

Package ‘KEGGdzPathwaysGEO’

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Type Package

Title KEGG Disease Datasets from GEO

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Description This is a collection of 24 data sets for which the phenotype is a disease with a corresponding pathway in the KEGG database. This collection of datasets were used as gold standard in comparing gene set analysis methods by the PADOG package.

Depends R (>= 2.13.0)

Imports Biobase, BiocGenerics

License GPL-2

biocViews MicroarrayData, GEO, ExperimentData

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KEGGdzPathwaysGEO-package

GEO Data Sets used to compare gene set analysis methods by PADOG package

Description

This is a collection of 24 data sets for which the phenotype is a disease with a corresponding pathway in the KEGG database. This collection of datasets were used as gold standard in comparing gene set analysis methods by the PADOG package.

GEOID	Pubmed	Ref.	Disease/Target pathway	KEGGID	Tissue
GSE1297	14769913	<i>pmid14769913</i>	Alzheimer's Disease	hsa05010	Hippocampal CA1
GSE5281	17077275	<i>pmid17077275</i>	Alzheimer's Disease	hsa05010	Brain, Entorhinal Cortex
GSE5281	17077275	<i>pmid17077275</i>	Alzheimer's Disease	hsa05010	Brain, hippocampus
GSE5281	17077275	<i>pmid17077275</i>	Alzheimer's Disease	hsa05010	Brain, Primary visual cortex
GSE20153	20926834	<i>pmid20926834</i>	Parkinson's disease	hsa05012	Lymphoblasts
GSE20291	15965975	<i>pmid15965975</i>	Parkinson's disease	hsa05012	Postmortem brain putamen
GSE8762	17724341	<i>pmid17724341</i>	Huntington's disease	hsa05016	Lymphocytes (blood)
GSE4107	17317818	<i>pmid17317818</i>	Colorectal Cancer	hsa05210	Mucosa
GSE8671	18171984	<i>pmid18171984</i>	Colorectal Cancer	hsa05210	Colon
GSE9348	20143136	<i>pmid20143136</i>	Colorectal Cancer	hsa05210	Colon
GSE14762	19252501	<i>pmid19252501</i>	Renal Cancer	hsa05211	Kidney
GSE781	14641932	<i>pmid14641932</i>	Renal Cancer	hsa05211	Kidney
GSE15471	19260470	<i>pmid19260470</i>	Pancreatic Cancer	hsa05212	Pancreas
GSE16515	19732725	<i>pmid19732725</i>	Pancreatic Cancer	hsa05212	Pancreas
GSE19728	-	-	Glioma	hsa05214	Brain
GSE21354	-	-	Glioma	hsa05214	Brain, Spine
GSE6956	18245496	<i>pmid18245496</i>	Prostate Cancer	hsa05215	Prostate
GSE6956	18245496	<i>pmid18245496</i>	Prostate Cancer	hsa05215	Prostate
GSE3467	16365291	<i>pmid16365291</i>	Thyroid Cancer	hsa05216	Thyroid
GSE3678	-	-	Thyroid Cancer	hsa05216	Thyroid
GSE9476	17910043	<i>pmid17910043</i>	Acute myeloid leukemia	hsa05221	Blood, Bone marrow
GSE18842	20878980	<i>pmid20878980</i>	Non-Small Cell Lung Cancer	hsa05223	Lung
GSE19188	20421987	<i>pmid20421987</i>	Non-Small Cell Lung Cancer	hsa05223	Lung

GSE3585 17045896 *pmid17045896* Dilated cardiomyopathy hsa05414 Heart

Details

Package: KEGGdzPathwaysGEO
 Type: Package
 Version: 1.0
 Date: 2012-07-23
 License: GPL-2

Author(s)

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References

Tarca AL, Draghici S, Bhatti G, Romero R (2012) Down-weighting overlapping genes improves gene set analysis. *BMC Bioinformatics* 13:136.

