

Package ‘WallomicsData’

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Title Datasets for Multi-Omics Integration in a Plant Abiotic Stress
Context

Version 1.0

Description

Datasets from the WallOmics project. Contains phenomics, metabolomics, proteomics and transcriptomics data collected from two organs of five ecotypes of the model plant *Arabidopsis thaliana* exposed to two temperature growth conditions. Exploratory and integrative analyses of these data are presented in Durufle et al (2020) <[doi:10.1093/bib/bbaa166](https://doi.org/10.1093/bib/bbaa166)> and Durufle et al (2020) <[doi:10.3390/cells9102249](https://doi.org/10.3390/cells9102249)>.

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Altitude_Cluster	<i>Altitude Cluster</i>
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Description

The **Altitude Cluster factor** identifies the environment height from which is originated a given plant from the sample under study, either high altitude (denoted *High*), moderate altitude (*Low*) or the reference group's environment height (*Col*, the lowest of all).

Usage

```
data("Altitude_Cluster")
```

Format

A factor with 3 levels.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the data
data("Altitude_Cluster")

# Count how many samples are in each group
table(Altitude_Cluster)
```

Ecotype

Ecotype

Description

The **Ecotype factor** identifies the genotype specifically designed for a given ecosystem of the *A. thaliana* from which the studied sample comes from. We have a population of reference as well as 4 newly-described Pyrenean populations, namely:

- Columbia, denoted *Col* (originating from Poland, acts as the reference ecotype)
- Grip, denoted *Grip*
- Herran, denoted *Hern*
- L'Hospitalet-près-l'Andorre, denoted *Hosp*
- Chapelle Saint Roch, denoted *Roch*

Usage

```
data("Ecotype")
```

Format

A factor with 5 levels of *A. thaliana* genotypes.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the data
data("Ecotype")

# Count how many samples are in each group
table(Ecotype)
```

Genetic_Cluster

Genetic Cluster

Description

The **Genetic Cluster factor** identifies the genetic group from which comes from the studied sample, either **Genetics Cluster 1** (constituted of *Grip* and *Roch* genotypes), **Genetics Cluster 2** (*Hern* and *Hosp* genotypes) or **Genetics Cluster 3** (*Col* genotype). See [Ecotype](#) for more information on genotypes.

Usage

```
data("Genetic_Cluster")
```

Format

A factor with 3 levels.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the data
data("Genetic_Cluster")

# Count how many samples are in each group
table(Genetic_Cluster)
```

Metabolomics_Rosettes *Metabolomics Rosettes*

Description

A dataset containing metabolomics variables measured on rosettes of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Metabolomics_Rosettes")
```

Format

A data frame with 30 rows and 6 variables:

- **Pectin_RGI**: Rhamnogalacturonan I ($\mu\text{g}/100\text{mg}$)
- **Pectin_HG**: Homogalacturonan ($\mu\text{g}/100\text{mg}$)
- **XG**: Xyloglucan ($\mu\text{g}/100\text{mg}$)
- **Pectin_linearity**: Linearity of pectin (Ratio)
- **Contribution_RG**: Contribution of rhamnogalacturonan to pectin population (Ratio)
- **RGI_branching**: Branching of Rhamnogalacturonan I (Ratio)

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```

# Load the dataset
data("Metabolomics_Rosettes")

# Look at simple statistics
summary(Metabolomics_Rosettes)

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# A graphical representation
plot(x = as.factor(substr(row.names(Metabolomics_Rosettes), 1, 7)),
     y = Metabolomics_Rosettes$Pectin_linearity, col = "white", lty = 0,
     xlab = "Genotype x Temperature groups",
     ylab = "Pectin linearity (Ratio)",
     main = "Pectin linearity distribution by genotype and growth temperature")
grid()
abline(h = 1, lty = 2)
points(x = as.factor(substr(row.names(Metabolomics_Rosettes), 1, 7)),
      y = Metabolomics_Rosettes$Pectin_linearity, type = "p", pch = 19, lwd = 5,
      col = colors)

```

Metabolomics_Stems *Metabolomics Stems*

Description

A dataset containing metabolomics variables measured on floral stems of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Metabolomics_Stems")
```

