

Package 'KEGGandMetacoreDzPathwaysGEO'

August 26, 2025

Type Package

Title Disease Datasets from GEO

Version 1.29.0

Date 2014-04-25

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Description This is a collection of 18 data sets for which the phenotype is a disease with a corresponding pathway in either KEGG or metacore database. This collection of datasets were used as gold standard in comparing gene set analysis methods.

Depends R (>= 2.15.0)

Imports Biobase, BiocGenerics

biocViews ExperimentData, GEO

License GPL-2

git_url <https://git.bioconductor.org/packages/KEGGandMetacoreDzPathwaysGEO>

git_branch devel

git_last_commit 8f277db

git_last_commit_date 2025-04-15

Repository Bioconductor 3.22

Date/Publication 2025-08-26

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KEGGandMetacoreDzPathwaysGEO-package

GEO Data Sets used to compare gene set analysis methods.

Description

This is a collection of 18 GEO datasets for which the phenotype is a disease with a corresponding pathway in either of the two popular gene to pathway annotation databases, KEGG and Metacore. These datasets were used as gold standard in comparing gene set analysis methods in the research article:

Tarca AL, Bhatti G, Romero R (2013) A Comparison of Gene Set Analysis Methods in Terms of Sensitivity, Prioritization and Specificity. PLoS ONE 8(11): e79217. doi:10.1371/journal.pone.0079217

GEOID	Pubmed	Ref.	Disease/Target pathway	KEGGID
GSE1145	-	-	Dilated cardiomyopathy	hsa5414
GSE11906	19852842	<i>pmid19852842</i>	COPD	Chronic obstructive pulm
GSE14924_CD4	19710498	<i>pmid19710498</i>	Acute myeloid leukemia	hsa5221
GSE14924_CD8	19710498	<i>pmid19710498</i>	Acute myeloid leukemia	hsa5221
GSE16759	20126538	<i>pmid20126538</i>	Alzheimer's disease	hsa5010
GSE19420	22802091	<i>pmid22802091</i>	Type II diabetes mellitus	hsa4930
GSE20164	20926834	<i>pmid20926834</i>	Parkinson's disease	hsa5012
GSE23878	21281787	<i>pmid21281787</i>	Colorectal cancer	hsa5210
GSE24739_G0	21436996	<i>pmid21436996</i>	Chronic myeloid leukemia	hsa5220
GSE24739_G1	21436996	<i>pmid21436996</i>	Chronic myeloid leukemia	hsa5220
GSE30153	21886837	<i>pmid21886837</i>	Lupus Erythematosus Systemic	Lupus Erythematosus Sy
GSE32676	22261810	<i>pmid22261810</i>	Pancreatic cancer	hsa5212
GSE38666_epithelia	23762861	<i>pmid23762861</i>	Ovarian cancer	Ovarian Neoplasms1
GSE38666_stroma	23762861	<i>pmid23762861</i>	Ovarian cancer	Ovarian Neoplasms1
GSE4183	19461970	<i>pmid19461970</i>	Colorectal cancer	hsa5210
GSE42057	23590301	<i>pmid23590301</i>	Chronic obstructive pulmonary disease	Chronic obstructive pulm
GSE7305	17640886	<i>pmid17640886</i>	Endometrial cancer	hsa5213
GSE22780	-	-	Pancreatic Neoplasms	Pancreatic Neoplasms

Details

Package: KEGGandMetacoreDzPathwaysGEO
 Type: Package
 Version: 0.99.4

Date: 2014-02-28
License: GPL-2

Author(s)

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References

Tarca AL, Bhatti G, Romero R (2013) A Comparison of Gene Set Analysis Methods in Terms of Sensitivity, Prioritization and Specificity. PLoS ONE 8(11): e79217. doi:10.1371/journal.pone.0079217

See Also

<http://www.bioconductor.org/packages/release/data/experiment/html/KEGGdzPathwaysGEO.html>