Examples

```
mysets=data(package="KEGGdzPathwaysGEO")$results[, "Item"]
mysets
data(GSE8671)

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

GSE1297

Gene Expression Omnibus (GEO) Data Set Id: GSE1297

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1297>

Usage

```
data(GSE1297)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE1297"@ lab : chr "Landfield"@ contact : chr "emblal@uky.edu"@ title : chr "Incipient Alzheimer's Disease: Microarray Correlation Analyses"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1297"@ pubMedIds : chr "14769913"@ 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:
0x3f9e5268> ..@ phenoData:Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots
.. ..@ varMetadata : 'data.frame': 2 obs. of 1 variable: .. .. .$ labelDescription: chr [1:2] "GEO
Sample ID" "Control/Disease status" .. ..@ data : 'data.frame': 16 obs. of 2 variables: .. .. .$
Sample: chr [1:16] "GSM21215" "GSM21217" "GSM21218" "GSM21219" .. .. .$ Group
: chr [1:16] "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': 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] 2 15 0 .. .. .$ : int [1:3] 2 16 0 .. .. .$ : int [1:3] 1 3 0 .. .. .$ : int [1:3] 1
0 0
```

Details

Samples belonging to the Severe and Control groups are included. The sample, GSM21207, was excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE1297>

Examples

```
data(GSE1297)
```

GSE14762

Gene Expression Omnibus (GEO) Data Set Id: GSE14762

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14762>

Usage

```
data(GSE14762)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE14762"@ lab : chr "Lab of Computational Biology"@ contact : chr "NA"@ title : chr "Renal Cell Carcinoma: Hypoxia and Endocytosis"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14762"@ pubMedIds : chr "19252501"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets: chr "05211"@ disease : chr "Renal 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: 0x3f9eaa60> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:@ ..\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data :'data.frame': 21 obs. of 2 variables:@ ..\$ Sample: chr [1:21] "GSM368649" "GSM368650" "GSM368651" "GSM368652"@ ..\$ 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] 2 15 0@ ..\$: int [1:3] 2 16 0@ ..\$: int [1:3] 1 3 0@ ..\$: int [1:3] 1 0 0

Details

The sample, GSM368647, was excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE14762>

Examples

```
data(GSE14762)
```

GSE15471

Gene Expression Omnibus (GEO) Data Set Id: GSE15471

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15471>

Usage

```
data(GSE15471)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE15471"@ lab : chr "AI and Bioinformatics"@ contact : chr "badea.liviu@gmail.com"@ title : chr "Whole-Tissue Gene Expression Study of Pancreatic Ductal Adenocarcinoma"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15471"@ pubMedIds : chr "19260470"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "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: 0x3f9f19b8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 3 obs. of 1 variable:@ .\$. labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID"@ data :'data.frame': 70 obs. of 3 variables:@ .\$. Sample: chr [1:70] "GSM388076" "GSM388078" "GSM388080" "GSM388082"@ .\$. Group : chr [1:70] "c" "c" "c" "c"@ .\$. Block : chr [1:70] "30162" "40728" "41027" "30057"@ 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': 70 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

Details

Samples, GSM388077, GSM388079, GSM388081, GSM388116, GSM388118, GSM388120 were excluded because they were replicates. Samples, GSM388111 and GSM388150, were excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE15471>

Examples

```
data(GSE15471)
```

GSE16515

*Gene Expression Omnibus (GEO) Data Set Id: GSE16515***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16515>

Usage

```
data(GSE16515)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE16515"@ lab : chr "NA"@ contact : chr "wang.liewei@mayo.edu"@ title : chr "Expression data from Mayo Clinic Pancreatic Tumor and Normal samples"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16515"@ pubMedIds : chr "19732725"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "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: 0x3f9f8150> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:@ ..\$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID"@ data : 'data.frame': 30 obs. of 3 variables:@ ..\$ Sample: chr [1:30] "GSM414928" "GSM414930" "GSM414934" "GSM414938"@ ..\$ Group : chr [1:30] "c" "c" "c" "c"@ ..\$ Block : chr [1:30] "16" "53" "11" "54"@ 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] 2 15 0@ ..\$: int [1:3] 2 16 0@ ..\$: int [1:3] 1 3 0@ ..\$: int [1:3] 1 0 0

Details

Only those samples that consisted of both tumor and normal expression data were included. Samples, GSM414931 and GSM414932, were excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE16515>

