

# Package ‘pRolocdata’

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**Type** Package

**Title** Data accompanying the pRoloc package

**Version** 1.29.0

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**Description** Mass-spectrometry based spatial proteomics data sets and protein complex separation data. Also contains the time course expression experiment from Mulvey et al. 2015.

**Depends** R (>= 3.6.3), MSnbase

**Imports** Biobase, utils

**Suggests** pRoloc (>= 1.13.8), testthat

**License** GPL-2

**BugReports** <https://github.com/lgatto/pRolocdata/issues>

**URL** <https://github.com/lgatto/pRolocdata>

**biocViews** ExperimentData, Homo\_sapiens\_Data, MassSpectrometryData, Arabidopsis\_thaliana\_Data, Drosophila\_melanogaster\_Data, Mus\_musculus\_Data, StemCell, Proteome

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## R topics documented:

andreyev2010	2
andy2011	3
at_chloro	4
baers2018	5
beltran2016	6
davies2018	7

dunkley2006	8
E14TG2a	10
fabre2015r1	11
foster2006	11
groen2014	12
hall2009	14
havugimana2012	14
hirst2018	15
hyperLOPIT2015	16
hyperLOPITU2OS2017	18
itzhak2016dynamic	20
itzhak2016stcSILAC	21
itzhak2017	21
kirkwood2013	23
Kozik_con	23
krahmer2018pcp	24
kristensen2012r1	25
lopimsSyn2	26
mulvey2015	26
nikolovski2012	27
nikolovski2014	29
orre2019	30
pRolocdata	31
pRolocmetadata	31
rodriguez2012r1	32
Shin2020	33
stekhoven2014	34
tan2009	34
ToxoLopit	36
trotter20010	36
yeast2018	37

## **Index** **39**

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andreyev2010	<i>Six sub-cellular fraction data from mouse macrophage-like RAW264.7 cells from Andreyev et al. (2009)</i>
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### **Description**

Data from Andreyev AY, Shen Z, Guan Z, Ryan A, Fahy E, Subramaniam S, Raetz CR, Briggs S, Dennis EA. Application of proteomic marker ensembles to subcellular organelle identification. *Mol Cell Proteomics*. 2010 Feb;9(2):388-402. DOI:<http://dx.doi.org/10.1074/mcp.M900432-MCP200>. PubMed PMID:19884172; PubMed Central PMCID:PMC2830848.

The 6 subcellular fractions are nuclei, mitochondria, cytoplasm, endoplasmic reticulum, plasma membrane and dense microsomal fraction.

### **Usage**

```
data("andreyev2010")
data("andreyev2010rest")
data("andreyev2010activ")
```

## Details

andreyev2010 is the full data where missing values were replaced by 0. andreyev2010rest and andreyev2010activ contain the resting (control) and Kdo2-lipid A-treated (activated) data respectively, which have been normalised (each reporter intensity was normalised by the sum over all replicates).

## Source

These data were generated from supplemental tables S1 (quantitative data) and 2 (organelle markers) (<http://www.mcponline.org/content/9/2/388/suppl/DC1>). See inst/scripts/andreyev2010.R for details.

## Examples

```
data(andreyev2010rest, verbose = TRUE)
data(andreyev2010activ, verbose = TRUE)

library("pRoloc")
par(mfrow = c(1, 2))
plot2D(andreyev2010rest, main = "Resting (control)")
plot2D(andreyev2010activ, main = "Kdo2-lipid A-treated")
addLegend(andreyev2010activ)
```

---

andy2011

*LOPIT experiment on Human Embryonic Kidney fibroblast HEK293T cells from Breckels et al. (2013)*

---

## Description

This is a LOPIT dataset from a standard LOPIT experimental design on Human Embryonic Kidney (HEK293T) fibroblast cells. See below for more details.

Note: this data was originally called andy2011. It is still available under that name but might be deprecated in the future and hence it is advised to use HEK293T2011.

## Usage

```
data(HEK293T2011)
data(HEK293T2011hpa)
data(HEK293T2011goCC)
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## Details

This is a LOPIT experiment. Normalised intensities for 1371 proteins for eight iTRAQ 8-plex labelled fractions. This dataset was used in testing the phenotype discovery algorithm from Breckels et al., *The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation*, J Proteomics, 2013, 88:129-40, see phenoDisco. New phenotype clusters identified from algorithm application are available as pd.2013 feature meta-data and the markers used as input for the analysis are available as markers feature meta-data.

The HEK293T2011goCC instance contains binary assay data. Its columns represent GO CC terms that have been observed for the object's features. A 1 indicates that a GO term has been associated to a given feature (protein); a 0 means not such association was found in the GO ontology.

The HEK293T2011hpa instance contains binary assay data. Its columns represent subcellular locations that have been observed from microscopy images from the Human Protein Atlas, for each protein. A 1 indicates that a subcellular term has been associated to a given feature (protein); a 0 means not such association was found. This matrix of terms was generated from version 13, released on 11/06/2014 of the Human Protein Atlas.

### Source

The data was generated by A. Christoforou at the Cambridge Centre for Proteomics.

<http://www.bio.cam.ac.uk/proteomics/>.

### References

Breckels LM, Gatto L, Christoforou A, Groen AJ, Lilley KS and Trotter MWB. *The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation*. J Proteomics. 2013 Aug 2;88:129-40. doi: 10.1016/j.jprot.2013.02.019. Epub 2013 Mar 21. PubMed PMID: 23523639

### Examples

```
data(HEK293T2011)
HEK293T2011
pData(HEK293T2011)
head(exprs(HEK293T2011))
## Organelle marker proteins
table(fData(HEK293T2011)$markers)
## PhenoDisco assignment results
table(fData(HEK293T2011)$pd.2013)

data(HEK293T2011goCC)
dim(HEK293T2011goCC)
head(featureNames(HEK293T2011goCC))
exprs(HEK293T2011goCC)[1:10, 1:5]
```

---

at\_chloro

*The AT\_CHLORO data base*

---

### Description

AT\_CHLORO is a comprehensive chloroplast proteome database with subplastidial localization and curated information on envelope proteins.

The assayData contains the raw spectral counts for 3 chloroplastic fractions (the envelope, the stroma and the thylakoids) and for a complete chloroplast sample. The percentage of occurrence in each of the sub-chloroplast fraction as calculated in Ferro et al. (2010) are available as feature meta data (Percent\_ENV, Percent\_STR and Percent\_THY).

### Usage

```
data(at_chloro)
```

**Format**

The data is an instance of class MSnSet from package MSnbase.

**Source**

Myriam Ferro Exploring the Dynamics of Proteomes (EDyP) Laboratoire Biologie a Grande Echelle (BGE) U1038 INSERM/CEA/UJF Institut de Recherches en Technologies et Sciences pour le Vivant (iRTSV) CEA/Grenoble

**References**

Ferro M, Brugiere S, Salvi D, Seigneurin-Berny D, Court M, Moyet L, Ramus C, Miras S, Mellal M, Le Gall S, Kieffer-Jaquinod S, Bruley C, Garin J, Joyard J, Masselon C, Rolland N. AT\_CHLORO, a comprehensive chloroplast proteome database with subplastidial localization and curated information on envelope proteins. *Mol Cell Proteomics*. 2010 Jun;9(6):1063-84. Epub 2010 Jan 10. PubMed PMID: 20061580; PubMed Central PMCID: PMC2877971

**Examples**

```
data(at_chloro)
dim(at_chloro)
pData(at_chloro)
head(exprs(at_chloro))
fvarLabels(at_chloro)
table(fData(at_chloro)$markers)
## check exprs data and 'TotalSpectralCount' feature meta data
all(fData(at_chloro)$TotalSpectralCount == rowSums(exprs(at_chloro)))
## create a set with the percentage of occurrence, as in Ferro et al. 2010
## rows that have no 'TOT' in the feature vars of interest
sel <- apply(fData(at_chloro)[, c("Percent_ENV", "Percent_STR", "Percent_THY")],
            1, function(.x) length(grep("TOT", .x)) == 0)
## new MSnSet
at_chloro2 <- at_chloro[sel, 1:3]
## columns of interest
perc <- c("Percent_ENV", "Percent_STR", "Percent_THY")
## create a new intensity matrix
exprs2 <- matrix(as.numeric(as.matrix(fData(at_chloro2)[, perc])), ncol
= 3)
colnames(exprs2) <- sampleNames(at_chloro2)
rownames(exprs2) <- featureNames(at_chloro2)
summary(rowSums(exprs2))
exprs(at_chloro2) <- exprs2
validObject(at_chloro2)
```

**Description**

Data from 'Spatial mapping of a cyanobacterial proteome reveals distinct subcellular compartment organisation and dynamic metabolic pathways' (submitted).

Cyanobacteria are complex prokaryotes, incorporating a Gram-negative cell wall and internal thylakoid membranes. However, localisation of proteins within cyanobacterial cells is poorly understood. Using subcellular fractionation and quantitative proteomics we report the most extensive subcellular map of the proteome of a cyanobacterial cell, identifying ~67% of *Synechocystis* sp. PCC 6803 proteins, ~1000 more than previous studies. 1711 proteins were assigned to six specific subcellular regions.

This dataset is composed of two combined replicated 10-plex LOPIT experiments.

Protein markers for the plasma membrane, thylakoid membrane, cytosol, and small and large ribosomal subunits were curated from a literature review. A Support Vector Machine (SVM) classifier was employed on the combined dataset, with a radial basis function kernel, using class specific weights for classification of unassigned proteins to one of the 5 defined sub-cellular niches, TM, PM, soluble, small ribosomal subunit, large ribosomal subunit. The weights used in classification were set to be inversely proportional to the subcellular class frequencies to account for class imbalance. Algorithmic performance of the SVM on the dataset was estimated (as described in Trotter et al 2010). Scoring thresholds were calculated per subcellular niche and were set based on concordance with existing subcellular knowledge annotation to attain a 7.5% false discovery rate (FDR). Unassigned proteins were then classified to 1 of the 5 compartments according to the SVM prediction if greater than the calculated class threshold.

### Usage