Format

A data frame with 30 rows and 6 variables:

- **Pectin_RGI**: Rhamnogalacturonan I ($\mu\text{g}/100\text{mg}$)
- **Pectin_HG**: Homogalacturonan ($\mu\text{g}/100\text{mg}$)
- **XG**: Xyloglucan ($\mu\text{g}/100\text{mg}$)
- **Pectin_linearity**: Linearity of pectin (Ratio)
- **Contribution_RG**: Contribution of rhamnogalacturonan to pectin population (Ratio)
- **RGI_branching**: Branching of Rhamnogalacturonan I (Ratio)

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Metabolomics_Stems")

# Look at simple statistics
summary(Metabolomics_Stems)

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# A graphical representation
plot(x = as.factor(substr(row.names(Metabolomics_Stems), 1, 7)),
     y = Metabolomics_Stems$Pectin_linearity, col = "white", lty = 0,
     xlab = "Genotype x Temperature groups",
     ylab = "Pectin linearity (Ratio)",
     main = "Pectin linearity distribution by genotype and growth temperature")
grid()
abline(h = 1, lty = 2)
points(x = as.factor(substr(row.names(Metabolomics_Stems), 1, 7)),
       y = Metabolomics_Stems$Pectin_linearity, type = "p", pch = 19, lwd = 5,
       col = colors)
```

Metadata

Metadata

Description

Bioinformatics Annotation and description, using the WallProtDB database, of all the Cell Wall Proteins (CWPs) identified on rosettes and floral stems of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for additional information.

Usage

```
data("Metadata")
```

Format

A data frame with 474 rows and 4 variables:

- **Acc_number**: GenBank accession number (gene name)
- **Functional_classes**: Functional classes of the CWPs
- **Protein_families**: Protein families of the CWPs
- **Putative_functions**: Putative functions of the CWPs

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Metadata")

# Look at the dataset's dimensions
dim(Metadata)
head(Metadata)

# How many functional classes ?
table(Metadata$Functional_classes)

# How many protein families ?
table(Metadata$Protein_families)
```

Phenomics_Rosettes *Phenomics Rosettes*

Description

A dataset containing phenotypic variables measured on rosettes of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Phenomics_Rosettes")
```

Format

A data frame with 30 rows and 5 variables:

- **Mass:** rosette mass (g)
- **Diameter:** rosette diameter (cm)
- **Leaves_number:** total number of leaves
- **Density:** rosette density (g/cm²)
- **Area:** projected rosette area (cm²)

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```

# Load the data
data("Phenomics_Rosettes")

# Look at simple statistics
dim(Phenomics_Rosettes)
summary(Phenomics_Rosettes)

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# A graphical representation: Leaves number distribution
plot(x = as.factor(substr(row.names(Phenomics_Rosettes), 1, 7)),
     y = Phenomics_Rosettes$Leaves_number, col = "white", lty = 0,
     xlab = "Genotype x Temperature groups",
     ylab = "Number of rosette leaves",
     main = "Rosette leaves' distribution by genotype and growth temperature"
    )
grid()
points(x = as.factor(substr(row.names(Phenomics_Rosettes), 1, 7)),
      y = Phenomics_Rosettes$Leaves_number, type = "p", pch = 19, lwd = 5,
      col = colors)

```

Phenomics_Stems

Phenomics Stems

Description

A dataset containing phenotypic variables measured on floral stems of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Phenomics_Stems")
```

Format

A data frame with 30 rows and 4 variables:

- **Mass:** floral stems mass (g)
- **Diameter:** floral stems diameter (mm)
- **Length:** length of the floral stems (cm)
- **Number_lateral_stems:** number of lateral stems)

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the data
data("Phenomics_Stems")

# Look at simple statistics
dim(Phenomics_Stems)
summary(Phenomics_Stems)

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# A graphical representation: Lateral stems distribution
plot(x = as.factor(substr(row.names(Phenomics_Stems), 1, 7)),
     y = Phenomics_Stems$Number_lateral_stems, col = "white", lty = 0,
     xlab = "Genotype x Temperature groups",
     ylab = "Number of lateral stems",
     main = "Lateral stems' distribution by genotype and growth temperature"
    )
grid()
points(x = as.factor(substr(row.names(Phenomics_Stems), 1, 7)),
      y = Phenomics_Stems$Number_lateral_stems, type = "p", pch = 19, lwd = 5,
      col = colors)
```