Examples

```
data(GSE16515)
```

GSE18842

Gene Expression Omnibus (GEO) Data Set Id: GSE18842

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18842>

Usage

```
data(GSE18842)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE18842"@ lab : chr "NA"@ contact : chr "efarez@ugr.es"@ title : chr "Gene expression analysis of human lung cancer and control samples"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18842"@ pubMedIds : chr "20878980"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Paired"@ targetGeneSets : chr "05223"@ disease : chr "Non Small Cell Lung 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: 0x3f9fe140> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 3 obs. of 1 variable:@ ..\$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID"@ data :'data.frame': 88 obs. of 3 variables:@ ..\$ Sample: chr [1:88] "GSM466948" "GSM466950" "GSM466953" "GSM466955"@ ..\$ Group : chr [1:88] "c" "c" "c" "c"@ ..\$ Block : chr [1:88] "2" "3" "9" "10"@ 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': 88 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

Details

Only those samples were included that were paired.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE18842>

Examples

```
data(GSE18842)
```

GSE19188

*Gene Expression Omnibus (GEO) Data Set Id: GSE19188***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188>

Usage

```
data(GSE19188)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE19188"@ lab : chr "NA"@ contact : chr "j.philipsen@erasmusmc.nl"@ title : chr "Expression data for early stage NSCLC"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188"@ pubMedIds : chr "20421987"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets : chr "05223"@ disease : chr "Non Small Cell Lung 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: 0x3fa048d8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:@ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 153 obs. of 2 variables:@ Sample: chr [1:153] "GSM475657" "GSM475658" "GSM475660" "GSM475663"@ Group : chr [1:153] "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': 153 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

Samples, GSM475659, GSM475666 and GSM475781, were excluded during Quality Control.

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19188>

```
data(GSE19188)
```

GSE19728 *Gene Expression Omnibus (GEO) Data Set Id: GSE19728*

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728>

```
data(GSE19728)
```

```

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "GSE19728" .. ..
..@ lab : chr "NA" .. ..@ contact : chr "yaozhq11@hotmail.com" .. ..@ title : chr "Expression
data from different grades (WHO) of astrocytomas (ACM)" .. ..@ abstract : chr "" .. ..@ url
: chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728" .. ..@ pubMedIds : chr
"NA" .. ..@ samples : list() .. ..@ hybridizations : list() .. ..@ normControls : list() ...
..@ preprocessing : list() .. ..@ other :List of 3 .. .. .$ design : chr "Not Paired" .. .. .$
targetGeneSets : chr "05214" .. .. .$ disease : chr "Glioma" .. ..@ .__classVersion__:Formal
class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 2 .. ..@ .Data:
: int [1:3] 1 0 0 .. ..@ .Data: : int [1:3] 1 1 0 ..@ assayData :<environment: 0x3fa0a8c8>
..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots .. ..@
varMetadata : 'data.frame': 2 obs. of 1 variable: .. ..@ .Data: : int [1:3] 1 1 0 ..@
labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status" .. ..@ data : 'data.frame': 21 obs. of 2 variables: .. ..@
Sample: chr [1:21] "GSM492649" "GSM525014" "GSM525015" "GSM525016" ... ..@ .Data: : int [1:3] 1 1 0 ..@
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 .. ..@ .Data: : int [1:3] 1 1 0 ..@ featureData :Formal class 'AnnotatedDataFrame'
[package "Biobase"] with 4 slots .. ..@ varMetadata : 'data.frame': 0 obs. of 1 variable: ..
..@ .Data: : int [1:3] 1 1 0 ..@ 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 .. ..@ .Data: : 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: ..
..@ .Data: : int [1:3] 1 1 0 ..@ 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 .. ..@ .Data: : int [1:3] 1 1 0 ..@
__classVersion__:Formal class 'Versions' [package "Biobase"] with 1 slots .. ..@ .Data:List of 4
.. ..@ .Data: : int [1:3] 2 15 0 .. ..@ .Data: : int [1:3] 2 16 0 .. ..@ .Data: : int [1:3] 1 3 0 .. ..@ .Data: : int [1:3] 1
0 0

```

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19728>

Examples

```
data(GSE19728)
```

GSE20153

Gene Expression Omnibus (GEO) Data Set Id: GSE20153

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153>

Usage

```
data(GSE20153)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE20153"@ lab : chr "NA"@ contact : chr "middletf@upstate.edu"@ title : chr "Expression analysis of lymphoblast cells lines in Parkinson's disease"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153"@ pubMedIds : chr "20926834"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets: chr "05012"@ disease : chr "Parkinson'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: 0x2cb8a330> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:@ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data :'data.frame': 16 obs. of 2 variables:@ Sample: chr [1:16] "GSM505297" "GSM505298" "GSM505299" "GSM505300"@ Group : chr [1:16] "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': 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] 2 15 0@ .\$. : int [1:3] 2 16 0@ .\$. : int [1:3] 1 3 0@ .\$. : int [1:3] 1 0 0

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20153>

Examples