Examples

```
mysets=data(package="KEGGandMetacoreDzPathwaysGEO")$results[, "Item"]
mysets
data(GSE1145)

set=mysets[1]
data(list=set, package="KEGGandMetacoreDzPathwaysGEO")
```

GSE1145

Data Set Id: GSE1145

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1145>

Usage

```
data(GSE1145)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE1145"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1145"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05414"\$ disease : chr "Dilated cardiomyopathy"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x29f44c0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA

```

NA .. ..@ data : 'data.frame': 26 obs. of 2 variables: .. .. .$ Sample: chr [1:26] "GSM18442"
"GSM18443" "GSM18444" "GSM18445" ... .. .$ Group : chr [1:26] "c" "c" "c" "c" ... ..
..@ 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': 54675 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 ..@ annotation : chr
"hgu133plus2" ..@ protocolData : Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4
slots .. ..@ varMetadata : 'data.frame': 0 obs. of 1 variable: .. .. .$ labelDescription: chr(0)
.. ..@ data : 'data.frame': 26 obs. of 0 variables .. ..@ 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 ..@ __classVersion__: Formal class
'Versions' [package "Biobase"] with 1 slots .. ..@ .Data: List of 4 .. .. .$ : int [1:3] 3 0 0 ..
.. .$ : int [1:3] 2 20 0 .. .. .$ : int [1:3] 1 3 0 .. .. .$ : int [1:3] 1 0 0

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1145>

Examples

```
data(GSE1145)
```

GSE11906

Data Set Id: GSE11906

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11906>

Usage

```
data(GSE11906)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData : Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE11906"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE11906"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other : List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Pulmonary Disease Chronic Obstructive"\$ disease : chr "Pulmonary Disease Chronic Obstructive"@ __classVersion__: Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data: List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData : <environment: 0x3483a70> ..@ phenoData : Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data : 'data.frame': 88 obs. of 2 variables:\$ Sample: chr [1:88] "GSM101095.CEL.gz" "GSM101097.CEL.gz" "GSM252799.CEL.gz" "GSM101098.CEL.gz"\$ Group : chr [1:88] "c" "c" "c" "c"


```

.. .. @ varMetadata : 'data.frame': 0 obs. of 1 variable: .. .. $ labelDescription: chr(0) .. ..
.. @ data : 'data.frame': 54675 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 .. @ annotation : chr
"hgu133plus2" .. @ protocolData : Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4
slots .. .. @ varMetadata : 'data.frame': 0 obs. of 1 variable: .. .. $ labelDescription: chr(0)
.. .. @ data : 'data.frame': 20 obs. of 0 variables .. .. @ 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 .. @ .__classVersion__: Formal class
'Versions' [package "Biobase"] with 1 slots .. .. @ .Data: List of 4 .. .. $ : int [1:3] 3 0 0 .. ..
.. $ : int [1:3] 2 20 0 .. .. $ : int [1:3] 1 3 0 .. .. $ : int [1:3] 1 0 0

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Examples

```
data(GSE14924_CD4)
```