Proteomics_Rosettes_CW

Proteomics Rosettes Cell Wall

Description

A dataset containing the identification and quantification of Cell Wall Proteins (CWPs) performed using LC-MS/MS analysis on rosettes of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for additional information.

Usage

```
data("Proteomics_Rosettes_CW")
```

Format

A data frame with 30 rows and 364 variables.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Proteomics_Rosettes_CW")

# Look at data frame dimensions
dim(Proteomics_Rosettes_CW)

# Look at the first rows and columns
head(Proteomics_Rosettes_CW[,c(1:10)])

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# PCA on proteomics
res.pca <- prcomp(Proteomics_Rosettes_CW, center = TRUE, scale. = TRUE)
plot(res.pca$x[, "PC1"], res.pca$x[, "PC2"], pch = 19, xlab = "PC1", ylab = "PC2", lwd = 5,
     main = "Individuals' plot (1 x 2) - PCA on Rosettes Cell Wall Proteomics",
     col = colors)
text(res.pca$x[, "PC1"], res.pca$x[, "PC2"], labels = row.names(res.pca$x), cex = 0.8, pos = 3)
```

Proteomics_Stems_CW *Proteomics Stems Cell Wall*

Description

A dataset containing the identification and quantification of Cell Wall Proteins (CWPs) performed using LC-MS/MS analysis on floral stems of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for additional information.

Usage

```
data("Proteomics_Stems_CW")
```

Format

A data frame with 30 rows and 414 variables.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Proteomics_Stems_CW")

# Look at data frame dimensions
dim(Proteomics_Stems_CW)

# Look at the first rows and columns
head(Proteomics_Stems_CW[,c(1:10)])

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# PCA on proteomics
res.pca <- prcomp(Proteomics_Stems_CW, center = TRUE, scale. = TRUE)
plot(res.pca$x[, "PC1"], res.pca$x[, "PC2"], pch = 19, xlab = "PC1", ylab = "PC2", lwd = 5,
     main = "Individuals' plot (1 x 2) - PCA on Stems Cell Wall Proteomics",
     col = colors)
text(res.pca$x[, "PC1"], res.pca$x[, "PC2"], labels = row.names(res.pca$x), cex = 0.8, pos = 3)
```

Temperature

Temperature

Description

The **Temperature factor** identifies the temperature at which the studied sample was exposed all along its growth, either 22°C (optimal condition) or 15°C (high altitude condition).

Usage

```
data("Temperature")
```

Format

A factor with 2 levels.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the data
data("Temperature")

# Count how many samples are in each group
```

```
table(Temperature)
```

Transcriptomics_Rosettes

Transcriptomics Rosettes

Description

A dataset containing all the transcripts obtained by RNA-seq performed, according to the standard Illumina protocols, on rosettes of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Transcriptomics_Rosettes")
```

Format

A data frame with 30 rows and 19763 variables.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Transcriptomics_Rosettes")

# Look at data frame dimensions
dim(Transcriptomics_Rosettes)

# Look at the first rows and columns
head(Transcriptomics_Rosettes[,c(1:10)])

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# PCA on transcriptomics
res.pca <- prcomp(Transcriptomics_Rosettes, center = TRUE, scale. = TRUE)
plot(res.pca$x[, "PC1"], res.pca$x[, "PC2"], pch = 19, xlab = "PC1", ylab = "PC2", lwd = 5,
     main = "Individuals' plot (1 x 2) - PCA on Rosettes' Transcriptomics",
     col = colors)
text(res.pca$x[, "PC1"], res.pca$x[, "PC2"], labels = row.names(res.pca$x), cex = 0.8, pos = 3)
```

Transcriptomics_Rosettes_CW

Transcriptomics Rosettes Cell Wall

Description

A dataset containing the transcripts encoding Cell Wall Proteins (CWPs) sorted from the 19 763 transcripts (see [Transcriptomics_Rosettes](#)) obtained by RNA-seq performed, according to the standard Illumina protocols, on rosettes of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Transcriptomics_Rosettes_CW")
```

