Package 'dressCheck'

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Title data and software for checking Dressman JCO 25(5) 2007

Description data and software for checking Dressman JCO 25(5) 2007

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Suggests survival, chron

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c119 *an N=119 expression set based on CEL files from JCO.zip*

Description

an N=119 expression set based on CEL files from JCO.zip

Usage

```
data(c119)
```

Format

The format is:
Formal class 'ExpressionSet' [package "Biobase"] with 6 slots
..@ assayData :<environment: 0x191bb50>
..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata :'data.frame': 14 obs. of 1 variable:
.. ..$ labelDescription: chr [1:14] NA NA NA NA ...
.. .. ..@ data :'data.frame': 119 obs. of 14 variables:
.. ..$ fixedid : Factor w/ 119 levels ".08","1024","1447",..: 53 54 4 6 16 17 18 25 27 29 ...
.. ..$ OVC.TumorID : Factor w/ 119 levels "0.08","1024",..: 53 54 4 6 16 17 18 25 27 29 ...
.. ..$ Survival : int [1:119] 185 183 132 74 78 118 142 87 118 107 ...
.. ..$ dead : int [1:119] 0 0 1 1 1 1 0 1 0 0 ...
.. ..$ Assigned.Stage: int [1:119] 3 3 3 3 3 3 3 3 3 3 ...
.. ..$ GRADE : Factor w/ 11 levels "","," 2/3","1",..: 7 5 7 5 5 7 5 7 5 7 ...
.. ..$ Debulk : Factor w/ 5 levels "O","Optimal",..: 3 3 3 1 3 1 1 1 1 1 ...
.. ..$ CA125.POST : Factor w/ 88 levels "","10","10.5",..: 40 80 24 63 43 27 80 75 73 2 ...
.. ..$ CR : int [1:119] 1 1 1 1 1 1 1 1 1 1 ...
.. ..$ X : logi [1:119] NA NA NA NA NA NA ...
.. ..$ X.1 : logi [1:119] NA NA NA NA NA NA ...
.. ..$ X.2 : logi [1:119] NA NA NA NA NA NA ...
.. ..$ celName : chr [1:119] "0074_1772_h133a_872.cel" "0074_1773_h133a_922.cel" "0074_1774_h133a_1451.cel"
"0074_1775_h133a_1526.cel" ...
.. ..$ rundate : chr [1:119] "09/20/02" "09/20/02" "09/20/02" "09/20/02" ...
.. .. ..@ dimLabels : chr [1:2] "rowNames" "columnNames"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. ..@ .Data:List of 1
.. ..$: int [1:3] 1 1 0
..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable:
.. ..$ labelDescription: chr(0)
.. .. ..@ data :'data.frame': 22283 obs. of 0 variables
.. .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns"
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. ..@ .Data:List of 1
.. ..$: int [1:3] 1 1 0

..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots
.. .. ..@ name : chr ""
.. .. ..@ lab : chr ""
.. .. ..@ contact : chr ""
.. .. ..@ title : chr ""
.. .. ..@ abstract : chr ""
.. .. ..@ url : chr ""
.. .. ..@ pubMedIds : chr ""
.. .. ..@ samples : list()
.. .. ..@ hybridizations : list()
.. .. ..@ normControls : list()
.. .. ..@ preprocessing :List of 2
.. ..$ filenames : chr [1:119] "/data/stvjc/ANDERSON/SOURCE/JCO-OvCa/DukeWebSite/CELS/0074_1772_h133a_87
"/data/stvjc/ANDERSON/SOURCE/JCO-OvCa/DukeWebSite/CELS/0074_1773_h133a_922.cel" "/data/stvjc/ANDERSON
OvCa/DukeWebSite/CELS/0074_1774_h133a_1451.cel" "/data/stvjc/ANDERSON/SOURCE/JCO-
OvCa/DukeWebSite/CELS/0074_1775_h133a_1526.cel" ...
.. ..$ affyversion: chr NA
.. .. ..@ other :List of 1
.. ..$: chr ""
.. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. ..@ .Data:List of 1
.. ..$: int [1:3] 1 0 0
..@ annotation : chr "hgu133a"
..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots
.. .. ..@ .Data:List of 4
.. ..$: int [1:3] 2 10 0
.. ..$: int [1:3] 2 3 11
.. ..$: int [1:3] 1 1 0
.. ..$: int [1:3] 1 0 0

Details

CEL files were obtained from https://discovery.genome.duke.edu/express/resources/1144/PlatinumJCO.zip and imported to R using justRMA in Bioconductor's affy package.

