Package ‘PREDAsampledata’

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

Version 0.47.0

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

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Contents

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

Description

An AffyBatch object containint 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 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(AffybatchRCC)
AffybatchRCC
```

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

Description

An ExpressionSet object containint 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 comparet 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)
```

`SODEGIRCNanalysisResults` *SODEGIR analysis results on Copy Number data*

Description

PREDAResults object containing SODEGIR analysis results on Copy Number data

Usage

```
data(SODEGIRCNanalysisResults)
```

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(SODEGIRCNanalysisResults)
str(SODEGIRCNanalysisResults)
```

`SODEGIRCNDataForPREDA` *Copy Number input data for PREDA analysis*

Description

DataForPREDA object containing Copy Number input data for PREDA analysis

Usage

```
data(SODEGIRCNDataForPREDA)
```

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(SODEGIRCNDataForPREDA)
str(SODEGIRCNDataForPREDA)
```

`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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