Package ‘qPLEXdata’

April 18, 2024

Type Package

Title Data accompanying qPLEXanalyzer package

Version 1.21.0

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 devel

git_last_commit 148accf

git_last_commit_date 2023-10-24

Repository Bioconductor 3.19

Date/Publication 2024-04-18

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`exp1_specificity` *exp1_specificity dataset*

Description

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.

`exp2_Xlink` *exp2_Xlink dataset*

Description

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).

Value

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

`exp3_OHT_ESR1` *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` *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)
```

Format

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 (ER and IgG).

Value

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

`exp7_NCOA3` *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)
```

Format

An object of class `list` related to peptides quantification. It consists of qPLEX-RIME data of 10 samples divided into two conditions (NCOA3 and IgG).

Value

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

`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.

`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

```
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.

`qPLEXdata` *Available datasets in the qPLEXdata package*

Description

This function lists the datasets available in qPLEXdata package

Usage

```
qPLEXdata()
```

Value

A list of datasets

Examples

```
qPLEXdata()
```

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