
pbmc_10x()
```

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raerdata

*raerdata*

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**Description**

A collection of datasets and databases to demonstrate RNA-editing analysis approaches using the raer package.

**Details**

[atlases](#) a collection of RNA editing databases

[NA12878](#) Whole genome and RNA sequencing data from the NA12878 cell line

[GSE99249](#) RNA sequencing data from a study that examined RNA editing in WT, ADAR1KO, and ADAR1-p150 HEK293T cells treated with and without interferon beta.

[pbmc\\_10x](#) single cell RNA sequencing data from human PBMCs from 10x Genomics

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rediportal\_full\_mm10 *Databases of known RNA editing sites*

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**Description**

Databases of known RNA editing sites

**Usage**

rediportal\_full\_mm10()

rediportal\_coords\_mm10()

rediportal\_full\_hg38()

rediportal\_coords\_hg38()

gabay\_sites\_mm10()

gabay\_sites\_hg38()

**Details**

rediportal\_full\_hg38() will download the human REDiportal database for hg38 which has been converted into a GRanges object. The GRanges is supplemented with additional columns of information provided by the REDiportal database, including gene location, repeat type, dbSNP annotation, and potential for amino-acid recoding.

rediportal\_coords\_hg38() will download the human REDiportal database for hg38 which has been converted into a GRanges object, which only contains the coordinates of the editing site.

rediportal\_full\_mm10() will download the mouse REDiportal database for mm10 which has been converted into a GRanges object. The GRanges is supplemented with additional columns of information provided by the REDiportal database, including gene location, repeat type, dbSNP annotation, and potential for amino-acid recoding.

rediportal\_coords\_mm10() will download the mouse REDiportal database for mm10 which has been converted into a GRanges object, which only contains the coordinates of the editing site.

gabay\_sites\_hg38() will download high-confidence human CDS editing sites (hg38).

gabay\_sites\_mm10() will download high-confidence mouse CDS editing sites (lifted-over from hg38 to mm10).

**Value**

A GRanges object.

**Examples**

```
gabay_sites_hg38()
```

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