GSE14924_CD8

Data Set Id: GSE14924_CD8

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Usage

```
data(GSE14924_CD8)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots .. @ experimentData : Formal class 'MIAME' [package "Biobase"] with 13 slots @ name : chr "GSE14924_CD8" @ lab : chr "" @ contact : chr "" @ title : chr "" @ abstract : chr "" @ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924_CD8" @ pubMedIds : chr "" @ samples : list() @ hybridizations : list() @ normControls : list() @ preprocessing : list() @ other : List of 3 \$ design : chr "Not Paired" \$ targetGeneSets: chr "05221" \$ disease : chr "Acute myeloid leukemia" @ .__classVersion__: Formal class 'Versions' [package "Biobase"] with 1 slots @ .Data: List of 2 \$: int [1:3] 1 0 0 \$: int [1:3] 1 1 0 .. @ assayData : <environment: 0x3474e00> .. @ phenoData : Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots @ varMetadata : 'data.frame': 2 obs. of 1 variable: \$ labelDescription: chr [1:2] NA NA @ data : 'data.frame': 21 obs. of 2 variables: \$ Sample: chr [1:21] "GSM372731" "GSM372732" "GSM372733" "GSM372734" \$ Group : chr [1:21] "c" "c" "c" "c" @ 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': 54675 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 ..@ annotation : chr
"hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4
slots .. .. ..@ varMetadata : 'data.frame': 0 obs. of 1 variable: .. .. ..$ labelDescription: chr(0)
.. .. ..@ data : 'data.frame': 21 obs. of 0 variables .. .. ..@ 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 ..@ .__classVersion__:Formal class
'Versions' [package "Biobase"] with 1 slots .. .. ..@ .Data:List of 4 .. .. ..$ : int [1:3] 3 0 0 .. ..
..$ : int [1:3] 2 20 0 .. .. ..$ : int [1:3] 1 3 0 .. .. ..$ : int [1:3] 1 0 0
```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14924>

Examples

```
data(GSE14924_CD8)
```

GSE16759

Data Set Id: GSE16759

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16759>

Usage

```
data(GSE16759)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE16759"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16759"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05010"\$ disease : chr "Alzheimer's disease"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3472060> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data : 'data.frame': 8 obs. of 2 variables:\$ Sample: chr [1:8] "GSM420149" "GSM420150" "GSM420151" "GSM420152"\$ Group : chr [1:8] "c" "c" "c" "c"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data

```
:'data.frame': 8 obs. of 0 variables .. ..@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"
.. ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@
.Data:List of 1 .. ..@ .$. : int [1:3] 1 1 0 ..@ .__classVersion__:Formal class 'Versions' [package
"Biobase"] with 1 slots .. ..@ .Data:List of 4 .. ..@ .$. : int [1:3] 3 0 0 .. ..@ .$. : int [1:3] 2 20 0
.. ..@ .$. : int [1:3] 1 3 0 .. ..@ .$. : int [1:3] 1 0 0
```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16759>

Examples

```
data(GSE16759)
```

GSE19420

Data Set Id: GSE19420

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19420>

Usage

```
data(GSE19420)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE19420"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19420"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets : chr "Diabetes Mellitus Type2"@ disease : chr "Diabetes Mellitus Type2"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2@ .\$. : int [1:3] 1 0 0@ .\$. : int [1:3] 1 1 0 ..@ assayData :<environment: 0x3472418> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:@ labelDescription: chr [1:2] NA NA@ data : 'data.frame': 24 obs. of 2 variables:@ Sample: chr [1:24] "GSM482934" "GSM482938" "GSM482945" "GSM482947"@ .\$. Group : chr [1:24] "c" "c" "c" "c"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:@ labelDescription: chr(0)@ data : 'data.frame': 24 obs. of 0 variables@ 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 ..@

```

.__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 4
.. .. ..$ : int [1:3] 3 0 0 .. .. ..$ : int [1:3] 2 20 0 .. .. ..$ : int [1:3] 1 3 0 .. .. ..$ : int [1:3] 1 0
0

```

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19420>

Examples

```
data(GSE19420)
```

GSE20164

Data Set Id: GSE20164

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20164>

Usage

```
data(GSE20164)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE20164"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20164"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets : chr "Parkinson disease"\$ disease : chr "Parkinson disease"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x346d510> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 11 obs. of 2 variables:\$ Sample: chr [1:11] "GSM506013" "GSM506014" "GSM506019" "GSM506020"\$ Group : chr [1:11] "c" "c" "c" "c"@ 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': 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 ..@ annotation : chr "hgu133a" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 11 obs. of 0 variables@ 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 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20164>

Examples

```
data(GSE20164)
```

GSE22780

Data Set Id: GSE22780

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22780>

Usage

