Package ‘qPLEXdata’

January 9, 2024

Type  Package
Title  Data accompanying qPLEXanalyzer package
Version  1.20.0
Date  2023-07-10
Description  qPLEX-RIME and Full proteome TMT mass spectrometry datasets.
Depends  R (>= 3.5), qPLEXanalyzer
Imports  utils, knitr, MSnbase, dplyr
Suggests  statmod
VignetteBuilder  knitr
License  GPL-2
biocViews  ExperimentData, MassSpectrometryData, Proteome
NeedsCompilation  no
git_url  https://git.bioconductor.org/packages/qPLEXdata
git_branch  RELEASE_3_18
git_last_commit  a5d56e2
git_last_commit_date  2023-10-24
Repository  Bioconductor 3.18
Date/Publication  2024-01-09

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R topics documented:

exp1_specificity  ................................................................. 2
exp2_Xlink  ................................................................. 2
exp3_OHT_ESR1  ............................................................... 3
exp4_OHT_FP  ................................................................. 3
exp5_PDX  ................................................................. 4
exp6_ER  ................................................................. 4
In this experiment we have used the qPLEX-RIME approach to identify ER specific interactors. We performed replicate ER RIME pull-downs in five independent biological replicates and an equal number of matched IgG mock samples was included.

Usage

data(exp1_specificity)

Format

An object of class list related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (ER and IgG).

Value

An object of class list related to peptides quantification.

An ER qPLEX-RIME experiment was performed to compare two different ways of cell crosslinking. MCF7 cells were double crosslinked with DSG/formaldehyde (double) or with formaldehyde alone (single). Four biological replicates were obtained for each condition along with two IgG pooled samples from each replicate.

Usage

data(exp2_Xlink)

Format

An object of class list related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into three conditions (FA, DSG.FA and IgG).
**exp3_OHT_ESR1**

**Value**

An object of class list related to peptides quantification.

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**exp3_OHT_ESR1 dataset**

**Description**

Three ER qPLEX-RIME (10plex) experiments were performed to investigate the dynamics of the ER complex assembly upon 4-hydrotamoxifen (OHT) treatment at 2h, 6h and 24h or at 24h post-treatment with the drug-vehicle alone (ethanol). Two biological replicates of each condition were included in each experiment to finally consider a total of six replicates per time point. Additionally, MCF7 cells were treated with OHT or ethanol and cross-linked at 24h post-treatment in each experiment to be used for mock IgG pull-downs and to enable discrimination of non-specific binding in the same experiment. This is a timecourse experiment to study the effect of tamoxifen in ER interactome using qPLEX-RIME method.

**Usage**

`data(exp3_OHT_ESR1)`

**Format**

An object of class list related to peptides quantification. It consists of qPLEX-RIME data from three experimental runs. Each run contains 10 samples divided into five conditions (IgG, vehicle, tam.2h, tam.6h and tam.24h).

**Value**

An object of class list related to peptides quantification.

---

**exp4_OHT_FP dataset**

**Description**

We performed two 10plex-TMT time-course experiments to study the effect of 4-hydrotamoxifen (OHT) on total protein levels. MCF7 cells were treated with OHT for 2h, 6h, 24h or for 24h with the drug-vehicle alone (ethanol) and a total number of four biological replicates were obtained. This is a timecourse experiment to study the effect of tamoxifen on full proteome.

**Usage**

`data(exp4_OHT_FP)`
An object of class `list` related to peptides quantification. It consists of total proteome data from two experimental runs. Each run contains 10 samples divided into four conditions (vehicle, tam.2h, tam.6h and tam.24h).

**Value**

An object of class `list` related to peptides quantification.

---

**exp5_PDX**

**exp5_PDX dataset**

**Description**

An ER qPLEX-RIME experiment was performed using three independent ER+ human Patient Derived Xenograft (PDX) tumour material. Cryosections of each tumour were double-crosslinked and each tumour was split in two parts that were used for ER and IgG RIME pull-down assays. One of the tumours was split in three different parts to be used as ER or IgG qPLEX-RIME in order to assess technical variability.

**Usage**

`data(exp5_PDX)`

**Format**

An object of class `list` related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (PDX and IgG).

**Value**

An object of class `list` related to peptides quantification.

---

**exp6_ER**

**exp6_ER dataset**

**Description**

An ER qPLEX-RIME experiment was performed using five independent ER-positive human breast cancer tumours. Cryosections of each tumour were double-crosslinked and each tumour was split in two parts that were used for ER and IgG RIME pull-down assays.

**Usage**

`data(exp6_ER)`

**Format**

An object of class `list` related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (PDX and IgG).

**Value**

An object of class `list` related to peptides quantification.
exp7_NCOA3

**Format**
An object of class `list` related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (ER and IgG).

**Value**
An object of class `list` related to peptides quantification.

**exp7_NCOA3 dataset**

**Description**
In this experiment we have used the qPLEX-RIME method to identify and characterize NCOA3 (SRC-3) associated proteins. We performed NCOA3 RIME pull-downs in five independent biological replicates and in five matched IgG mock samples.

**Usage**
data(exp7_NCOA3)

**exp8_CBP**

**exp8_CBP dataset**

**Description**
A qPLEX-RIME experiment was designed for the characterization of the CBP (CREB-binding protein) interactome. Five independent biological replicates of CBP RIME pull-downs and five IgG RIME pull-downs were prepared for this experiment.

**Usage**
data(exp8_CBP)

**Format**
An object of class `list` related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (CBP and IgG).
Value

An object of class `list` related to peptides quantification.

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### exp9_PolII

#### exp9_PolII dataset

**Description**

The qPLEX-RIME method was applied for the characterization of the largest and catalytic component of RNA polymerase II (RPB1). Particularly, the phosphorylated form at Serine 5 in the C-terminal domain (CTD) was used as the bait protein. Five biological replicates of RNA polymerase II RIME pull-downs and five IgG pull-downs were included for the identification and characterization of RNA polymerase II-associated proteins.

**Usage**

```r
data(exp9_PolII)
```

**Format**

An object of class `list` related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (PolII and IgG).

**Value**

An object of class `list` related to peptides quantification.

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### qPLEXdata

#### Available datasets in the qPLEXdata package

**Description**

This function lists the datasets available in qPLEXdata package.

**Usage**

```r
qPLEXdata()
```

**Value**

A list of datasets

**Examples**

```r
qPLEXdata()
```
Index

* datasets
  exp1_specificity, 2
  exp2_Xlink, 2
  exp3_OHT_ESR1, 3
  exp4_OHT_FP, 3
  exp5_PDX, 4
  exp6_ER, 4
  exp7_NCOA3, 5
  exp8_CBP, 5
  exp9_PolII, 6

* data
  exp1_specificity, 2
  exp2_Xlink, 2
  exp3_OHT_ESR1, 3
  exp4_OHT_FP, 3
  exp5_PDX, 4
  exp6_ER, 4
  exp7_NCOA3, 5
  exp8_CBP, 5
  exp9_PolII, 6

exp1_specificity, 2
exp2_Xlink, 2
exp3_OHT_ESR1, 3
exp4_OHT_FP, 3
exp5_PDX, 4
exp6_ER, 4
exp7_NCOA3, 5
exp8_CBP, 5
exp9_PolII, 6

list, 2–6
qPLEXdata, 6