The CEL files had names `> sampleNames(c119)[1:5] [1] "0074_1772_h133a_872.cel" "0074_1773_h133a_922.cel" [3] "0074_1774_h133a_1451.cel" "0074_1775_h133a_1526.cel" [5] "0074_1776_h133a_1784.cel"` in which the patient identifiers are embedded as the tokens between the last underscore and the `.cel` suffix. 'fixedid' is the extracted identifier, which is of the same form as the sample identifiers in the clinical data, `OVCclinicalinfo.xls` distributed at the Duke website https://discovery.genome.duke.edu/express/resources/193/OVCclinicalinfo.xls

The phenoData component of c119 was derived from OVCclinicalinfo.xls and linked to samples by associating the variable `OVC TumorID` in the spreadsheet with the sample identifiers extracted from the CEL filenames.

Examples

```
data(c119)
## maybe str(c119) ; plot(c119) ...
```

corrp116 *Dressman's RMA+SFR corrected quantifications for 116 ovarian cancer samples*

Description

Dressman's RMA+SFR corrected quantifications for 116 ovarian cancer samples

Usage

```
data(corrp116)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 6 slots ..@ assayData :<environment: 0x1a30350> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 14 obs. of 1 variable: .. ..$ labelDescription: chr [1:14] NA NA NA NA ... .@ data :'data.frame': 116 obs. of 14 variables: .. ..$ fixedid : Factor w/ 119 levels ".08","1024","1447",..: 12 35 8 18 28 25 46 47 13 45 ... .$ OVC.TumorID : Factor w/ 119 levels "0.08","1024",..: 12 35 8 18 28 25 46 47 13 45 ... .$ Survival : int [1:116] 15 95 33 142 98 87 16 16 18 16 ... .$ dead : int [1:116] 1 0 1 0 1 1 1 1 1 1 ... .$ Assigned.Stage: int [1:116] 3 3 4 3 3 3 3 4 3 3 ... .$ GRADE : Factor w/ 11 levels ""," 2/3","1",..: 5 5 5 5 7 7 5 5 5 5 ... .$ Debulk : Factor w/ 5 levels "O","Optimal",..: 3 3 1 1 1 1 1 1 1 3 ... .$ CA125.POST : Factor w/ 88 levels "","10","10.5",..: 64 10 77 80 73 75 70 4 21 33 ... .$ CR : int [1:116] 0 1 1 1 1 1 1 1 1 0 ... .$ X : logi [1:116] NA NA NA NA NA NA ... .$ X.1 : logi [1:116] NA NA NA NA NA NA ... .$ X.2 : logi [1:116] NA NA NA NA NA NA ... .$ celName : chr [1:116] "0074_1830_h133a_1665.cel" "0074_2033_h133a_2505.cel" "0074_2398_h133a_1578.cel" "0074_1778_h133a_1846.cel" ... .$ rundate : chr [1:116] "10/23/02" "01/03/03" "05/30/03" "09/20/02" ... .@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. ..$ labelDescription: chr(0) .. .. ..@ data :'data.frame': 22115 obs. of 0 variables .. .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "" .. .. ..@ lab : chr "" .. .. ..@ contact : chr "" .. .. ..@ title : chr "" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "" .. .. ..@ pubMedIds : chr "" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other : list() .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 0 0 ..@ annotation : chr(0) ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 4 .. ..$: int [1:3] 2 9 0 .. ..$: int [1:3] 2 3 10 .. ..$: int [1:3] 1 1 0 .. ..$: int [1:3] 1 0 0

Examples

