

# Package ‘KOdata’

September 22, 2026

**Type** Package

**Title** LINCS Knock-Out Data Package

**Version** 1.38.0

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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.

**License** MIT + file LICENSE

**LazyData** TRUE

**RoxygenNote** 5.0.1

**Depends** R (>= 3.3.0)

**biocViews** ExpressionData, CancerData, Homo\_sapiens\_Data

**NeedsCompilation** no

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

**git\_branch** RELEASE\_3\_23

**git\_last\_commit** 1b7a03b

**git\_last\_commit\_date** 2026-04-28

**Repository** Bioconductor 3.23

**Date/Publication** 2026-09-22

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|----------------|--------------------------------------------------------------------|
| gene_cell_info | <i>Baseline expression information for genes across cell lines</i> |
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**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\_symbola character vector
- cella character vector
- basex\_affxa numeric vector
- basex\_rnaseqa numeric vector
- copy\_numbera numeric vector
- is\_expresseda logical vector

**Value**

A data.frame object

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|        |                                                                     |
|--------|---------------------------------------------------------------------|
| KOdata | <i>KOdata: an R data package designed to be used with KEGGlincs</i> |
|--------|---------------------------------------------------------------------|

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**Description**

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

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|         |                             |
|---------|-----------------------------|
| KO_data | <i>LINCS knock-out data</i> |
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**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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## \* **datasets**

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