```
data("baers2018")
```

### Examples

```
data(baers2018)

library("pRoloc")
par(mfrow = c(1, 2))
plot2D(baers2018, main = "Markers")
addLegend(baers2018, where = "bottomright")
plot2D(baers2018, fcol = "Localisation", main = "Localisation")
```

---

beltran2016

*Data from Beltran et al. 2016*

---

### Description

The data contain the spatial proteomics data for 5 time points (24, 48, 72, 96 and 120) and two conditions (HMCV infection and MOCK), totalling 10 MSnSet object. Each contains expression data for 1748 to 2220 proteins along 6 fractions quantified by TMT 6-plex.

### Usage

```
data(beltran2016HCMV24)
data(beltran2016HCMV48)
data(beltran2016HCMV72)
data(beltran2016HCMV96)
data(beltran2016HCMV120)
data(beltran2016MOCK24)
data(beltran2016MOCK48)
```

```
data(beltran2016MOCK72)
data(beltran2016MOCK96)
data(beltran2016MOCK120)
```

### Format

The data is an instance of class MSnSet from package MSnbase.

### References

Jean Beltran PM, Mathias RA, Cristea IM. *A Portrait of the Human Organelle Proteome In Space and Time during Cytomegalovirus Infection*. Cell Syst. 2016 Oct 26;3(4):361-373.e6. doi: 10.1016/j.cels.2016.08.012. Epub 2016 Sep 15. PubMed PMID: 27641956; PubMed Central PMCID: PMC5083158.

### Examples

```
## load the two 24 hours datasets
data(beltran2016MOCK24)
data(beltran2016HCMV24)
beltran2016MOCK24
beltran2016HCMV24

## the expression data
head(exprs(beltran2016MOCK24))
head(exprs(beltran2016HCMV24))

## abstract
abstract(beltran2016HCMV24)

## plotting
library("pRoloc")
par(mfrow = c(1, 2))
plot2D(beltran2016HCMV24, main = "HCMV 24hpi")
plot2D(beltran2016MOCK24, main = "MOCK 24hpi")

## Combine the data as a list and keep only common features
ml <- MSnSetList(list(beltran2016HCMV24, beltran2016MOCK24))
ml <- commonFeatureNames(ml)

par(mfrow = c(1, 2))
plot2D(ml[[1]], main = "HCMV 24hpi")
plot2D(ml[[2]], main = "MOCK 24hpi")
```

---

davies2018

*AP-4 vesicles contribute to spatial control of autophagy via RUSC-dependent peripheral delivery of ATG9A*

---

### Description

Data from 'AP-4 vesicles contribute to spatial control of autophagy via RUSC-dependent peripheral delivery of ATG9A' Nature Communications.

Adaptor protein 4 (AP-4) is an ancient membrane trafficking complex, whose function has largely remained elusive. In humans, AP-4 deficiency causes a severe neurological disorder of unknown

aetiology. We apply unbiased proteomic methods, including 'Dynamic Organellar Maps', to find proteins whose subcellular localisation depends on AP-4. We identify three transmembrane cargo proteins, ATG9A, SERINC1 and SERINC3, and two AP-4 accessory proteins, RUSC1 and RUSC2. We demonstrate that AP-4 deficiency causes missorting of ATG9A in diverse cell types, including patient-derived cells, as well as dysregulation of autophagy. RUSC2 facilitates the transport of AP-4-derived, ATG9A-positive vesicles from the trans-Golgi network to the cell periphery. These vesicles cluster in close association with autophagosomes, suggesting they are the 'ATG9A reservoir' required for autophagosome biogenesis. Our study uncovers ATG9A trafficking as a ubiquitous function of the AP-4 pathway. Furthermore, it provides a potential molecular pathomechanism of AP-4 deficiency, through dysregulated spatial control of autophagy.

### Usage

```
data("davies2018ap4b1")
data("davies2018ap4e1")
data("davies2018wt")
```

### Format

The data is an instance of class MSnSet from package MSnbase.

### References

*AP-4 vesicles contribute to spatial control of autophagy via RUSC-dependent peripheral delivery of ATG9A* Alexandra K. Davies, Daniel N. Itzhak, James R. Edgar, Tara L. Archuleta, Jennifer Hirst, Lauren P. Jackson, Margaret S. Robinson & Georg H. H. Borner <https://doi.org/10.1038/s41467-018-06172-7>

### Examples

```
data(davies2018wt)
davies2018wt
pData(davies2018wt)
exprs(davies2018wt)[1:3,1:3]

library("pRoloc")
plot2D(davies2018wt,, main = "Davies 2018 HeLa - wt")
```

---

dunkley2006

*LOPIT data from Dunkley et al. (2006)*

---

### Description

This is the data from Dunkley et al., *Mapping the Arabidopsis organelle proteome*, PNAS 2006 (PMID 16618929). See below for more details.

### Usage

```
data(dunkley2006)
data(dunkley2006goCC)
```



## Format

The data is an instance of class MSnSet from package MSnbase.

## Details

This is a LOPIT experiment. Normalised intensities for 689 proteins for four iTRAQ 4-plex labelled fraction and 2 membrane preparation in duplicate (16 samples, see phenoData(dunkley2006) for more details) are provided.

Partial least square discriminant analysis (PLSDA) has originally been applied to the test data fData(dunkley)\$markers); assignment results are available with fData(dunkley)\$assigned) for 5 organelles.

This dataset was also used in testing the phenotype discovery algorithm from Breckels et al., *The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation*, J Proteomics, In Press., see phenoDisco. New phenotype clusters identified from algorithm application are available as pd.2013 feature meta-data.

The dunkley2006goCC instance contains binary assay data. Its columns represent GO CC terms that have been observed for the object's features. A 1 indicates that a GO term has been associated to a given feature (protein); a 0 means not such association was found in the GO ontology.

## Source

Supporting Information on <http://www.pnas.org/content/103/17/6518.abstract>.

## References

Dunkley TP, Hester S, Shadforth IP, Runions J, Weimar T, Hanton SL, Griffin JL, Bessant C, Brandizzi F, Hawes C, Watson RB, Dupree P, Lilley KS. *Mapping the Arabidopsis organelle proteome*. Proc Natl Acad Sci U S A. 2006 Apr 25;103(17):6518-23. Epub 2006 Apr 17. PubMed PMID: 16618929; PubMed Central PMCID: PMC1458916.

Breckels LM, Gatto L, Christoforou A, Groen AJ, Lilley KS and Trotter MWB. *The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation* J Proteomics. In Press.

## Examples

```
data(dunkley2006)
dunkley2006
phenoData(dunkley2006)
## Input training data (organelle markers)
table(fData(dunkley2006)$markers)
## PLSDA assignment results
table(fData(dunkley2006)$assigned)
## PhenoDisco results
table(fData(dunkley2006)$pd.2013)
```

---

E14TG2a

*LOPIT experiment on Mouse E14TG2a Embryonic Stem Cells from Breckels et al. (2016)*

---

### Description

This is data from a standard LOPIT experimental design on Mouse E14TG2a embryonic stem cells. See below for more details.

### Usage

```
data(E14TG2aS1)
data(E14TG2aS2)
data(E14TG2aR)
data(E14TG2aS1yLoc)
data(E14TG2aS1goCC)
```

### Format

The data is an instance of class MSnSet from package MSnbase.

### Details

This is a LOPIT experiment. Normalised intensities of proteins from eight iTRAQ 8-plex labelled fractions are available for 2 replicates (indexed 1 and 2) using stringent and relaxed setting (S and R, respectively).

The E14TG2aS1goCC instance contains binary assay data. Its columns represent GO CC terms that have been observed for the object's features. A 1 indicates that a GO term has been associated to a given feature (protein); a 0 means not such association was found in the GO ontology.

The E14TG2aS1yLoc instance contains 34 sequence and annotation features obtained from a feature selection of the sequence and annotation features from the computational classifier YLoc. These features include: variants of psuedo amino acid counts, autocorrelation, sum of charge, prosite patterns, Gene Ontology terms and the number of signal peptides. These features are described in detail in Breckels et al (2015).

### Source

The data was generated by A. Christoforou at the Cambridge Centre for Proteomics, Cambridge. <http://www.bio.cam.ac.uk/proteomics/>.

### Examples

```
data(E14TG2aS1)
E14TG2aS1
pData(E14TG2aS1)
head(exprs(E14TG2aS1))
```

---

fabre2015r1

*Data from Fabre et al. 2015*

---

### Description

Duplicated experimental data from Fabre et al. 2015, *Deciphering preferential interactions within supramolecular protein complexes: the proteasome case*. Protein complexes were separated by glycerol density gradient centrifugation. Proteins have been quantified by label-free (iBAQ) mass spectrometry.

### Usage

```
data("fabre2015r1")
data("fabre2015r2")
```

### References

Fabre B, Lambour T, Garrigues L, Amalric F, Vigneron N, Menneteau T, Stella A, Monsarrat B, Van den Eynde B, Burlet-Schiltz O, Bousquet-Dubouch MP. Deciphering preferential interactions within supramolecular protein complexes: the proteasome case. *Mol Syst Biol.* 2015 Jan 5;11(1):771. doi: 10.15252/msb.20145497. PubMed PMID: 25561571.

### Examples

```
data(fabre2015r1)
experimentData(fabre2015r1)
library("pRoloc")
plot2D(fabre2015r1)
addLegend(fabre2015r1, where = "topright")
```

---

foster2006

*PCP data from Foster et al. (2006)*

---

### Description

This is the data from Foster et al., *A Mammalian Organelle Map by Protein Correlation Profiling*, *Cell* 2006 (PMID 16615899). See below for more details.

### Usage