```
data(corrp116)
## maybe str(corrp116) ; plot(corrp116) ...
```

`DrAsGiven` *Quantifications of 119 ovarian cancer samples as distributed at Duke's platinum.php*

Description

Quantifications of 119 ovarian cancer samples as distributed at Duke's platinum.php

Usage

```
data(DrAsGiven)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 6 slots ..@ assayData :<environment: 0x18b5f34> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 11 obs. of 1 variable: .. ..$ labelDescription: chr [1:11] NA NA NA NA ... .@ data :'data.frame': 119 obs. of 11 variables: .. ..$ OVC.TumorID : Factor w/ 119 levels "0.08","1024",..: 1 2 3 4 5 6 7 8 9 10 ... .$ Survival : int [1:119] 14 13 75 132 108 74 33 33 148 13 ... .$ X0...alive...1...dead: int [1:119] 1 1 1 1 1 1 1 0 1 ... .$ Assigned.Stage : int [1:119] 4 4 3 3 3 3 3 4 3 3 ... .$ GRADE : Factor w/ 11 levels "","2/3","1",..: 7 7 5 7 7 5 5 5 5 7 ... .$ Debulk : Factor w/ 5 levels "O","Optimal",..: 3 3 3 3 1 1 3 1 1 3 ... .$ CA125.POST : Factor w/ 88 levels "","10","10.5",..: 74 10 76 24 50 63 82 77 73 79 ... .$ response.0.NR..1.CR : int [1:119] 0 1 1 1 1 1 1 1 1 0 ... .$ X : logi [1:119] NA NA NA NA NA NA ... .$ X.1 : logi [1:119] NA NA NA NA NA NA ... .$ X.2 : logi [1:119] NA NA NA NA NA NA ... .@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 0 obs. of 1 variable: .. ..$ labelDescription: chr(0) .. .. ..@ data :'data.frame': 22115 obs. of 0 variables .. .. ..@ dimLabels : chr [1:2] "featureNames" "featureColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "" .. .. ..@ lab : chr "" .. .. ..@ contact : chr "" .. .. ..@ title : chr "" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "" .. .. ..@ pubMedIds : chr "" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other : list() .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 0 0 ..@ annotation : chr(0) ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 4 .. ..$: int [1:3] 2 9 0 .. ..$: int [1:3] 2 3 10 .. ..$: int [1:3] 1 1 0 .. ..$: int [1:3] 1 0 0

Examples

```
data(DrAsGiven)
## maybe str(DrAsGiven) ; plot(DrAsGiven) ...
```

`E2F3sig.probes` *Affymetrix probe identifiers for the E2F3 pathway signature of Bild et al.*

Description

Affymetrix probe identifiers for the E2F3 pathway signature of Bild et al.

Usage

```
data(E2F3sig.probes)
```

Format

The format is: chr [1:298] "223320_s_at" "213485_s_at" "209735_at" "239579_at" ...

Examples

```
data(E2F3sig.probes)
## maybe str(E2F3sig.probes) ; plot(E2F3sig.probes) ...
```

`e2f3Wts` *Coefficients to weight components of E2F3 pathway to score for activity, derived from SVD applied to Bild's data*

Description

Coefficients to weight components of E2F3 pathway to score for activity, derived from SVD applied to Bild's data

Usage

```
data(e2f3Wts)
```

Format

The format is: Named num [1:298] -0.0613 0.0589 -0.0626 -0.0596 -0.0541 ... - attr(*, "names")= chr [1:298] "223320_s_at" "213485_s_at" "209735_at" "239579_at" ...

Examples

```
data(e2f3Wts)
## maybe str(e2f3Wts) ; plot(e2f3Wts) ...
```

platsigprobes *affymetrix probe identifiers for the platinum responsiveness signature*

Description

affymetrix probe identifiers for the platinum responsiveness signature

Usage

```
data(platsigprobes)
```

Format

The format is: Named chr [1:246] "208926_at" "1557227_s_at" "201730_s_at" ... - attr(*, "names")= chr [1:246] "NEU1" "TPR1" "TPR2" "TPR3" ...