```
data(GSE22780)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE22780"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22780"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets : chr "Pancreatic Neoplasms"\$ disease : chr "Pancreatic Neoplasms"@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33b93f0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] NA NA NA@ data : 'data.frame': 16 obs. of 3 variables:\$ Sample: chr [1:16] "GSM563305" "GSM563307" "GSM563309" "GSM563311"\$ Group : chr [1:16] "c" "c" "c" "c"\$ Block : chr [1:16] "1" "2" "3" "4"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data : 'data.frame': 16 obs. of 0 variables@ 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 ..@ .._classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE22780>

Examples

```
data(GSE22780)
```

GSE23878	<i>Data Set Id: GSE23878</i>
----------	------------------------------

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE23878>

Usage

```
data(GSE23878)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE23878"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE23878"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets: chr "05210"\$ disease : chr "Colorectal cancer"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3466988> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] NA NA NA@ data : 'data.frame': 38 obs. of 3 variables:\$ Sample: chr [1:38] "GSM588863" "GSM588864" "GSM588865" "GSM588867"\$ Group : chr [1:38] "c" "c" "c" "c"\$ Block : chr [1:38] "2" "3" "8" "11"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data : 'data.frame': 38 obs. of 0 variables@ 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 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE23878>

Examples

```
data(GSE23878)
```

GSE24739_G0

*Data Set Id: GSE24739_G0***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739>

Usage

```
data(GSE24739_G0)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE24739_G0"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739_G0"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05220"\$ disease : chr "Chronic myeloid leukemia"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x34626d8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 12 obs. of 2 variables:\$ Sample: chr [1:12] "GSM609354" "GSM609355" "GSM609356" "GSM609357"\$ Group : chr [1:12] "c" "c" "c" "c"@ 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': 54613 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 12 obs. of 0 variables@ 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 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739>

Examples

```
data(GSE24739_G0)
```

GSE24739_G1

*Data Set Id: GSE24739_G1***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739>

Usage

```
data(GSE24739_G1)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE24739_G1"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739_G1"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets : chr "05220"@ disease : chr "Chronic myeloid leukemia"@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2@ ..\$: int [1:3] 1 0 0@ ..\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3460810> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:@ ..\$ labelDescription: chr [1:2] NA NA@ data : 'data.frame': 12 obs. of 2 variables:@ ..\$ Sample: chr [1:12] "GSM609366" "GSM609367" "GSM609368" "GSM609369"@ ..\$ Group : chr [1:12] "c" "c" "c" "c"@ ..@ 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': 54613 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:@ ..\$ labelDescription: chr(0)@ data : 'data.frame': 12 obs. of 0 variables@ 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 ..@ .._classVersion_:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4@ ..\$: int [1:3] 3 0 0@ ..\$: int [1:3] 2 20 0@ ..\$: int [1:3] 1 3 0@ ..\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE24739>

Examples

```
data(GSE24739_G1)
```

GSE30153

*Data Set Id: GSE30153***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30153>

Usage

```
data(GSE30153)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE30153"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30153"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Lupus Erythematosus Systemic"\$ disease : chr "Lupus Erythematosus Systemic"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x345d438> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 26 obs. of 2 variables:\$ Sample: chr [1:26] "GSM746743" "GSM746744" "GSM746745" "GSM746746"\$ Group : chr [1:26] "c" "c" "c" "c"@ 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': 34853 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 26 obs. of 0 variables@ 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 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE30153>

Examples

```
data(GSE30153)
```

GSE32676

*Data Set Id: GSE32676***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32676>

Usage

```
data(GSE32676)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE32676"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32676"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05212"\$ disease : chr "Pancreatic cancer"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3456c68> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data : 'data.frame': 32 obs. of 2 variables:\$ Sample: chr [1:32] "GSM811029" "GSM811030" "GSM811031" "GSM811032"\$ Group : chr [1:32] "c" "c" "c" "c"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data : 'data.frame': 32 obs. of 0 variables@ 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 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE32676>

Examples

```
data(GSE32676)
```

GSE38666_epithelia

*Data Set Id: GSE38666_epithelia***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Usage