```
data(foster2006)
```

### Format

The data is an instance of class MSnSet from package MSnbase.

## Details

This is a PCP experiment. Label-free quantification has been done on a total of 26 high and low density-separated fractions (see `pData(foster2006)`). A total of 1555 proteins have been quantified in a subset of the fractions. The proteins are described in the `featureData` slot. Chi<sup>2</sup> calculations, as defined in the PCP experiment, has been performed using marker proteins for a total of 8 organelles, as well as the authors' original assignment and notes are available in the `featureData` slot.

## Source

Supplemental data on [http://www.cell.com/abstract/S0092-8674\(06\)00369-2](http://www.cell.com/abstract/S0092-8674(06)00369-2).

## References

Foster LJ, de Hoog CL, Zhang Y, Zhang Y, Xie X, Mootha VK, Mann M. *A mammalian organelle map by protein correlation profiling*. Cell. 2006 Apr 7;125(1):187-99. PubMed PMID: 16615899.

## Examples

```
data(foster2006)
foster2006
phenoData(foster2006)
featureData(foster2006)
## organelle marker proteins
table(fData(foster2006)$train)
```

---

groen2014

*LOPIT experiments on Arabidopsis thaliana roots, from Groen et al. (2014)*

---

## Description

This is the data from Groen et al. *Identification of Trans Golgi Network proteins in Arabidopsis thaliana root tissue* J. Proteome Res, 2014, Feb 7; 13(2):763-776. See below for more details.

## Usage

```
data(groen2014r1)
data(groen2014r2)
data(groen2014r3)
data(groen2014cmb)
data(groen2014r1goCC)
```

## Format

An instance of class `MSnSet` from package `MSnbase`.

## Details

This is a LOPIT experiment. Normalised intensities for proteins for four iTRAQ 4-plex labelled fractions are available for 3 replicates (r1, r2 and r3 respectively). The 3 replicates have also been combined as described in Groen et al. and Trotter et al. (2010) to generate a fourth dataset (cmb), also shown in the example code below.

The groen2014r1goCC instance contains binary assay data. Its columns represent GO CC terms that have been observed for the object's features. A 1 indicates that a GO term has been associated to a given feature (protein); a 0 means not such association was found in the GO ontology.

## Source

<http://pubs.acs.org/doi/abs/10.1021/pr4008464>

## References

Groen AJ, Sancho-Andres G, Breckels LM, Gatto L, Aniento F, and Lilley KS. *Identification of Trans Golgi Network proteins in Arabidopsis thaliana root tissue*. J. Proteome Res, 2014, Feb 7; 13(2):763-776. DOI:10.1021/pr4008464, PMID: 24344820.

Trotter MWB, Sadowski PG, Dunkley TPJ, Groen AJ and Lilley KS. *Improved sub-cellular resolution via simultaneous analysis of organelle proteomics data across varied experimental conditions*. Proteomics 2010 10(23):4213-4219. PMID 21058340.

Sadowski PG, Groen AJ, Dupree P and Lilley KS. *Sub-cellular localization of membrane proteins*. Proteomics 2008 8(19):3991-4011. PMID 18780351.

Dunkley TP, Hester S, Shadforth IP, Runions J, Weimar T, Hanton SL, Griffin JL, Bessant C, Brandizzi F, Hawes C, Watson RB, Dupree P, Lilley KS. *Mapping the Arabidopsis organelle proteome*. Proc Natl Acad Sci U S A. 2006 Apr 25;103(17):6518-23. Epub 2006 Apr 17. PubMed PMID: 16618929; PubMed Central PMCID: PMC1458916.

## Examples

```
data(groen2014r1)
data(groen2014r2)
data(groen2014r3)
data(groen2014cmb)

## The combine dataset can generated manually using
cmb <- combine(groen2014r1, updateFvarLabels(groen2014r2))
cmb <- filterNA(cmb)
cmb <- combine(cmb, updateFvarLabels(groen2014r3))
cmb <- filterNA(cmb)
fData(cmb) <- fData(cmb)[, c(1,2,5)]
cmb

## or can simply be loaded directly
data(groen2014cmb)

## check datasets are the same
all.equal(cmb, groen2014cmb, check.attributes=FALSE)
```

---

hall12009

*LOPIT data from Hall et al. (2009)*

---

### Description

This is the data from Hall et al. *The Organelle Proteome of the DT40 Lymphocyte Cell Line* Mol Cell Proteomics. 2009 Jun;8(6):1295-305. (PMID: PMC2690488).

### Usage

```
data(hall12009)
```

### Format

An instance of class MSnSet from package MSnbase.

### Details

See reference.

### Source

<http://www.mcponline.org/content/8/6/1295.abstract>

### References

Hall SL, Hester S, Griffin JL, Lilley KS, Jackson AP. *The organelle proteome of the DT40 lymphocyte cell line* Mol Cell Proteomics. 2009 Jun;8(6):1295-305. doi: 10.1074/mcp.M800394-MCP200. Epub 2009 Jan 30. PubMed PMID: 19181659; PubMed Central PMCID: PMC2690488.

### Examples

```
data(hall12009)
pData(hall12009)
library("pRoloc")
plot2D(hall12009)
```

---

havugimana2012

*Data from Havugimana et al. 2012*

---

### Description

Data from Havugimana et al. 2012, *A census of human soluble protein complexes*. The protein complexes were fractionated by ion exchange chromatography, Isoelectric focusing and sucrose density gradient centrifugation. Proteins were quantified by spectral counting.

### Usage

```
data("havugimana2012")
```

## References

Havugimana PC, Hart GT, Nepusz T, Yang H, Turinsky AL, Li Z, Wang PI, Boutz DR, Fong V, Phanse S, Babu M, Craig SA, Hu P, Wan C, Vlasblom J, Dar VU, Bezginov A, Clark GW, Wu GC, Wodak SJ, Tillier ER, Paccanaro A, Marcotte EM, Emili A. A census of human soluble protein complexes. *Cell*. 2012 Aug 31;150(5):1068-81. doi: 10.1016/j.cell.2012.08.011. PubMed PMID: 22939629; PubMed Central PMCID: PMC3477804.

## Examples

```
data(havugimana2012)
experimentData(havugimana2012)
```

---

hirst2018

*Data from Hirst et al. 2018*

---

## Description

From the supplementary file notes:

These are the SILAC ratio data from 2046 proteins with complete profiles across all nine organellar maps.

Each profile consists of five ratios, corresponding to five subcellular fractions obtained by differential centrifugation (3000 x g pellet, 6000 x g pellet, 12000 x g pellet, 24000 x g pellet, 80000 x g pellet). The centrifugation speeds are available in the MSnSet object.

Each ratio shows the abundance of the total membrane SILAC heavy spike-in relative to the abundance in a given subfraction.

Maps were made from three cell lines (control HeLa, and two independent AP5Z1 KO HeLa cell lines, called AP5KNC2 and AP5KOC6), each in triplicate (replicates R1, R2, and R3). The sample are code as "CTRL" (HeLa control), "C2" (AP5KNC2 AP5Z1 KO cells) and "C6" (AP5KNC6 AP5Z1 KO cells).

Marker proteins used to define organellar clusters in Supplemental Figure 1 in the manuscript are annotated as feature variable markers.

Finally, the ratios in the hirst2018 data were normalised by their sum (using `normalise(, method = "sum")`).

The feature data also contains information about the comparison of organellar maps made from control or AP5 ablated cells, revealing putative proteins that undergo subcellular localisation shifts. Each protein receives an M score (magnitude of movement), and an R score (reproducibility of movement, i.e. correlation between replicates). In addition, the reproducibility of movement between the two AP5 KO cell lines is scored (Correlation C2 vs C6). Note however that the authors themselves claim that:

‘The cutoffs chosen in Fig 1C ( $M > 1.5$ ,  $R > 0.5$ ) correspond to an estimated FDR of 23%. Please note that the actual FDR is probably lower than this estimated FDR, because the mock data lack the additional cell line and the clonal correlation filter.’

The re-localisation candidates are those that have an M score  $> 1.5$  and a R score  $> 0.5$ , and are marked with a hit feature variable set to TRUE.

## Usage

```
data(hirst2018)
```

**Format**

The data is an instance of class MSnSet from package MSnbase.

**References**

Hirst J, Itzhak DN, Antrobus R, Borner GHH, Robinson MS. Role of the AP-5 adaptor protein complex in late endosome-to-Golgi retrieval. *PLoS Biol.* 2018 Jan 30;16(1):e2004411. doi: 10.1371/journal.pbio.2004411. eCollection 2018 Jan. PubMed PMID: 29381698; PubMed Central PMCID: PMC5806898.

**Examples**

```
## load the two 24 hours datasets
data(hirst2018)
hirst2018

## experimental design
table(pData(hirst2018)[, -2])

## the expression data
exprs(hirst2018)[1:5, 1:3]

## abstract
abstract(hirst2018)

## split data by samples
x <- split(hirst2018, "sample")

## These are the relocalisation hits
hits <- which(fData(hirst2018)$Hits)
reloc <- FeaturesOfInterest(description = "Relocation hits",
  featureNames(hirst2018)[hits])
reloc

## plotting
library("pRoloc")
par(mfrow = c(1, 3))
plot2D(x[[1]], main = "AP5KNC2")
highlightOnPlot(x[[1]], reloc)
plot2D(x[[2]], main = "AP5KNC6")
highlightOnPlot(x[[1]], reloc)
plot2D(x[[3]], main = "HeLa control")
highlightOnPlot(x[[1]], reloc)
addLegend(x[[3]], where = "topleft")
```

---

hyperLOPIT2015

*Protein and PMS-level hyperLOPIT datasets on Mouse E14TG2a embryonic stem cells from Christoforou et al. (2016).*

---

**Description**

This is a spatial proteomics dataset from a hyperLOPIT experimental design on Mouse E14TG2a embryonic stem cells.



## Usage

```
data(hyperLOPIT2015)
data(hyperLOPIT2015ms3r1)
data(hyperLOPIT2015ms3r2)
data(hyperLOPIT2015ms3r3)
data(hyperLOPIT2015ms2)
data(hyperLOPIT2015ms3r1psm)
data(hyperLOPIT2015ms3r2psm)
data(hyperLOPIT2015ms2psm)
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## Details

This is a hyperLOPIT experiment. Normalised intensities for proteins for TMT 10-plex labelled fractions are available for 3 replicates acquired in MS3 mode (hyperLOPIT2015ms3r1, hyperLOPIT2015ms3r2 and hyperLOPIT2015ms3r3) using an Orbitrap Fusion mass-spectrometer. The first two replicates have also been combined as described in Trotter et al (2010) to generate dataset hyperLOPIT2015 to increase organellar resolution. A dataset acquired in MS2 mode has also been acquired (hyperLOPIT2015ms2) which was also generated using the Orbitrap Fusion and using a TMT 10-plex experimental design.

