

Package ‘dressCheck’

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Title 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 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.ce1" "/data/stvjc/ANDERSON/SOURCE/JCO-OvCa/DukeWebSite/CELS/0074_1773_h133a_922.ce1" "/data/stvjc/ANDERSON/SOURCE/JCO-OvCa/DukeWebSite/CELS/0074_1774_h133a_1451.ce1" "/data/stvjc/ANDERSON/SOURCE/JCO-OvCa/DukeWebSite/CELS/0074_1775_h133a_1526.ce1" ...
.. .. ..$ 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.ce1" "0074_1773_h133a_922.ce1" [3] "0074_1774_h133a_1451.ce1" "0074_1775_h133a_1526.ce1" [5] "0074_1776_h133a_1784.ce1"` in which the patient identifiers are embedded as the tokens between the last underscore and the `.ce1` 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 NA\$ X.1 : logi [1:116] NA NA NA NA NA NA NA\$ X.2 : logi [1:116] NA 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.,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

```

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 ... .. .. 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 ... .. ..
..- 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 ... .. .. 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 ... .. .. 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 ... .. .. 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 ... .. .. 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 ... .. ..$ Annotation.Date : Factor w/ 2 levels "Mar 11, 2009",...:
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 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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