Examples

```
data(platsigprobes)
## maybe str(platsigprobes) ; plot(platsigprobes) ...
```

pwLines *A representation of Bild's HMEC lines for pathway signature identification*

Description

A representation of Bild's HMEC lines for pathway signature identification

Usage

```
data(pwLines)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 6 slots ..@ assayData :<environment: 0x192e1dc> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 28 obs. of 1 variable: .. ..$ labelDescription: chr [1:28] NA NA NA NA ... .@ data :'data.frame': 55 obs. of 28 variables: .. ..$ gsmid : chr [1:55] "GSM70597" "GSM70598" "GSM70599" "GSM70600" ... .$ gsmlabel : Factor w/ 55 levels "BCAT-8","BCAT-9",..: 19 21 22 23 24 25 26 27 28 20 ... .$ perturb : chr [1:55] "GFP" "GFP" "GFP" "GFP" ... .$ title : Factor w/ 55 levels "BCAT-8","BCAT-9",..: 19 21 22 23 24 25 26 27 28 20 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ geo_accession : Factor w/ 55 levels "GSM70597","GSM70598",..: 1 2 3 4 5 6 7 8 9 10 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ status : Factor w/ 1 level "Public on Nov 07 2005": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3"

"V4" "V5" ... .$ submission_date : Factor w/ 1 level "Aug 17 2005": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ last_update_date : Factor w/ 1 level "Nov 07 2005": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ type : Factor w/ 1 level "RNA": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ channel_count : Factor w/ 1 level "1": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ source_name_ch1 : Factor w/ 1 level "mammary epithelial cells expressing oncogenes (or GFP control)": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ organism_ch1 : Factor w/ 1 level "Homo sapiens": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ characteristics_ch1 : Factor w/ 1 level "mammary epithelial cells expressing oncogenes (or GFP control)": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ molecule_ch1 : Factor w/ 1 level "total RNA": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ label_ch1 : Factor w/ 1 level "biotin": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ description : Factor w/ 1 level "RNA was extracted from human mammary epithelial cells expressing oncogenes (or GFP control)": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ data_processing : Factor w/ 1 level "Affymetrix Microarray Suite version 5.0": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ platform_id : Factor w/ 1 level "GPL570": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_name : Factor w/ 1 level "Joseph,R.,Nevins": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_department : Factor w/ 1 level "IGSP": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_institute : Factor w/ 1 level "Duke University": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_address : Factor w/ 1 level "2133 CIEMAS, 101 Science Dr.": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_city : Factor w/ 1 level "Durham": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_state : Factor w/ 1 level "NC": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_zip/postal_code: Factor w/ 1 level "27708": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ contact_country : Factor w/ 1 level "USA": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ supplementary_file : Factor w/ 1 level "NONE": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .$ data_row_count : Factor w/ 1 level "54675": 1 1 1 1 1 1 1 1 1 1 ... .- attr(*, "names")= chr [1:55] "V2" "V3" "V4" "V5" ... .@ dimLabels : chr [1:2] "sampleNames" "sampleColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. .. ..@ varMetadata :'data.frame': 16 obs. of 3 variables: .. ..$ Column : chr [1:16] "ID" "GB_ACC" "SPOT_ID" "Species Scientific Name" ... .$ Description : Factor w/ 15 levels "","A gene symbol, when one is available (from UniGene).",..: 3 5 15 13 12 1 11 1 10 14 ... .$ labelDescription: chr [1:16] NA NA NA NA ... .@ data :'data.frame': 54675 obs. of 16 variables: .. ..$ ID : Factor w/ 54676 levels "1007_s_at","1053_at",..: 1 2 3 4 5 6 7 8 9 10 ... .$ GB_ACC : Factor w/ 51277 levels "AF276507","AK074161",..: 82 21 83 85 17 16 84 87 19 15 ... .$ SPOT_ID : chr [1:54675] NA NA NA NA ... .$ Species.Scientific.Name : Factor w/ 2 levels "Homo sapiens",..: 1 1 1 1 1 1 1 1 1 1 ... .$ Annotation.Date : Factor w/ 2 levels "Mar 11, 2009",..: 1 1 1 1 1 1 1 1 1 1 ... .$ Sequence.Type : Factor w/ 4 levels "Consensus sequence",..:

2 2 2 2 2 2 2 2 2 ... .$ Sequence.Source : Factor w/ 3 levels "Affymetrix Proprietary Database",..: 1 2 1 2 1 2 1 1 2 1 ... .$ Target.Description : Factor w/ 51843 levels "J02843 /FEATURE=cds /DEFINITION=HUMCYPIIE Human cytochrome P450IIE1 (ethanol-inducible) gene, complete cds",..: 8 7 9 11 3 2 10 13 5 1 ... .$ Representative.Public.ID : Factor w/ 51339 levels "AF276507","AK074161",..: 82 21 83 85 17 16 84 87 19 15 ... .$ Gene.Title : Factor w/ 23061 levels "ADAM metallopeptidase domain 32",..: 34 59 42 54 41 76 72 58 19 33 ... .$ Gene.Symbol : Factor w/ 20828 levels "ADAM32","AFG3L1",..: 26 59 40 50 38 75 68 54 18 25 ... .$ ENTREZ_GENE_ID : Factor w/ 20828 levels "10406","11078",..: 63 59 51 64 48 62 61 3 60 24 ... .$ RefSeq.Transcript.ID : Factor w/ 20082 levels "","NM_000409",..: 17 22 19 26 2 25 24 32 23 4 ... .$ Gene.Ontology.Biological.Process: Factor w/ 8891 levels "","0000122 // negative regulation of transcription from RNA polymerase II promoter // inferred from electronic annotation /// 0006"| __truncated__,..: 20 11 36 8 39 18 5 23 35 49 ... .$ Gene.Ontology.Cellular.Component: Factor w/ 6677 levels "","0000151 // ubiquitin ligase complex // inferred from electronic annotation /// 0005634 // nucleus // inferred from electronic a"| __truncated__,..: 43 21 1 20 44 1 18 28 8 36 ... .$ Gene.Ontology.Molecular.Function: Factor w/ 8929 levels "","0000166 // nucleotide binding // inferred from electronic annotation /// 0001784 // phosphotyrosine binding // inferred from el"| __truncated__,..: 9 5 10 23 47 7 22 38 41 37 ... .@ dimLabels : chr [1:2] "featureNames" "featureColumns" .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 1 0 ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. .. ..@ name : chr "" .. .. ..@ lab : chr "" .. .. ..@ contact : chr "" .. .. ..@ title : chr "" .. .. ..@ abstract : chr "" .. .. ..@ url : chr "" .. .. ..@ pubMedIds : chr "" .. .. ..@ samples : list() .. .. ..@ hybridizations : list() .. .. ..@ normControls : list() .. .. ..@ preprocessing : list() .. .. ..@ other : list() .. .. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 1 .. ..$: int [1:3] 1 0 0 ..@ annotation : chr "hgu133plus2.db" ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 4 .. ..$: int [1:3] 2 10 0 .. ..$: int [1:3] 2 3 11 .. ..$: int [1:3] 1 1 0 .. ..$: int [1:3] 1 0 0

Examples

```
data(pwLines)
## maybe str(pwLines) ; plot(pwLines) ...
```

`Src.probes` *Affymetrix probe identifiers for the Src pathway signature of Bild et al.*

Description

Affymetrix probe identifiers for the Src pathway signature of Bild et al.

Usage

```
data(Src.probes)
```

Format

The format is: chr [1:73] "213485_s_at" "201128_s_at" "215867_x_at" "201879_at" ...

Examples

```
data(Src.probes)
## maybe str(Src.probes) ; plot(Src.probes) ...
```

`srcWts` *Coefficients to weight components of Src pathway to score for activity, derived from SVD applied to Bild's data*

Description

Coefficients to weight components of Src pathway to score for activity, derived from SVD applied to Bild's data

Usage

```
data(srcWts)
```

Format

The format is: Named num [1:73] -0.1251 -0.1335 -0.1313 -0.0893 -0.1321 ... - attr(*, "names")= chr [1:73] "213485_s_at" "201128_s_at" "215867_x_at" "201879_at" ...

Examples

```
data(srcWts)
## maybe str(srcWts) ; plot(srcWts) ...
```

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