The PSM-level cvs file are available in the extdata directory and have been processed as follows: imported MSnSet instances using readMSnSet2, PSMs with missing values were filtered out with filterNA, only PSMs with feature variable Quan.Usage "Used" and a TMT6plex modification were retained and the phenoData was matched and assigned from the respective protein-level data. Finally, marker proteins are annotated based on the combined protein-level data hyperLOPIT2015 and reporter tags are normalised using the "sum" method. The processing script is scripts/hyperlopit2015psm.R.

The TAGM feature data contains the allocation results from the Bayesian T-augmented Gaussian Mixture modelling approach as described in Crook et al. (2018).

## Source

The data was generated by A. Christoforou and C. Mulvey in the Cambridge Centre for Proteomics. <http://www.bio.cam.ac.uk/proteomics/>.

## References

*A draft map of the mouse pluripotent stem cell spatial proteome.* Christoforou A, Mulvey CM, Breckels LM, Geladaki A, Hurrell T, Hayward PC, Naake T, Gatto L, Viner R, Martinez Arias A, Lilley KS. Nat Commun. 2016 Jan 12;7:8992. doi: 10.1038/ncomms9992. PubMed PMID: 26754106; PubMed Central PMCID: PMC4729960.

*A Bayesian Mixture Modelling Approach For Spatial Proteomics* Oliver M Crook, Claire M Mulvey, Paul D. W. Kirk, Kathryn S Lilley, Laurent Gatto bioRxiv 282269; doi: <https://doi.org/10.1101/282269>

## Examples

```
data(hyperLOPIT2015)
hyperLOPIT2015
pData(hyperLOPIT2015)
head(exprs(hyperLOPIT2015))

data(hyperLOPIT2015ms3r1psm)
```

```
x <- combineFeatures(hyperLOPIT2015ms3r1psm,
  groupBy = fData(hyperLOPIT2015ms3r1psm)$Protein.Group.Accession,
  fun = median)
library("pRoloc")
par(mfrow = c(1, 2))
plot2D(hyperLOPIT2015ms3r1psm, main = "PSM-level")
plot2D(x, main = "Protein-level (using mean)")
```

---

hyperLOPITU2OS2017      *2017 and 2018 hyperLOPIT on U2OS cells*

---

## Description

This data contains 4 different datasets generated from U2OS cells. The lopitdcU2OS2018 was generated using the LOPIT-DC method and all other datasets have been generated using the hyperLOPIT protocol (see Christoforou et al. 2016 and Mulvey et al. 2017). The lopitdcU2OS2018 dataset contains 3 replicates, 10 fractions per replicate. The hyperLOPITU2OS2017 dataset contains 2 replicates, in which the quantitation was obtained using two sets of TMT 10-plex per replicate, producing a total of 40 quantitation channels, while in hyperLOPITU2OS2017b, 3 fractions with low protein yields have been removed (see example below). The hyperLOPITU2OS2018 dataset contains a third replicate, thus giving 57 quantitation channels in total.

## Usage

```
data("hyperLOPITU2OS2017")
```

## Format

An object of class MSnSet, defined in the MSnbase package.

## Details

The data (expression and feature variable) contain:

- UniProt Accession for Protein Group (no isoform information): Unique UniProt accession for quantified protein group reported by Proteome Discoverer (1% FDR) - isoform information not retained.
- Normalized TMT 10-plex Reporter Ion Distribution: ReplicateX TMT SetX-126 Normalized TMT 10-plex reporter ion values, representing the distribution of each protein across the fractionation scheme for each experiment. Protein-level reporter ion values were calculated by taking the median of all quantifiable PSMs for the protein group, then normalized so that the sum of all 10 channels was equal to 1. The numeric value in the tag name corresponds to the nominal mass of each TMT reporter ion. The N and C suffixes differentiate between the 15N or 13C isotopologue variants of TMT 10-plex reporter ions of the same nominal mass.
- UniProt Accession for Protein Group (with isoform information): Unique UniProt accession for quantified protein group reported by Proteome Discoverer (1% FDR) - isoform information retained.
- UniProt Protein Description: UniProt description for protein accession.
- Coverage: Percentage of protein sequence covered by identified peptides.
- Quantified Proteins: Number of quantified protein groups.

- Quantified Unique Peptides: Number of unique quantified peptides. Only these peptides were used for quantification.
- Quantified Peptides: Number of quantified peptides. Only peptides that were unique to a single protein group were used for quantification.
- Quantified PSMs: Number of quantified peptide-spectrum matches.
- Score - ReplicateX TMT SetX: Total score of identified protein group for each experiment. This score is equal to the sum of the individual peptide scores.
- Coverage - ReplicateX TMT SetX: Percentage of protein sequence covered by identified peptides for each experiment.
- Quantified Peptides - ReplicateX TMT SetX: Number of quantified peptides for each experiment. Only peptides that were unique to a single protein group were used for quantification.
- Quantified PSMs - ReplicateX TMT SetX: Number of quantified peptide-spectrum matches for each experiment.
- SVM Marker Set: Final marker set used for SVM classification of protein subcellular localization to 14 subcellular compartments.
- SVM Classification: Subcellular class to which the protein group was assigned by SVM classification. All proteins are assigned to a single class by SVM.
- SVM Score: Confidence score for localization assignment, ranging from 0 to 1. A score close to 0 represents a very low confidence assignment, whereas a score of 1 indicates a very high confidence assignment.
- Final SVM Classification (5% FDR) (assignment): Predicted localization, with SVM score thresholds determined empirically by comparison to GO annotation and protein database annotation. The SVM score thresholds were set individually for each class so that the false discovery rate of the SVM classification was equal or lower than 5%.

## References

Thul PJ et al. *A subcellular map of the human proteome*. Science. 2017 May 26;356(6340). pii: eaal3321. doi: 10.1126/science.aal3321. Epub 2017 May 11. PubMed PMID: 28495876.

## Examples

```
data(hyperLOPITU2OS2017)
hyperLOPITU2OS2017

library("pRoloc")
plot2D(hyperLOPITU2OS2017, addLegend = "bottomleft")

## removing low intensity fractions
sort(colSums(exprs(hyperLOPITU2OS2017)))
i <- order(colSums(exprs(hyperLOPITU2OS2017)))[1:3]
x <- hyperLOPITU2OS2017[, -i]
plot2D(x, mirrorY = TRUE)

data(hyperLOPITU2OS2017b)
## only difference if subsetting data
all.equal(hyperLOPITU2OS2017b, x)
processingData(hyperLOPITU2OS2017b)
processingData(x)
```

---

itzhak2016dynamic	<i>Global, quantitative and dynamic mapping of protein subcellular localization</i>
-------------------	---

---

## Description

Data from 'Global, quantitative and dynamic mapping of protein subcellular localization.

Subcellular localization critically influences protein function, and cells control protein localization to regulate biological processes. We have developed and applied Dynamic Organellar Maps, a proteomic method that allows global mapping of protein translocation events. We initially used maps statically to generate a database with localization and absolute copy number information for over 8700 proteins from HeLa cells, approaching comprehensive coverage. All major organelles were resolved, with exceptional prediction accuracy (estimated at >92%). Combining spatial and abundance information yielded an unprecedented quantitative view of HeLa cell anatomy and organellar composition, at the protein level. We subsequently demonstrated the dynamic capabilities of the approach by capturing translocation events following EGF stimulation, which we integrated into a quantitative model. Dynamic Organellar Maps enable the proteome-wide analysis of physiological protein movements, without requiring any reagents specific to the investigated process, and will thus be widely applicable in cell biology.

## Usage

```
data("itzhak2016helaCtrl")
data("itzhak2016helaEgf")
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## References

*Itzhak DN, Tyanova S, Cox J, Borner GH. Global, quantitative and dynamic mapping of protein subcellular localization. Elife. 2016 Jun 9;5:e16950.*

## Examples

```
data("itzhak2016helaCtrl")
helaCtrl <- itzhak2016helaCtrl
pData(helaCtrl)
exprs(helaCtrl)[1:3,1:3]

library("pRoloc")
plot2D(helaCtrl, main = "HeLa Ctrl", dims = c(1, 3))
```

---

itzhak2016stcSILAC      *Data from Itzhak et al. (2016)*

---

### Description

Data from Daniel N Itzhak, Stefka Tyanova, Jurgen Cox and Georg HH Borner. Global, quantitative and dynamic mapping of protein subcellular localization. DOI:<http://dx.doi.org/10.7554/eLife.16950> Published June 9, 2016 Cite as eLife 2016;10.7554/eLife.16950

It currently contains

- The second sheet contains the 6 replicates of the SILAC static data (*Static* data were used to generate six deep organellar maps) and is made available as itzhak2016stcSILAC.

### Usage

```
data("itzhak2016stcSILAC")
```

### Source

This data was generated from Supplementary file 9 (<https://elifesciences.org/content/5/e16950/supp-material9>). See `inst/scripts/itzhak2016.R` for details.

### Examples

```
data(itzhak2016stcSILAC)
itzhak2016stcSILAC
dim(itzhak2016stcSILAC)
pData(itzhak2016stcSILAC)

