Package ‘KOdata’

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Type Package

Title LINCS Knock-Out Data Package

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Description Contains consensus genomic signatures (CGS) for experimental cell-line specific gene knock-outs as well as baseline gene expression data for a subset of experimental cell-lines. Intended for use with package KEGGlincs.

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LazyData TRUE

RoxygenNote 5.0.1

Depends R (>= 3.3.0)

biocViews ExpressionData, CancerData, Homo_sapiens_Data

NeedsCompilation no

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Repository Bioconductor 3.19

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Contents

`gene_cell_info` *Baseline expression information for genes across cell lines*

Description

This data set contains baseline expression measurements for genes in cell lines [without any experimental perturbations] as profiled by the LINCS data consortium

Usage

```
data(gene_cell_info)
```

Format

A data frame with 1703457 observations on the following 6 variables.

- `pr_gene_symbol`a character vector
- `cell`a character vector
- `basex_affx`a numeric vector
- `basex_rnaseq`a numeric vector
- `copy_number`a numeric vector
- `is_expressed`a logical vector

Value

A data.frame object

`KOdata` *KOdata: an R data package designed to be used with KEGGlincs*

Description

KOdata: an R data package designed to be used with KEGGlincs

`KO_data` *LINCS knock-out data*

Description

This data set contains consensus genome signatures (CGS) that are the result of experimental knock-out studies conducted by the BROAD Institute.

Usage

```
data(KO_data)
```

Format

A data frame with 36720 observations on the following 9 variables.

- `cell_id` a character vector
- `pert_desc` a character vector
- `pert_time` a numeric vector
- `dn100_bing` a character vector
- `dn100_full` a character vector
- `dn50_lm` a character vector
- `up100_bing` a character vector
- `up100_full` a character vector
- `up50_lm` a character vector

Value

A data.frame object

References

http://lincsportal.ccs.miami.edu

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