

# Package ‘LINCSDataportal’

July 31, 2017

**Title** Query LINCS project data and metadata from LINCS Data Portal

**Version** 0.1.0

**Date** 2017-07-31

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## Description

Access, query and download of data and metadata from the Library of Integrated Network-based Cellular Signatures (LINCS) project (<http://www.lincsproject.org/>).

**Depends** R (>= 3.2.1)

**Imports** httr, utils, jsonlite

**License** GPL-3

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 6.0.1.9000

## R topics documented:

cell_metadata . . . . .	2
datalevels . . . . .	2
dataset_entities . . . . .	3
download_dataset . . . . .	3
find_dataset . . . . .	4
gene_metadata . . . . .	4
protein_metadata . . . . .	5
SM_metadata . . . . .	6
<b>Index</b>	<b>7</b>

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cell_metadata	<i>Retrieve metadata associated with a cell (cl) used in LINCS experiments.</i>
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**Description**

Retrieve metadata associated with a cell (cl) used in LINCS experiments.

**Usage**

```
cell_metadata(cl)
```

**Arguments**

cl	String representing a cell of interest
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**Value**

data frame with available cell metadata

**Examples**

```
cell_metadata("mcf7")
```

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datalevels	<i>Retrieve all available data level and associated dataset id for a given dataset id.</i>
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**Description**

Retrieve all available data level and associated dataset id for a given dataset id.

**Usage**

```
datalevels(lds_id)
```

**Arguments**

lds_id	String representing a dataset id (LDS-xxxx)
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**Value**

data frame with available data level and associated dataset id

**Examples**

```
datalevels("LDS-1233")
```

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dataset_entities	<i>Retrieve entities (gene, protein, small molecule, etc.) associated with a specific LINCS dataset</i>
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**Description**

Retrieve entities (gene, protein, small molecule, etc.) associated with a specific LINCS dataset

**Usage**

```
dataset_entities(lds_id)
```

**Arguments**

lds_id	String representing the dataset id (LDS-xxxx)
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**Value**

list of vectors with entities, measured or used to perturb the experiment associated to a given dataset.  
One vector per entity type.

**Examples**

```
dataset_entities("LDS-1266")  
dataset_entities("LDS-1173")
```

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download_dataset	<i>Download LINCS dataset packages, given dataset id's, from Lincs Data Portal.</i>
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**Description**

Download LINCS dataset packages, given dataset id's, from Lincs Data Portal.

**Usage**

```
download_dataset(lds_id, path = ".")
```

**Arguments**

lds_id	Vector of dataset ids (LDS-xxxx)
path	Path to local folder where the dataset package will be downloaded, default = current directory

**Examples**

```
## Not run:
download_dataset("LDS-1266")
download_dataset("LDS-1173", path = "/datasets")

## End(Not run)
```

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find_dataset	<i>Retrieve datasets from LINCS data portal associated with a term of interest (gene, protein, small molecule)</i>
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**Description**

Retrieve datasets from LINCS data portal associated with a term of interest (gene, protein, small molecule)

**Usage**

```
find_dataset(searchterm)
```

**Arguments**

searchterm	String representing the search term
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**Value**

data.frame containing dataset id and description

**Examples**

```
find_dataset("afatinib")
find_dataset("mcf7")
```

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gene_metadata	<i>Retrieve metadata associated with a gene measured in LINCS experiments.</i>
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**Description**

Retrieve metadata associated with a gene measured in LINCS experiments.

**Usage**

```
gene_metadata(ge)
```

**Arguments**

ge                      String representing a gene of interest

**Value**

data frame with available gene metadata

**Examples**

```
gene_metadata("BRCA1")
```

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protein_metadata	<i>Retrieve metadata associated with a protein measured or used in LINCS experiments.</i>
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**Description**

Retrieve metadata associated with a protein measured or used in LINCS experiments.

**Usage**

```
protein_metadata(pr)
```

**Arguments**

pr                      String representing a protein of interest

**Value**

data frame with available protein metadata

**Examples**

```
protein_metadata("ACK")
```

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SM_metadata	<i>Retrieve metadata associated with a Small Molecule (SM) used in LINCS experiments.</i>
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**Description**

Retrieve metadata associated with a Small Molecule (SM) used in LINCS experiments.

**Usage**

```
SM_metadata(sm)
```

**Arguments**

sm	String representng a small molecule of interest
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**Value**

data frame with available small molecule metadata

**Examples**

```
SM_metadata("afatinib")
```

# Index

cell\_metadata, [2](#)

datalevels, [2](#)

dataset\_entities, [3](#)

download\_dataset, [3](#)

find\_dataset, [4](#)

gene\_metadata, [4](#)

protein\_metadata, [5](#)

SM\_metadata, [6](#)