## only 1st replicate
dim(itzhak2016stcSILAC[, itzhak2016stcSILAC$rep == 1])

## filter out features with missing values
itzhak2016stcSILAC <- filterNA(itzhak2016stcSILAC)

library("pRoloc")
## Cell map
plot2D(itzhak2016stcSILAC)
## as in the paper
plot2D(itzhak2016stcSILAC, dims = c(1, 3))
```

---

itzhak2017

*Data from Itzhak et al. 2017*

---

## Description

The data from Itzhal et al. 2017 defines a spatial map for mouse primary neurons. The data are composed of 5 spatial maps, each containing 6 differential centrifugation fraction (as described in Itzhak et al. 2016, see [itzhak2016](#)).

The annotated marker proteins are available in the `itzhak2017markers` dataset.

This data corresponds to the *Mouse neuron Intensity and LFQ data* data from supplemental table S3 (Proteomic Mouse Neuron Data Generated in This Study, Related to Figure 5).

## Usage

```
data(itzhak2017)
data(itzhak2017markers)
```

## Format

The data is an instance of class `MSnSet` from package `MSnbase`.

## References

Itzhak DN, Davies C, Tyanova S, Mishra A, Williams J, Antrobus R, Cox J, Weekes MP, Borner GH. A Mass Spectrometry-Based Approach for Mapping Protein Subcellular Localization Reveals the Spatial Proteome of Mouse Primary Neurons. *Cell Rep.* 2017 Sep 12;20(11):2706-2718. doi: 10.1016/j.celrep.2017.08.063. PubMed PMID: 28903049; PubMed Central PMCID: PMC5775508.

## Examples

```
data(itzhak2017)
itzhak2017

## experimental design
table(pData(itzhak2017))

## the expression data
exprs(itzhak2017)[1:5, 1:5]

## abstract
abstract(itzhak2017)

## split data by samples
x <- split(itzhak2017, "map")

## plotting
library("pRoloc")
par(mfrow = c(2, 3))
for (i in 1:5)
  plot2D(x[[i]], main = paste("Map", i))
plot2D(itzhak2017, main = "All maps")
addLegend(itzhak2017, where = "bottomleft")
```

---

`kirkwood2013`*Data from Kirkwood et al. 2013.*

---

**Description**

Data from Kirkwood et al. 2013, *Characterization of native protein complexes and protein isoform variation using size-fractionation-based quantitative proteomics*. Protein complexes were separated by size exclusion chromatography and proteins were quantified by spectral counting.

**Usage**

```
data("kirkwood2013")
```

**References**

Kirkwood KJ, Ahmad Y, Larance M, Lamond AI. Characterization of native protein complexes and protein isoform variation using size-fractionation-based quantitative proteomics. *Mol Cell Proteomics*. 2013 Dec;12(12):3851-73. doi: 10.1074/mcp.M113.032367. Epub 2013 Sep 16. PubMed PMID: 24043423; PubMed Central PMCID: PMC3861729.

**Examples**

```
data(kirkwood2013)
experimentData(kirkwood2013)
```

---

`Kozik_con`*Small molecule enhancers of endosome-to-cytosol import augment anti-tumour immunity*

---

**Description**

Data from 'Small molecule enhancers of endosome-to-cytosol import augment anti-tumour immunity'

Efficient cross-presentation of antigens by dendritic cells (DCs) is critical for initiation of anti-tumour immune responses. Yet, several steps of antigen intracellular traffic during cross-presentation are incompletely understood: in particular, the molecular mechanisms and the relative importance of antigen import from endocytic compartments into the cytosol. Here, we asked whether antigen import into the cytosol is rate-limiting for cross-presentation and anti-tumour immunity. By screening 700 FDA-approved drugs, we identified 37 import enhancers. We focused on prazosin and tamoxifen, and generated proteomic organellar maps of drug-treated DCs, covering the subcellular localisations of over 2000 proteins. By combining organellar mapping, quantitative proteomics, microscopy, and bioinformatics, we conclude that import enhancers undergo lysosomal trapping leading to membrane permeation and antigen release into the cytosol. Enhancing antigen import facilitates cross-presentation of both soluble and cell-associated antigens. Systemic administration of prazosin also led to reduced growth of MC38 tumours and to a synergistic effect with checkpoint immunotherapy in a melanoma model. Thus, inefficient antigen import into the cytosol limits antigen cross-presentation, restraining the potency of anti-tumour immune responses and efficacy of checkpoint blockers.

**Usage**

```
data("Kozik_con")
data("Kozik_pra")
data("Kozik_tam")
```

**Format**

The data is an instance of class MSnSet from package MSnbase.

**Examples**

```
data(Kozik_con)
Kozik_con
pData(Kozik_con)
exprs(Kozik_con)[1:3,1:3]

library("pRoloc")
plot2D(Kozik_con, main = "dendritic cells control")
```

---

krahmer2018pcp

*Subcellular Reorganization in Diet-Induced Hepatic Steatosis*

---

**Description**

Data from 'Organellar Proteomics and Phospho-Proteomics Reveal Subcellular Reorganization in Diet-Induced Hepatic Steatosis' Developmental cell.

Lipid metabolism is highly compartmentalized between cellular organelles that dynamically adapt their compositions and interactions in response to metabolic challenges. Here, we investigate how diet-induced hepatic lipid accumulation, observed in non-alcoholic fatty liver disease (NAFLD), affects protein localization, organelle organization, and protein phosphorylation in vivo. We develop a mass spectrometric workflow for protein and phosphopeptide correlation profiling to monitor levels and cellular distributions of 6,000 liver proteins and 16,000 phosphopeptides during development of steatosis. Several organelle contact site proteins are targeted to lipid droplets (LDs) in steatotic liver, tethering organelles orchestrating lipid metabolism. Proteins of the secretory pathway dramatically redistribute, including the mis-localization of the COPI complex and sequestration of the Golgi apparatus at LDs. This correlates with reduced hepatic protein secretion. Our systematic in vivo analysis of subcellular rearrangements and organelle-specific phosphorylation reveals how nutrient overload leads to organellar reorganization and cellular dysfunction.

**Usage**

```
data("krahmer2018pcp")
data("krahmer2018phosphopcp")
```

**Format**

The data is an instance of class MSnSet from package MSnbase.



## References

*Organellar proteomics and phospho-proteomics reveal subcellular reorganization in diet-induced hepatic steatosis.* Krahmer N, Najafi B, Schueder F, Quagliarini F, Steger M, Seitz S, Kasper R, Salinas F, Cox J, Uhlenhaut NH, Walther TC. *Developmental Cell.* 2018 Oct 22;47(2):205-21. <https://doi.org/10.1016/j.devcel.2018.09.017>

## Examples

```
data(krahmer2018pcp)
krahmer2018pcp
pData(krahmer2018pcp)
exprs(krahmer2018pcp)[1:3,1:3]

library("pRoloc")
plot2D(krahmer2018pcp, fcol = "Organelle" , main = "Krahmer 2018")

data(krahmer2018phosphopcp)
krahmer2018phosphopcp
exprs(krahmer2018phosphopcp)[1:3,1:3]

plot2D(krahmer2018phosphopcp, main = "Krahmer 2018")
```

---

kristensen2012r1

*Data from Kristensen et al. 2012*

---

## Description

Triplicated experimental data from Kristensen et al. 2012, *A high-throughput approach for measuring temporal changes in the interactome.* Protein complexes were separated by size exclusion chromatography and protein were quantified using SILAC.

## Usage

```
data("kristensen2012r1")
data("kristensen2012r2")
data("kristensen2012r3")
```

## References

Kristensen AR, Gsponer J, Foster LJ. A high-throughput approach for measuring temporal changes in the interactome. *Nat Methods.* 2012 Sep;9(9):907-9. doi: 10.1038/nmeth.2131. Epub 2012 Aug 5. PubMed PMID: 22863883; PubMed Central PMCID: PMC3954081.

## Examples

```
data(kristensen2012r1)
experimentData(kristensen2012r1)
```

---

`lopimsSyn2`*LOPIMS data for the Synapter 2.0 paper*

---

**Description**

TODO

**Usage**

```
data("lopimsSyn1")
data("lopimsSyn2")
data("lopimsSyn2_0frags")
```

**Format**

These data are MSnSet instances, defined in the MSnbase package.

**Examples**

```
data(lopimsSyn1)
data(lopimsSyn2)
data(lopimsSyn2_0frags)

## Visualisation
library("pRoloc")
par(mfrow = c(1, 3))
plot2D(lopimsSyn1, main = "Synapter 1", addLegend = "topleft")
plot2D(lopimsSyn2, main = "Synapter 2")
plot2D(lopimsSyn2_0frags, main = "Synapter 2 (0 fragments)")
```

---

`mulvey2015`*Data from Mulvey et al. 2015*

---

**Description**

This is the data from Mulvey et al., *Dynamic proteomic profiling of extra-embryonic endoderm differentiation in mouse embryonic stem cells.*, Stem Cell. (PMID 26059426). See below for more details.

**Usage**

```
data(mulvey2015)
data(mulvey2015norm)
```

**Format**

The data is an instance of class MSnSet from package MSnbase.

## Details

While not a spatial proteomics data, it was analysed with the pRoLoc package.

During mammalian preimplantation development, the cells of the blastocyst's inner cell mass differentiate into the epiblast and primitive endoderm lineages, which give rise to the fetus and extra-embryonic tissues, respectively. Extra-embryonic endoderm (XEN) differentiation can be modeled in vitro by induced expression of GATA transcription factors in mouse embryonic stem cells. Here, we use this GATA-inducible system to quantitatively monitor the dynamics of global proteomic changes during the early stages of this differentiation event and also investigate the fully differentiated phenotype, as represented by embryo-derived XEN cells. Using mass spectrometry-based quantitative proteomic profiling with multivariate data analysis tools, we reproducibly quantified 2,336 proteins across three biological replicates and have identified clusters of proteins characterized by distinct, dynamic temporal abundance profiles. We first used this approach to highlight novel marker candidates of the pluripotent state and XEN differentiation. Through functional annotation enrichment analysis, we have shown that the downregulation of chromatin-modifying enzymes, the reorganization of membrane trafficking machinery, and the breakdown of cell-cell adhesion are successive steps of the extra-embryonic differentiation process. Thus, applying a range of sophisticated clustering approaches to a time-resolved proteomic dataset has allowed the elucidation of complex biological processes which characterize stem cell differentiation and could establish a general paradigm for the investigation of these processes.

## Source

Supporting Information on

## References

Mulvey CM, Schröter C, Gatto L, Dikicioglu D, Fidaner IB, Christoforou A, Deery MJ, Cho LT, Niakan KK, Martinez-Arias A, Lilley KS. Dynamic Proteomic Profiling of Extra-Embryonic Endoderm Differentiation in Mouse Embryonic Stem Cells. *Stem Cells*. 2015 Sep;33(9):2712-25. doi: 10.1002/stem.2067. Epub 2015 Jun 23. PubMed PMID: 26059426.

## Examples

```
data(mulvey2015)
library("pRoLoc")
plot2D(mulvey2015)
```

```
data(mulvey2015norm)
heatmap(exprs(mulvey2015))
```

---

nikolovski2012

*Meta-analysis from Nikolovski et al. (2012)*

---

## Description

This is the data used in Nikolovski et al. (2012). See below for details and references.

## Usage

```
data(nikolovski2012)
data(nikolovski2012imp)
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## Details

These data are a concatenation of 4 LOPIT experiments. Experiments 1 and 2 are from Dunkley et al. 2006 (see also dunkley2006). Experiments 3 and 4 are new.