```
data(GSE38666_epithelia)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE38666_epithelia"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets : chr "Ovarian Neoplasms1"\$ disease : chr "Ovarian Neoplasms1"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x3452868> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 30 obs. of 2 variables:\$ Sample: chr [1:30] "GSM947277" "GSM947278" "GSM947279" "GSM947280"\$ Group : chr [1:30] "c" "c" "c" "c"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 30 obs. of 0 variables@ 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 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Examples

```
data(GSE38666_epithelia)
```

GSE38666_stroma

*Data Set Id: GSE38666_stroma***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Usage

```
data(GSE38666_stroma)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE38666_stroma"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666_epithelia"@ PubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets: chr "Ovarian Neoplasms1"@ disease : chr "Ovarian Neoplasms1"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2@ .\$. : int [1:3] 1 0 0@ .\$. : int [1:3] 1 1 0 ..@ assayData :<environment: 0x33ff060> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:@ labelDescription: chr [1:2] NA NA@ data :'data.frame': 15 obs. of 2 variables:@ Sample: chr [1:15] "GSM947269" "GSM947270" "GSM947271" "GSM947272"@ .\$. Group : chr [1:15] "c" "c" "c" "c"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:@ labelDescription: chr(0)@ data :'data.frame': 15 obs. of 0 variables@ 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 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4@ .\$. : int [1:3] 3 0 0@ .\$. : int [1:3] 2 20 0@ .\$. : int [1:3] 1 3 0@ .\$. : int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE38666>

Examples

```
data(GSE38666_stroma)
```

GSE4183

*Data Set Id: GSE4183***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4183>

Usage

```
data(GSE4183)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE4183"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4183"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "05210"\$ disease : chr "Colorectal cancer"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33fff38> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data :'data.frame': 23 obs. of 2 variables:\$ Sample: chr [1:23] "GSM95473" "GSM95474" "GSM95475" "GSM95476"\$ Group : chr [1:23] "c" "c" "c" "c"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data :'data.frame': 23 obs. of 0 variables@ 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 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4183>

Examples

```
data(GSE4183)
```

GSE42057

Data Set Id: GSE42057

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42057>

Usage

```
data(GSE42057)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE42057"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42057"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets: chr "Pulmonary Disease Chronic Obstructive"\$ disease : chr "Pulmonary Disease Chronic Obstructive"@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33eca48> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] NA NA@ data : 'data.frame': 136 obs. of 2 variables:\$ Sample: chr [1:136] "GSM1031553" "GSM1031554" "GSM1031555" "GSM1031564"\$ Group : chr [1:136] "c" "c" "c" "c"@ 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': 12531 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data : 'data.frame': 136 obs. of 0 variables@ 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 ..@ __classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 2 15 0\$: int [1:3] 2 16 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE42057>

Examples

```
data(GSE42057)
```

GSE7305

*Data Set Id: GSE7305***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7305>

Usage

```
data(GSE7305)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE7305"@ lab : chr ""@ contact : chr ""@ title : chr ""@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7305"@ pubMedIds : chr ""@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets : chr "05213"\$ disease : chr "Endometrial cancer"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 2\$: int [1:3] 1 0 0\$: int [1:3] 1 1 0 ..@ assayData :<environment: 0x33e9dc0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] NA NA NA@ data : 'data.frame': 20 obs. of 3 variables:\$ Sample: chr [1:20] "GSM175776" "GSM175777" "GSM175778" "GSM175779"\$ Group : chr [1:20] "c" "c" "c" "c"\$ Block : chr [1:20] "1" "2" "3" "4"@ 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': 54675 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 ..@ annotation : chr "hgu133plus2" ..@ protocolData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 0 obs. of 1 variable:\$ labelDescription: chr(0)@ data : 'data.frame': 20 obs. of 0 variables@ 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 ..@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots@ .Data:List of 4\$: int [1:3] 3 0 0\$: int [1:3] 2 20 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE7305>

Examples

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data(GSE7305)
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