

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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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 NA ...
```

```
.. .. ..$ X.1 : logi [1:119] NA NA NA NA NA NA NA ...
```

```
.. .. ..$ X.2 : logi [1:119] NA 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_872.cel" "/data/stvjc/ANDERSON/SOURCE/JCO-OvCa/DukeWebSite/CELS/0074_1773_h133a_922.cel" "/data/stvjc/ANDERSON/SOURCE/JCO-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) ...

```

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 "0.08","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 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 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 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 NA\$ X.1 : logi [1:119] NA NA NA NA NA NA NA\$ X.2 : logi [1:119] NA 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	<i>Coefficients to weight components of E2F3 pathway to score for activity, derived from SVD applied to Bild's data</i>
---------	---

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	<i>affymetrix probe identifiers for the platinum responsiveness signature</i>
---------------	---

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.,Neveins": 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 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 2 ... .. ..$ Sequence.Source : Factor w/ 3 levels "Affymetrix Proprietary
Database",...: 1 2 1 2 1 2 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" | __trun-
cated__,...: 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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