In the LOPIT experiments by Dunkley et al. (2006), peripheral membrane proteins were removed by carbonate washing of the isolated membranes, while for experiments 3 and 4, no carbonate wash was performed and are, as such, enriched in peripheral and luminal proteins. See figure 1 in Nikolovski 2012 for a description of the design.

In nikolovski2012imp missing values have been imputed using partial least-squares regression.

The training set used for the Naive Bayesian classifier is available as the markers feature meta-data. Note that Nikolovski included a group of markers labelled 'others', which has been retained in these data sets. The results produced in this work are available in the preds feature variable (note that some organelles are marked with a '\*', which is undefined here).

## Source

Supporting Information on <http://www.plantphysiol.org/content/160/2/1037.long>, also available in the package's extdata directory.

## References

Nikolovski N, Rubtsov D, Segura MP, Miles GP, Stevens TJ, Dunkley TP, Munro S, Lilley KS, Dupree P. *Putative glycosyltransferases and other plant Golgi apparatus proteins are revealed by LOPIT proteomics*. Plant Physiol. 2012 Oct;160(2):1037-51. doi: 10.1104/pp.112.204263. Epub 2012 Aug 24. PMID: 22923678; PMCID: PMC3461528.

Dunkley TP, Hester S, Shadforth IP, Runions J, Weimar T, Hanton SL, Griffin JL, Bessant C, Brandizzi F, Hawes C, Watson RB, Dupree P, Lilley KS. *Mapping the Arabidopsis organelle proteome*. Proc Natl Acad Sci U S A. 2006 Apr 25;103(17):6518-23. Epub 2006 Apr 17. PubMed PMID: 16618929; PubMed Central PMCID: PMC1458916.

## Examples

```
data(nikolovski2012)
data(nikolovski2012imp)
table(is.na(nikolovski2012))
table(is.na(nikolovski2012imp))
phenoData(nikolovski2012)
table(fData(nikolovski2012)$markers)
all.equal(sort(featureNames(nikolovski2012)),
          sort(featureNames(nikolovski2012imp)))
library("pRoloc")
plot2D(nikolovski2012imp)
addLegend(nikolovski2012imp, where = "topright", bty = "n", cex = .7)
```

---

nikolovski2014

*LOPIMS data from Nikolovski et al. (2014)*

---

## Description

This is the data used in Nikolovski et al. (2014). See below for details and references.

## Usage

```
data(nikolovski2014)
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## Details

**Abstract:** The proteomic composition of the Arabidopsis Golgi apparatus is currently reasonably well documented; however little is known about the relative abundances between different proteins within this compartment. Accurate quantitative information of Golgi resident proteins is of great importance: it facilitates a better understanding of the biochemical processes which take place within this organelle, especially those of different polysaccharide synthesis pathways. Golgi resident proteins are challenging to quantify since the abundance of this organelle is relatively low within the cell. In this study an organelle fractionation approach, targeting the Golgi apparatus, was combined with a label free quantitative mass spectrometry (MS), data-independent acquisition (DIA) method employing ion mobility separation known as LC-IMS-MSE (or HDMSE), to simultaneously localize proteins to the Golgi apparatus and assess their relative quantity. In total 102 Golgi localised proteins were quantified. These data provide new insight into Golgi apparatus organization and demonstrate that organelle fractionation in conjunction with label free quantitative MS is a powerful and relatively simple tool to access protein organelle localisation and their relative abundances. The findings presented open a unique view on the organization of the plant Golgi apparatus, leading towards novel hypotheses centered on the biochemical processes of this organelle.

These data are a concatenation of 2 LOPIMS gradients, labelled gradient A and B, each with 10 fractions.

## Source

Supplemental Data downloaded from <http://www.plantphysiol.org/content/early/2014/08/13/pp.114.245589/suppl/DC1>, also available in the package's extdata directory.

## References

Nikolovski N, Shliaha PV, Gatto L, Dupree P, Lilley KS. Label free protein quantification for plant Golgi protein localisation and abundance. *Plant Physiol.* 2014 Aug 13. pii: pp.114.245589. [Epub ahead of print] PubMed PMID: 25122472.

## Examples

```
data(nikolovski2014)
pData(nikolovski2014)
library("pRoloc")
plot2D(nikolovski2014)
```

```
addLegend(nikolovski2014, where = "topright", bty = "n", cex = .7)

A <- pData(nikolovski2014)$gradient == "A"
par(mfrow = c(1, 2))
plot2D(nikolovski2014[, A], main = "Gradient A")
plot2D(nikolovski2014[, !A], main = "Gradient B")
```

---

orre2019

*SubCellBarCode: Proteome-wide Mapping of Protein Localization and Relocalization*

---

## Description

Data from 'SubCellBarCode: Proteome-wide Mapping of Protein Localization and Relocalization' Molecular cell.

Subcellular localization is a main determinant of protein function; however, a global view of cellular proteome organization remains relatively unexplored. We have developed a robust mass spectrometry-based analysis pipeline to generate a proteome-wide view of subcellular localization for proteins mapping to 12,418 individual genes across five cell lines. Based on more than 83,000 unique classifications and correlation profiling, we investigate the effect of alternative splicing and protein domains on localization, complex member co-localization, cell-type-specific localization, as well as protein relocalization after growth factor inhibition. Our analysis provides information about the cellular architecture and complexity of the spatial organization of the proteome; we show that the majority of proteins have a single main subcellular location, that alternative splicing rarely affects subcellular location, and that cell types are best distinguished by expression of proteins exposed to the surrounding environment. The resource is freely accessible via [www.subcellbarcode.org](http://www.subcellbarcode.org).

## Usage

```
data("orre2019a431")
data("orre2019h322")
data("orre2019hcc827")
data("orre2019hcc827gef")
data("orre2019hcc827rep1")
data("orre2019hcc827rep2")
data("orre2019hcc827rep3")
data("orre2019mcf7")
data("orre2019u251")
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## References

*SubCellBarCode: Proteome-wide Mapping of Protein Localization and Relocalization* Lukas Minus Orre, Mattias Vesterlund, Yanbo Pan, Taner Arslan, Yafeng Zhu, Alejandro Fernandez Woodbridge, Oliver Frings, Erik Fredlund, and Janne Lehtio <https://doi.org/10.1016/j.molcel.2018.11.035>

**Examples**

```
data(orre2019a431)
orre2019a431
pData(orre2019a431)
exprs(orre2019a431)[1:3,1:3]

library("pRoloc")
plot2D(orre2019a431,, main = "Orre 2019 A431")
```

---

pRolocdata                      *List of pRolocdata data sets*

---

**Description**

This function lists the data sets available in pRolocdata package by calling `data(package = "pRolocdata")`.

**Usage**

```
pRolocdata()
```

**Author(s)**

Laurent Gatto <lg390@cam.ac.uk>

**References**

See in the respective data sets' manual pages for references to publications.

**Examples**

```
pRolocdata()
```

---

pRolocmetadata                      *Extract pRoloc metadata*

---

**Description**

Extracts relevant metadata from an MSnSet instance. See `README.md` for a description and explanation of the metadata fields.

**Usage**

```
pRolocmetadata(x)
```

**Arguments**

x                      A pRolocdata data.

**Value**

An instance of class pRolocmetadata.

**Author(s)**

Laurent Gatto

**Examples**

```
library("pRolocdata")
data(dunkley2006)
data(dunkley2006)
pRolocmetadata(dunkley2006)
```

---

rodriguez2012r1*Spatial proteomics of human inducible goblet-like LS174T cells from Rodriguez-Pineiro et al. (2012)*

---

**Description**

Data from Rodriguez-Pineiro AM, van der Post S, Johansson ME, Thomsson KA, Nesvizhskii AI, Hansson GC. Proteomic study of the mucin granulae in an intestinal goblet cell model. *J Proteome Res.* 2012 Mar 2;11(3):1879-90. doi: 10.1021/pr2010988. Epub 2012 Feb 2. PubMed PMID:22248381; PubMed Central PMCID:PMC3292267.

**Usage**

```
data("rodriguez2012r1")
data("rodriguez2012r2")
data("rodriguez2012r3")
```

**Details**

As no marker were provided with the data, we transferred markers from the hyperLOPIT2015 (mouse) data using gene names to match between experiments. To validate our marker annotations, we compared the relative distributions of our markers (see figure below) to the PCA plot provided by the authors (Figure 3). Both show a similar separation of mitochondion/ER vs the rest along PC1 and ribosomes/lysosome vs rest along PC2. The data do not match exactly as the different marker protein are used.

