

# Package ‘PREDAsampledata’

July 11, 2024

**Title** expression and copy number data on clear cell renal carcinoma samples

**Version** 0.45.0

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**Description** Sample data for PREDA package. (annotations objects synchronized with GeneAnnot custom CDFs version 2.2.0)

**Depends** R (>= 2.10.0), methods, PREDA, Biobase, affy, annotate

**Suggests** hgu133plus2.db, hgu133plus2cdf

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**License** Artistic-2.0

**biocViews** ExperimentData, Tissue, CancerData, KidneyCancerData, MicroarrayData, TissueMicroarrayData, ArrayExpress

**git\_url** <https://git.bioconductor.org/packages/PREDAsampledata>

**git\_branch** devel

**git\_last\_commit** e2c1e10

**git\_last\_commit\_date** 2024-04-30

**Repository** Bioconductor 3.20

**Date/Publication** 2024-07-11

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`AffybatchRCC`*AffyBatch object for clear cell renal carcinoma (RCC) sample dataset*

---

**Description**

An AffyBatch object containing raw data from clear cell renal carcinoma (RCC) dataset CEL files

**Usage**

```
data(AffybatchRCC)
```

**Details**

The sample gene expression dataset includes 12 samples of clear cell renal carcinoma and 11 samples from normal kidney tissue.

**Source**

ArrayExpress dataset E-TABM-282

**References**

Ingrid Cifola, Roberta Spinelli, Luca Beltrame, Clelia Peano, Ester Fasoli, Stefano Ferrero, Silvano Bosari, Stefano Signorini, Francesco Rocco, Roberto Perego, Vanessa Proserpio, Francesca Raimondo, Paolo Mocarrelli, and Cristina Battaglia. Genomewide screening of copy number alterations and loh events in renal cell carcinomas and integration with gene expression profile. *Mol Cancer*, 7:6, 2008.

**Examples**

```
data(AffybatchRCC)
AffybatchRCC
```

---

`ExpressionSetRCC`*ExpressionSet object for clear cell renal carcinoma (RCC) sample dataset*

---

**Description**

An ExpressionSet object containing justRMA preprocessed data for clear cell renal carcinoma (RCC) dataset, using standard Affymetrix CDF

**Usage**

```
data(ExpressionSetRCC)
```

**Details**

The sample gene expression dataset includes 12 samples of clear cell renal carcinoma and 11 samples from normal kidney tissue.

**Source**

ArrayExpress dataset E-TABM-282

**References**

Ingrid Cifola, Roberta Spinelli, Luca Beltrame, Clelia Peano, Ester Fasoli, Stefano Ferrero, Silvano Bosari, Stefano Signorini, Francesco Rocco, Roberto Perego, Vanessa Proserpio, Francesca Raimondo, Paolo Mocarelli, and Cristina Battaglia. Genomewide screening of copy number alterations and loh events in renal cell carcinomas and integration with gene expression profile. *Mol Cancer*, 7:6, 2008.

**Examples**

```
data(ExpressionSetRCC)
ExpressionSetRCC
```

---

GEanalysisResults

*RCC gene expression sample dataset - PREDA analysis results*

---

**Description**

PREDA analysis results of RCC gene expression sample dataset. The PREDA analysis was focused on the detection of differentially expressed genomic regions in tumor samples compared to normal kidney cells.

**Usage**

```
data(GEanalysisResults)
```

**Source**

ArrayExpress dataset E-TABM-282

**References**

<http://www.xlab.unimo.it/PREDA>

**Examples**

```
data(GEanalysisResults)
str(GEanalysisResults)
```

SODEGIRCAnalysisResults

*SODEGIR analysis results on Copy Number data*

---

### **Description**

PREDAResults object containing SODEGIR analysis results on Copy Number data

### **Usage**

```
data(SODEGIRCAnalysisResults)
```

### **Details**

See also vignette from PREDA package

### **Source**

Copy number data data were obtained from ArrayExpress datasets E-TABM-283/E-TABM-284

### **References**

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

### **Examples**

```
data(SODEGIRCAnalysisResults)
str(SODEGIRCAnalysisResults)
```

---

SODEGIRCNDDataForPREDA *Copy Number input data for PREDA analysis*

---

### **Description**

DataForPREDA object containing Copy Number input data for PREDA analysis

### **Usage**

```
data(SODEGIRCNDDataForPREDA)
```

### **Details**

See also vignette from PREDA package

**Source**

Copy number data data were obtained from ArrayExpress datasets E-TABM-283/E-TABM-284

**References**

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

**Examples**

```
data(SODEGIRCNDDataForPREDA)
str(SODEGIRCNDDataForPREDA)
```

---

SODEGIRGEanalysisResults

*SODEGIR analysis results on Gene Expression data*

---

**Description**

PREDADataAndResults object containing SODEGIR analysis results on Gene Expression data

**Usage**

```
data(SODEGIRGEanalysisResults)
```

**Details**

See also vignette from PREDA package

**Source**

ArrayExpress dataset E-TABM-282

**References**

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

**Examples**

```
data(SODEGIRGEanalysisResults)
str(SODEGIRGEanalysisResults)
```

SODEGIRGEDataForPREDA *Gene Expression input data for PREDA analysis*

---

**Description**

DataForPREDA object containing Gene Expression input data for PREDA analysis

**Usage**

```
data(SODEGIRGEDataForPREDA)
```

**Details**

See also vignette from PREDA package

**Source**

ArrayExpress dataset E-TABM-282

**References**

<http://www.xlab.unimo.it/PREDA> <http://www.xlab.unimo.it/SODEGIR>

Silvio Bicciato, Roberta Spinelli, Mattia Zampieri, Eleonora Mangano, Francesco Ferrari, Luca Beltrame, Ingrid Cifola, Clelia Peano, Aldo Solari, and Cristina Battaglia. A computational procedure to identify significant overlap of differentially expressed and genomic imbalanced regions in cancer datasets. *Nucleic Acids Res*, 37(15):5057-70, August 2009.

**Examples**

```
data(SODEGIRGEDataForPREDA)  
str(SODEGIRGEDataForPREDA)
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