Format

A data frame with 30 rows and 364 variables.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Transcriptomics_Rosettes_CW")

# Look at data frame dimensions
dim(Transcriptomics_Rosettes_CW)

# Look at the first rows and columns
head(Transcriptomics_Rosettes_CW[,c(1:10)])

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# PCA on transcriptomics
res.pca <- prcomp(Transcriptomics_Rosettes_CW, center = TRUE, scale. = TRUE)
plot(res.pca$x[, "PC1"], res.pca$x[, "PC2"], pch = 19, xlab = "PC1", ylab = "PC2", lwd = 5,
     main = "Individuals' plot (1 x 2) - PCA on Rosettes Cell Wall Transcriptomics",
     col = colors)
text(res.pca$x[, "PC1"], res.pca$x[, "PC2"], labels = row.names(res.pca$x), cex = 0.8, pos = 3)
```

Transcriptomics_Stems *Transcriptomics Stems*

Description

A dataset containing all the transcripts obtained by RNA-seq performed, according to the standard Illumina protocols, on floral stems of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Transcriptomics_Stems")
```

Format

A data frame with 30 rows and 22570 variables.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Transcriptomics_Stems")

# Look at data frame dimensions
dim(Transcriptomics_Stems)

# Look at the first rows and columns
head(Transcriptomics_Stems[,c(1:10)])

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# PCA on transcriptomics
res.pca <- prcomp(Transcriptomics_Stems, center = TRUE, scale. = TRUE)
plot(res.pca$x[, "PC1"], res.pca$x[, "PC2"], pch = 19, xlab = "PC1", ylab = "PC2", lwd = 5,
     main = "Individuals' plot (1 x 2) - PCA on Stems' Transcriptomics",
     col = colors)
text(res.pca$x[, "PC1"], res.pca$x[, "PC2"], labels = row.names(res.pca$x), cex = 0.8, pos = 3)
```

Transcriptomics_Stems_CW

Transcriptomics Stems Cell Wall

Description

A dataset containing the transcripts encoding Cell Wall Proteins (CWPs) sorted from the 22 570 transcripts (see [Transcriptomics_Stems](#)) obtained by RNA-seq performed, according to the standard Illumina protocols, on floral stems of five *A. thaliana* genotypes at two growth temperatures. See [Ecotype](#) and [Temperature](#) for more information.

Usage

```
data("Transcriptomics_Stems_CW")
```

Format

A data frame with 30 rows and 414 variables.

Source

doi: [10.3390/cells9102249](https://doi.org/10.3390/cells9102249)

Examples

```
# Load the dataset
data("Transcriptomics_Stems_CW")

# Look at data frame dimensions
dim(Transcriptomics_Stems_CW)

# Look at the first rows and columns
head(Transcriptomics_Stems_CW[,c(1:10)])

# Create a colors' vector
colors <- c(rep("#A6CEE3",3), rep("#1F78B4",3), rep("#B2DF8A",3), rep("#33A02C",3),
            rep("#FB9A99",3), rep("#E31A1C",3), rep("#FDBF6F",3), rep("#FF7F00",3),
            rep("#CAB2D6",3), rep("#6A3D9A",3))

# PCA on transcriptomics
res.pca <- prcomp(Transcriptomics_Stems_CW, center = TRUE, scale. = TRUE)
plot(res.pca$x[, "PC1"], res.pca$x[, "PC2"], pch = 19, xlab = "PC1", ylab = "PC2", lwd = 5,
     main = "Individuals' plot (1 x 2) - PCA on Stems Cell Wall Transcriptomics",
     col = colors)
text(res.pca$x[, "PC1"], res.pca$x[, "PC2"], labels = row.names(res.pca$x), cex = 0.8, pos = 3)
```

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