**Source**

The supplementary file is pr2010988\_si\_003.xls. See scripts/rodriguez-pineiro2012.R for data preparation.

**Examples**

```
data(rodriguez2012r1)
data(rodriguez2012r2)
data(rodriguez2012r3)

library("pRoloc")
par(mfrow = c(2, 2))
plot2D(rodriguez2012r1)
addLegend(rodriguez2012r1, cex = .7, where = "topleft")
plot2D(rodriguez2012r2)
```



```

plot2D(rodriuez2012r3)

## compare to figure 3
dev.new()
plot2D(markerMSnSet(rodriuez2012r1),
      mirrorX = TRUE, mirrorY = TRUE,
      main = "Our markers")
addLegend(markerMSnSet(rodriuez2012r1), where = "bottomright")

```

Shin2020

*Spatial proteomics defines the content of trafficking vesicles captured by golgin tethers*

## Description

Data from 'Spatial proteomics defines the content of trafficking vesicles captured by golgin tethers' Intracellular traffic between compartments of the secretory and endocytic pathways is mediated by vesicle-based carriers. The precise and complete proteomes of carriers destined for many organelles are ill-defined because the vesicular intermediates are transient, low-abundance and difficult to purify. Here, we combine vesicle relocalisation with organelle proteomics and Bayesian analysis to define the content of different endosome-derived vesicles destined for the trans-Golgi network (TGN). The golgin coiled-coil proteins golgin-97, golgin-245 and GCC88, shown previously to capture endosome-derived vesicles at the TGN, were individually relocalised to mitochondria and the content of subsequently re-routed vesicles was determined by organelle proteomics. Our findings revealed 45 integral and 51 peripheral membrane proteins re-routed by golgin-97, evidence for a distinct class of vesicles shared by golgin-97 and GCC88, and various cargoes specific to individual golgins. These results illustrate a general strategy for analysing intracellular sub-proteomes by combining acute cellular re-wiring with high-resolution spatial proteomics.

## Usage

```

data("Shin2019MitoControlrep1")
data("Shin2019MitoGcc88rep1")
data("Shin2019MitoGol97rep1")

```

## Format

The data is an instance of class MSnSet from package MSnbase.

## References

*Spatial proteomics defines the content of trafficking vesicles captured by golgin tethers.* John J.H. Shin, Oliver M. Crook, Alicia C. Borgeaud, Jerome Cattin-Ortola, Sew-Yeu Peak-Chew, Jessica Chadwick, Kathryn S. Lilley, Sean Munro.

## Examples

```

data(Shin2019MitoControlrep1)
Shin2019MitoControlrep1
pData(Shin2019MitoControlrep1)
exprs(Shin2019MitoControlrep1)[1:3,1:3]

```

```
library("pRoloc")  
plot2D(Shin2019MitoControlrep1, main = "Shin 2019 HeK 293T WT")
```

---

stekhoven2014

*Data from Stekhoven et al. 2014*

---

### Description

Proteomics data provide unique insights into biological systems, including the predominant subcellular localization (SCL) of proteins, which can reveal important clues about their functions. Here we analyzed data of a complete prokaryotic proteome expressed under two conditions mimicking interaction of the emerging pathogen *Bartonella henselae* with its mammalian host. Normalized spectral count data from cytoplasmic, total membrane, inner and outer membrane fractions allowed us to identify the predominant SCL for 82 proteins. The spectral count proportion of total membrane versus cytoplasmic fractions indicated the propensity of cytoplasmic proteins to co-fractionate with the inner membrane, and enabled us to distinguish cytoplasmic, peripheral inner membrane and bona fide inner membrane proteins. Principal component analysis and k-nearest neighbor classification training on selected marker proteins or predominantly localized proteins, allowed us to determine an extensive catalog of at least 74 expressed outer membrane proteins, and to extend the SCL assignment to 94% of the identified proteins, including 18 silico methods gave no prediction. Suitable experimental proteomics data combined with straightforward computational approaches can thus identify the predominant SCL on a proteome-wide scale. Finally, we present a conceptual approach to identify proteins potentially changing their SCL in a condition-dependent fashion.

### Usage

```
data("stekhoven2014")
```

### References

Stekhoven DJ, Omasits U, Quebatte M, Dehio C, Ahrens CH. *Proteome-wide identification of predominant subcellular protein localizations in a bacterial model organism*. J Proteomics. 2014 Mar 17;99:123-37. doi:10.1016/j.jprot.2014.01.015. Epub 2014 Jan 28. PubMed PMID: 24486812.

### Examples

```
data(stekhoven2014)  
library("pRoloc")  
plot2D(stekhoven2014)
```

---

tan2009

*LOPIT data from Tan et al. (2009)*

---

### Description

This is the data from Tan et al., *Mapping organelle proteins and protein complexes in Drosophila melanogaster*, J Proteome Res. 2009 Jun;8(6):2667-78. See below for more details.

## Usage

```
data(tan2009r1)
data(tan2009r2)
data(tan2009r3)
data(tan2009r1goCC)
```

## Format

The data is an instance of class MSnSet from package MSnbase.

## Details

This is a LOPIT experiment. Normalised intensities for proteins for four iTRAQ 4-plex labelled fractions are available for 3 replicates (r1, r2 and r3 respectively). The partial least square discriminant analysis results from the paper are available as PLSDA feature meta-data and the markers used in analysis are available as markers feature meta-data (Note: the ER and Golgi organelle markers were combined in original PLSDA analysis).

Replicate 1 was also used in testing the phenotype discovery algorithm from Breckels et al., *The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation*, J Proteomics, In Press., see phenoDisco. New phenotype clusters identified from algorithm application are available as pd.2013 feature meta-data.

The tan2009r1goCC instance contains binary assay data. Its columns represent GO CC terms that have been observed for the object's features. A 1 indicates that a GO term has been associated to a given feature (protein); a 0 means not such association was found in the GO ontology.

## Source

Supporting Information on <http://pubs.acs.org/doi/full/10.1021/pr800866n>

## References

Mapping organelle proteins and protein complexes in Drosophila melanogaster. Tan DJ, Dvinge H, Christoforou A, Bertone P, Martinez Arias A, Lilley KS. J Proteome Res. 2009 Jun;8(6):2667-78. PMID: 19317464

Breckels LM, Gatto L, Christoforou A, Groen AJ, Lilley KS and Trotter MWB. *The Effect of Organelle Discovery upon Sub-Cellular Protein Localisation* J Proteomics. In Press.

## Examples

```
data(tan2009r1)
tan2009r1
pData(tan2009r1)
head(exprs(tan2009r1))
# Organelle markers
table(fData(tan2009r1)$markers)
# PLSDA assignment results
table(fData(tan2009r1)$PLSDA)
```

---

ToxoLopit	<i>Whole-cell spatial proteome of Toxoplasma: molecular anatomy of an apicomplexan cell</i>
-----------	---

---

### Description

Data from 'Whole-cell spatial proteome of Toxoplasma: molecular anatomy of an apicomplexan cell'

Apicomplexan parasites are the causative agents of major human diseases and food insecurity and owe their considerable success to novel, highly specialized cell compartments and structures. These adaptations facilitate the recognition and non-destructive penetration of their host cells, and elaborate reengineering of these cells to promote growth, dissemination and active countering of host defense responses. The evolution of apicomplexan compartments is concomitant with great proteomic novelty that defines these new cell organizations and functions and, hence, approximately half of their proteins are unique and uncharacterized. Consequently, apicomplexan cells are relatively poorly understood. Here we employ the hyperLOPIT cell spatial proteomic method to the apicomplexan *Toxoplasma gondii* and define the steady-state subcellular location of thousands of proteins simultaneously giving comprehensive definition to these cells and their compartments. These data, moreover, provide new insight into the spatial organizations of protein expression, adaptation to hosts, and the underlying evolutionary trajectories of these parasites.

### Usage

```
data("Barylyuk2020ToxoLopit")
```

### Format

The data is an instance of class MSnSet from package MSnbase.

### Examples

```
data(Barylyuk2020ToxoLopit)
Barylyuk2020ToxoLopit
pData(Barylyuk2020ToxoLopit)
exprs(Barylyuk2020ToxoLopit)[1:3,1:3]

library("pRoloc")
plot2D(Barylyuk2020ToxoLopit, main = "Davies 2018 HeLa - wt")
```

---

trotter20010	<i>LOPIT data sets used in Trotter et al. (2010)</i>
--------------	--

---

### Description

The two Arabidopsis LOPIT data sets `trotter2010shallow` and `trotter2010steep` have been used in Trotter et al. (2010) to illustrate improvement of sub-cellular resolution upon data fusion. The data have originally been published in Dunkley et al. (2006) and Sadowski et al. (2008), respectively.

The feature metadata contains the cellular compartment from TAIR8 and the pRoloc Arabidopsis markers (see [pRolocmarkers](#)).

**Usage**

```
data(trotter2010)
data(trotter2010shallow)
data(trotter2010steep)
```

**Format**

The data are instances of class MSnSet from package MSnbase. trotter2010 corresponds to the combined steep and shallow data.

**Source**

Supporting information available on <http://onlinelibrary.wiley.com/doi/10.1002/pmic.201000359/abstract>

**References**

Trotter MWB, Sadowski PG, Dunkley TPJ, Groen AJ and Lilley KS. *Improved sub-cellular resolution via simultaneous analysis of organelle proteomics data across varied experimental conditions*. Proteomics 2010 10(23):4213-4219. PMID 21058340.

Sadowski PG, Groen AJ, Dupree P and Lilley KS. *Sub-cellular localization of membrane proteins*. Proteomics 2008 8(19):3991-4011. PMID 18780351.

