

# Package ‘yeastRNASeq’

July 11, 2023

**Title** Yeast RNA-Seq Experimental Data from Lee et al. 2008

**Version** 0.39.0

**Author** James H. Bullard and Kasper D. Hansen

**Description** A selection of RNA-Seq data from a yeast transcriptome experiment.

**biocViews** ExperimentData, Saccharomyces\_cerevisiae\_Data,  
SequencingData, RNASeqData

**Maintainer** J. Bullard <bullard@stat.berkeley.edu>

**License** GPL

**Depends** R (>= 2.4)

**Suggests** Biobase, ShortRead, IRanges

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

**git\_branch** devel

**git\_last\_commit** b4e15e7

**git\_last\_commit\_date** 2023-04-25

**Date/Publication** 2023-07-11

## R topics documented:

geneLevelData . . . . .	2
yeastAligned . . . . .	2
yeastAnno . . . . .	3
<b>Index</b>	<b>4</b>

---

`geneLevelData`*Yeast gene-level counts from: Lee et al. PloS Genetics 2008.*

---

**Description**

Gene counts for an Illumina sequencing experiment. These counts represent summarizations over the data in the `yeastAligned` object using the annotation from the `yeastAnno` object, both from this package.

**Usage**

```
data(geneLevelData)
```

**Source**

A citation for the dataset may be generated using `citation("yeastRNASeq")`.

**See Also**

The package vignette.

---

`yeastAligned`*AlignedRead list*

---

**Description**

A four element list of `AlignedRead` objects from the `ShortRead` package from 4 yeast lanes of a Solexa experiment: Lee et al. PloS Genetics 2008.

The data represents a random subsample of reads from 4 lanes (2 wild-type, 2 mutant lanes)

**Usage**

```
data(yeastAligned)
```

**Source**

A citation for the dataset may be generated using `citation("yeastRNASeq")`.

**See Also**

The package vignette.

---

yeastAnno

*Yeast Annotation*

---

### **Description**

Annotation for *S. cerevisiae* downloaded from Ensembl using the **biomaRt** package in the fall of 2009 and post-processed. This file should not be used for analyses purposes, but rather demonstrates some functionality of various packages.

### **Usage**

```
data(geneLevelData)
```

### **Source**

A citation for the dataset may be generated using `citation("yeastRNASeq")`.

### **See Also**

The package vignette.

# Index

## \* datasets

geneLevelData, [2](#)

yeastAligned, [2](#)

yeastAnno, [3](#)

geneLevelData, [2](#)

yeastAligned, [2](#)

yeastAnno, [3](#)