```
data(GSE20153)
```

GSE20291

Gene Expression Omnibus (GEO) Data Set Id: GSE20291

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20291>

Usage

```
data(GSE20291)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE20291"@ lab : chr "NA"@ contact : chr "middletf@upstate.edu"@ title : chr "Transcriptional analysis of putamen in Parkinson's disease"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20291"@ pubMedIds : chr "15965975"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets : chr "05012"\$ disease : chr "Parkinson'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: 0x2cb9b7d8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 33 obs. of 2 variables:\$ Sample: chr [1:33] "GSM508594" "GSM508683" "GSM508686" "GSM508687"\$ Group : chr [1:33] "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': 33 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

Details

Samples, GSM508611 and GSM606622, were excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE20291>

Examples

```
data(GSE20291)
```

GSE21354

Gene Expression Omnibus (GEO) Data Set Id: GSE21354

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21354>

Usage

```
data(GSE21354)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE21354"@ lab : chr "NA"@ contact : chr "yaozhq11@hotmail.com"@ title : chr "gene expression profiling of three type of grade II gliomas"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21354"@ pubMedIds : chr "NA"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets : chr "05214"\$ disease : chr "Glioma"@ .__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: 0x2cba1008> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 17 obs. of 2 variables:\$ Sample: chr [1:17] "GSM492649" "GSM525014" "GSM525015" "GSM525016"\$ Group : chr [1:17] "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': 17 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

Details

Sample, GSM492652, was excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE21354>

Examples

```
data(GSE21354)
```

GSE3467

Gene Expression Omnibus (GEO) Data Set Id: GSE3467

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467>

Usage

```
data(GSE3467)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE3467"@ lab : chr "Davuluri Lab"@ contact : chr "sandya.liyanarachchi@osumc.edu"@ title : chr "The role of micro-RNA genes in papillary thyroid carcinoma"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467"@ pubMedIds : chr "16365291"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets: chr "05216"\$ disease : chr "Thyroid 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: 0x2cba7f60> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID"@ data : 'data.frame': 18 obs. of 3 variables:\$ Sample: chr [1:18] "GSM77362" "GSM77364" "GSM77366" "GSM77368"\$ Group : chr [1:18] "c" "c" "c" "c"\$ Block : chr [1:18] "14" "26" "50" "69"@ 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': 18 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

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3467>

Examples

```
data(GSE3467)
```

GSE3585

*Gene Expression Omnibus (GEO) Data Set Id: GSE3585***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585>

Usage

```
data(GSE3585)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE3585"@ lab : chr "Unit Cancer Genome Research"@ contact : chr "r.kuner@dkfz.de"@ title : chr "Dilated Cardiomyopathy and Non Failing Biopsies"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585"@ pubMedIds : chr "17045896"@ 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: 0x2cbaeeb8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 12 obs. of 2 variables:\$ Sample: chr [1:12] "GSM82381" "GSM82382" "GSM82383" "GSM82384"\$ 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': 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': 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] 2 15 0\$: int [1:3] 2 16 0\$: int [1:3] 1 3 0\$: int [1:3] 1 0 0

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3585>

Examples

```
data(GSE3585)
```

GSE3678

Gene Expression Omnibus (GEO) Data Set Id: GSE3678

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678>

Usage

```
data(GSE3678)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experiment-Data :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE3678"@ lab : chr "NA"@ contact : chr "ismael_reyes@nymc.edu"@ title : chr "PTC versus paired normal thyroid tissue"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678"@ pubMedIds : chr "NA"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Paired"\$ targetGeneSets: chr "05216"\$ disease : chr "Thyroid 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: 0x2cbb46e8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID"@ data :'data.frame': 14 obs. of 3 variables:\$ Sample: chr [1:14] "GSM85215" "GSM85216" "GSM85217" "GSM85218"\$ Group : chr [1:14] "c" "c" "c" "c"\$ Block : chr [1:14] "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': 14 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

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE3678>

Examples

```
data(GSE3678)
```

GSE4107

*Gene Expression Omnibus (GEO) Data Set Id: GSE4107***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107>

