

# Package ‘qPLEXdata’

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**Type** Package

**Title** Data accompanying qPLEXanalyzer package

**Version** 1.26.0

**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>

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**git\_last\_commit** d03cb23

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|                  |                                 |
|------------------|---------------------------------|
| exp1_specificity | <i>exp1_specificity dataset</i> |
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**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.

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|------------|---------------------------|
| exp2_Xlink | <i>exp2_Xlink dataset</i> |
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**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.

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`exp3_OHT_ESR1`*exp3\_OHT\_ESR1 dataset*

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**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*

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**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.

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`exp5_PDX`*exp5\_PDX dataset*

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**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*

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**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*

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**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*

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**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\_PolIII

*exp9\_PolIII dataset*

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**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_PolIII)
```

**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*

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**Description**

This function lists the datasets available in qPLEXdata package

**Usage**

```
qPLEXdata()
```

**Value**

A list of datasets

**Examples**

```
qPLEXdata()
```

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