**Examples**

```
library(pRoloc)
## Replication of figure 4 from Trotter et al.
## individual data sets
data(trotter2010)
data(trotter2010steep)
data(trotter2010shallow)

par(mfrow = c(2,3))
plot2D(trotter2010shallow, fcol = "TAIR8", main = "Shallow (TAIR8)")
plot2D(trotter2010steep, fcol = "TAIR8", main = "Steep (TAIR8)")
plot2D(trotter2010, fcol = "TAIR8", main = "Combined (TAIR8)")
addLegend(trotter2010, where = "bottomleft", fcol = "TAIR8", ncol = 2)
plot2D(trotter2010shallow, main = "Shallow (markers)")
plot2D(trotter2010steep, main = "Steep (markers)")
plot2D(trotter2010, main = "Combined (markers)")
addLegend(trotter2010, where = "bottomleft", ncol = 2)
```

---

 yeast2018

*Saccharomyces cerevisiae* spatial proteomics (2018)
 

---

**Description**

Data from 'The subcellular organisation of *Saccharomyces cerevisiae*' (submitted).

This dataset represents four biological replicate hyperLOPIT experiments performed in *Saccharomyces cerevisiae* cultured to early-mid exponential phase, in synthetic media with glucose as sole carbon source (SD-His media (Breker et al 2013)). These were carried out to produce a map of

the spatial proteome of this organism under no-perturbed conditions. The associated quantitation data from these experiments were combined using the method described in reference. This dataset contains quantitative information for 2,847 proteins that were common across our four biological replicate experiments and information regarding localisation for all of the proteins in the combined experiment. Overall this dataset describes 936 proteins that localise to one of 12 subcellular locations in *S. cerevisiae* under our experimental conditions.

### Usage

```
data("yeast2018")
```

### Examples

```
data(yeast2018)

library("pRoloc")
par(mfrow = c(1, 2))
plot2D(yeast2018, main = "Markers")
addLegend(yeast2018, where = "bottomleft", cex = .7)
plot2D(yeast2018, fcol = "predicted.location", main = "Localisation")
```

# Index

## \* datasets

- andreyev2010, [2](#)
  - andy2011, [3](#)
  - at\_chloro, [4](#)
  - baers2018, [5](#)
  - beltran2016, [6](#)
  - davies2018, [7](#)
  - dunkley2006, [8](#)
  - E14TG2a, [10](#)
  - fabre2015r1, [11](#)
  - foster2006, [11](#)
  - groen2014, [12](#)
  - hall2009, [14](#)
  - havugimana2012, [14](#)
  - hirst2018, [15](#)
  - hyperLOPIT2015, [16](#)
  - hyperLOPITU20S2017, [18](#)
  - itzhak2016dynamic, [20](#)
  - itzhak2016stcSILAC, [21](#)
  - itzhak2017, [21](#)
  - kirkwood2013, [23](#)
  - Kozik\_con, [23](#)
  - krahmer2018pcp, [24](#)
  - kristensen2012r1, [25](#)
  - lopimsSyn2, [26](#)
  - mulvey2015, [26](#)
  - nikolovski2012, [27](#)
  - nikolovski2014, [29](#)
  - orre2019, [30](#)
  - rodriguez2012r1, [32](#)
  - Shin2020, [33](#)
  - stekhoven2014, [34](#)
  - tan2009, [34](#)
  - ToxoLopit, [36](#)
  - trotter20010, [36](#)
  - yeast2018, [37](#)
- 
- andreyev2010, [2](#)
  - andreyev2010activ (andreyev2010), [2](#)
  - andreyev2010rest (andreyev2010), [2](#)
  - andy2011, [3](#)
  - andy2011goCC (andy2011), [3](#)
  - andy2011hpa (andy2011), [3](#)
  - at\_chloro, [4](#)
  - baers2018, [5](#)
  - Barylyuk2020ToxoLopit (ToxoLopit), [36](#)
  - beltran2016, [6](#)
  - beltran2016HCMV120 (beltran2016), [6](#)
  - beltran2016HCMV24 (beltran2016), [6](#)
  - beltran2016HCMV48 (beltran2016), [6](#)
  - beltran2016HCMV72 (beltran2016), [6](#)
  - beltran2016HCMV96 (beltran2016), [6](#)
  - beltran2016MOCK120 (beltran2016), [6](#)
  - beltran2016MOCK24 (beltran2016), [6](#)
  - beltran2016MOCK48 (beltran2016), [6](#)
  - beltran2016MOCK72 (beltran2016), [6](#)
  - beltran2016MOCK96 (beltran2016), [6](#)
  - davies2018, [7](#)
  - davies2018ap4b1 (davies2018), [7](#)
  - davies2018ap4e1 (davies2018), [7](#)
  - davies2018wt (davies2018), [7](#)
  - dunkley2006, [8](#)
  - dunkley2006goCC (dunkley2006), [8](#)
  - E14TG2a, [10](#)
  - E14TG2aR (E14TG2a), [10](#)
  - E14TG2aS1 (E14TG2a), [10](#)
  - E14TG2aS1goCC (E14TG2a), [10](#)
  - E14TG2aS1yLoc (E14TG2a), [10](#)
  - E14TG2aS2 (E14TG2a), [10](#)
  - fabre2015 (fabre2015r1), [11](#)
  - fabre2015r1, [11](#)
  - fabre2015r2 (fabre2015r1), [11](#)
  - foster2006, [11](#)
  - groen2014, [12](#)
  - groen2014cmb (groen2014), [12](#)
  - groen2014r1 (groen2014), [12](#)
  - groen2014r1goCC (groen2014), [12](#)
  - groen2014r2 (groen2014), [12](#)
  - groen2014r3 (groen2014), [12](#)
  - hall2009, [14](#)
  - havugimana2012, [14](#)
  - HEK293T2011 (andy2011), [3](#)
  - HEK293T2011goCC (andy2011), [3](#)
  - HEK293T2011hpa (andy2011), [3](#)

- hirst2018, 15  
 hyperLOPIT2015, 16  
 hyperLOPIT2015goCC (hyperLOPIT2015), 16  
 hyperLOPIT2015ms2 (hyperLOPIT2015), 16  
 hyperLOPIT2015ms2psm (hyperLOPIT2015), 16  
 hyperLOPIT2015ms3r1 (hyperLOPIT2015), 16  
 hyperLOPIT2015ms3r1psm (hyperLOPIT2015), 16  
 hyperLOPIT2015ms3r2 (hyperLOPIT2015), 16  
 hyperLOPIT2015ms3r2psm (hyperLOPIT2015), 16  
 hyperLOPIT2015ms3r3 (hyperLOPIT2015), 16  
 hyperLOPITU20S2017, 18  
 hyperLOPITU20S2017b (hyperLOPITU20S2017), 18  
 hyperLOPITU20S2018 (hyperLOPITU20S2017), 18  
  
 itzhak2016, 22  
 itzhak2016 (itzhak2016stcSILAC), 21  
 itzhak2016dynamic, 20  
 itzhak2016helaCtrl (itzhak2016dynamic), 20  
 itzhak2016helaEgf (itzhak2016dynamic), 20  
 itzhak2016stcSILAC, 21  
 itzhak2017, 21  
 itzhak2017markers (itzhak2017), 21  
  
 kirkwood2013, 23  
 Kozik\_con, 23  
 Kozik\_pra (Kozik\_con), 23  
 Kozik\_tam (Kozik\_con), 23  
 krahmer2018pcp, 24  
 krahmer2018phosphopcp (krahmer2018pcp), 24  
 kristensen2012 (kristensen2012r1), 25  
 kristensen2012r1, 25  
 kristensen2012r2 (kristensen2012r1), 25  
 kristensen2012r3 (kristensen2012r1), 25  
  
 lopimsSyn1 (lopimsSyn2), 26  
 lopimsSyn2, 26  
 lopimsSyn2\_0frags (lopimsSyn2), 26  
 lopitdcU20S2018 (hyperLOPITU20S2017), 18  
  
 mulvey2015, 26  
 mulvey2015norm (mulvey2015), 26  
  
 nikolovski2012, 27  
 nikolovski2012imp (nikolovski2012), 27  
 nikolovski2014, 29  
  
 orre2019, 30  
 orre2019a431 (orre2019), 30  
 orre2019h322 (orre2019), 30  
 orre2019hcc827 (orre2019), 30  
 orre2019hcc827gef (orre2019), 30  
 orre2019hcc827rep1 (orre2019), 30  
 orre2019hcc827rep2 (orre2019), 30  
 orre2019hcc827rep3 (orre2019), 30  
 orre2019mcf7 (orre2019), 30  
 orre2019u251 (orre2019), 30  
  
 print.pRolocmetadata (pRolocmetadata), 31  
 pRolocdata, 31  
 pRolocmarkers, 36  
 pRolocmetadata, 31  
  
 rodriguez-pineiro2012 (rodriguez2012r1), 32  
 rodriguez2012 (rodriguez2012r1), 32  
 rodriguez2012r1, 32  
 rodriguez2012r2 (rodriguez2012r1), 32  
 rodriguez2012r3 (rodriguez2012r1), 32  
  
 Shin2019MitoControlrep1 (Shin2020), 33  
 Shin2019MitoControlrep2 (Shin2020), 33  
 Shin2019MitoControlrep3 (Shin2020), 33  
 Shin2019MitoGcc88rep1 (Shin2020), 33  
 Shin2019MitoGcc88rep2 (Shin2020), 33  
 Shin2019MitoGcc88rep3 (Shin2020), 33  
 Shin2019MitoGol97rep1 (Shin2020), 33  
 Shin2019MitoGol97rep2 (Shin2020), 33  
 Shin2019MitoGol97rep3 (Shin2020), 33  
 Shin2020, 33  
 stekhoven2014, 34  
 synechocystis (baers2018), 5  
  
 tan2009, 34  
 tan2009r1 (tan2009), 34  
 tan2009r1goCC (tan2009), 34  
 tan2009r2 (tan2009), 34  
 tan2009r3 (tan2009), 34  
 ToxoLopit, 36  
 trotter20010, 36  
 trotter2010 (trotter20010), 36  
 trotter2010shallow (trotter20010), 36  
 trotter2010steep (trotter20010), 36  
  
 U20S (hyperLOPITU20S2017), 18  
  
 yeast2018, 37