Usage

```
data(GSE4107)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE4107"@ lab : chr "CRC research lab"@ contact : chr "hong.yi@sgh.com.sg;fbap8570@yahoo.com"@ title : chr "Expression profiling in early onset colorectal cancer"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107"@ pubMedIds : chr "17317818"@ 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: 0x41550490> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data :'data.frame': 22 obs. of 2 variables:\$ Sample: chr [1:22] "GSM93938" "GSM93939" "GSM93941" "GSM93943"\$ Group : chr [1:22] "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': 22 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

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE4107>

Examples

```
data(GSE4107)
```

GSE5281_EC	<i>Gene Expression Omnibus (GEO) Data Set Id: GSE5281. GSE5281_EC contains data for Entorhinal cortex samples from the data set GSE5281.</i>
------------	--

Description

GSE5281_EC contains data for Entorhinal cortex samples from the data set GSE5281. For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281>

Usage

```
data(GSE5281_EC)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE5281_EC"@ lab : chr "NIH Neuroscience Microarray Consortium"@ contact : chr "bhamill@mednet.ucla.edu"@ title : chr "Alzheimer's disease and the normal aged brain (steph-affy-human-433773)"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281"@ pubMedIds : chr "17077275"@ 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: 0x415573e8> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data :'data.frame': 21 obs. of 2 variables:\$ Sample: chr [1:21] "GSM119615" "GSM119616" "GSM119617" "GSM119618"\$ 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] 2 15 0 .. ..@ .$. : int [1:3] 2 16 0 .. ..@ .$. : int [1:3] 1 3 0 .. ..@ .$. : int [1:3] 1
0 0
```

Details

GSE5281_EC contains data for Entorhinal cortex samples from the data set GSE5281. The samples, GSM119626 and GSM238763, were excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281>

Examples

```
data(GSE5281_EC)
```

GSE5281_HIP	<i>Gene Expression Omnibus (GEO) Data Set Id: GSE5281.GSE5281_HIP contains data for hippocampus samples from the data set GSE5281.</i>
-------------	--

Description

GSE5281_HIP contains data for hippocampus samples from the data set GSE5281. For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281>

Usage

```
data(GSE5281_HIP)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE5281_HIP"@ lab : chr "NIH Neuroscience Microarray Consortium"@ contact : chr "bhamill@mednet.ucla.edu"@ title : chr "Alzheimer's disease and the normal aged brain (steph-affy-human-433773)"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281"@ pubMedIds : chr "17077275"@ 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: 0x4155cc18> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata :'data.frame': 2 obs. of 1 variable:@ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data :'data.frame': 23 obs. of 2 variables:@ .\$. Sample: chr [1:23] "GSM119628" "GSM119629" "GSM119630" "GSM119631"@ .\$. Group : chr [1:23] "c" "c" "c" "c"@ dimLabels : chr [1:2] "sampleNames" "sampleColumns"@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1

```
The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "GSE5281_VCX" ..
.. ..@ lab : chr "NIH Neuroscience Microarray Consortium" .. ..@ contact : chr "bhamill@mednet.ucla.edu"
.. ..@ title : chr "Alzheimer's disease and the normal aged brain (steph-affy-human-433773)" .. ..
..@ abstract : chr "" .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281"
.. ..@ pubMedIds : chr "17077275" .. ..@ 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: 0x2cbb3168> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"]
with 4 slots .. .. .@ varMetadata :'data.frame': 2 obs. of 1 variable: .. .. .$. labelDescription:
chr [1:2] "GEO Sample ID" "Control/Disease status" .. .. .@ data :'data.frame': 31 obs. of 2 vari-
ables: .. .. .$. Sample: chr [1:31] "GSM119677" "GSM119678" "GSM119679" "GSM119680"
... .. .$. Group : chr [1:31] "c" "c" "c" "c" ... .. .@ dimLabels : chr [1:2] "sampleNames"
"sampleColumns" .. .. .@ .__classVersion__:Formal class 'Versions' [package "Biobase"] with 1
slots .. .. .@ .Data:List of 1 .. .. .$. : int [1:3] 1 1 0 ..@ featureData :Formal class 'Anno-
tatedDataFrame' [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: .. ..
..$. labelDescription: chr(0) .. .. .@ data :'data.frame': 31 obs. of 0 variables .. .. .@ dimLabels
: chr [1:2] "sampleNames" "sampleColumns" .. .. .@ .__classVersion__:Formal class 'Versions'
[package "Biobase"] with 1 slots .. .. .@ .Data:List of 1 .. .. .$. : 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
```

Details

GSE5281_VCX contains data for Visual Cortex samples from the data set GSE5281.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE5281>

Examples

```
data(GSE5281_VCX)
```

GSE6956AA

*Gene Expression Omnibus (GEO) Data Set Id: GSE6956.
GSE6956AA contains data for African-American Men from the data
set GSE6956*

Description

GSE6956AA contains data for African-American Men from the data set GSE6956. For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6956>

Usage

```
data(GSE6956AA)
```

```

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData
:Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "GSE6956AA" ..
.. ..@ lab : chr "The Laboratory of Human Carcinogenesis" .. ..@ contact : chr "NA" .. ..@
title : chr "Tumor Immunobiological Differences in Prostate Cancer between African-American and
European-American Men" .. ..@ abstract : chr "" .. ..@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=
.. ..@ PubMedIds : chr "18245496" .. ..@ samples : list() .. ..@ hybridizations : list() ..
.. ..@ normControls : list() .. ..@ preprocessing : list() .. ..@ other :List of 3 .. .. ..$
design : chr "Paired" .. .. ..$ targetGeneSets: chr "05215" .. .. ..$ disease : chr "Prostate
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: 0x2cb95870> .. ..@ phenoData :Formal class 'AnnotatedDataFrame'
[package "Biobase"] with 4 slots .. .. ..@ varMetadata : 'data.frame': 3 obs. of 1 variable: .. ..
..$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID" .. .. ..@ data
: 'data.frame': 10 obs. of 3 variables: .. .. ..$ Sample: chr [1:10] "GSM160404" "GSM160424"
"GSM160427" "GSM160428" ... .. ..$ Group : chr [1:10] "c" "c" "c" "c" ... .. ..$ Block :
chr [1:10] "65" "51" "16" "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': 22277 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': 10 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

```

GSE6956AA contains data for African-American Men from the data set GSE6956.

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE6956>

```
data(GSE6956AA)
```

GSE6956C *Gene Expression Omnibus (GEO) Data Set Id: GSE6956. GSE6956C contains data for European-American Men from the data set GSE6956.*

GSE781

*Gene Expression Omnibus (GEO) Data Set Id: GSE781***Description**

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE781>

Usage

```
data(GSE781)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experiment-Data :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE781"@ lab : chr "NA"@ contact : chr "mlenburg@bu.edu"@ title : chr "Normal and Renal Cell Carcinoma Kidney Tissue, Human"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE781"@ pubMedIds : chr "14641932"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3@ design : chr "Not Paired"@ targetGeneSets : chr "05211"@ disease : chr "Renal 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: 0x2a6cbd18> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:@ \$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 17 obs. of 2 variables:@ \$ Sample: chr [1:17] "GSM11805" "GSM11823" "GSM12075" "GSM12098"@ \$ Group : chr [1:17] "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': 17 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

Details

Samples run on the chip, hgu133a, are included.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE781>

Examples

```
data(GSE781)
```

GSE8671

Gene Expression Omnibus (GEO) Data Set Id: GSE8671

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671>

Usage

```
data(GSE8671)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experiment-Data :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE8671"@ lab : chr "NA"@ contact : chr "marra@imcr.uzh.ch"@ title : chr "Transcriptome profile of human colorectal adenomas."@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671"@ pubMedIds : chr "18171984"@ 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: 0x383c9608> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 3 obs. of 1 variable:\$ labelDescription: chr [1:3] "GEO Sample ID" "Control/Disease status" "Pair ID"@ data : 'data.frame': 64 obs. of 3 variables:\$ Sample: chr [1:64] "GSM215051" "GSM215052" "GSM215053" "GSM215054"\$ Group : chr [1:64] "c" "c" "c" "c"\$ Block : chr [1:64] "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': 64 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

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8671>

Examples

```
data(GSE8671)
```

GSE8762

Gene Expression Omnibus (GEO) Data Set Id: GSE8762

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762>

Usage

```
data(GSE8762)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE8762"@ lab : chr "Laboratory of Neurogenetics"@ contact : chr "kuhnam@mail.nih.gov"@ title : chr "Lymphocyte gene expression data from moderate stage HD patients and controls"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762"@ pubMedIds : chr "17724341"@ samples : list()@ hybridizations : list()@ normControls : list()@ preprocessing : list()@ other :List of 3\$ design : chr "Not Paired"\$ targetGeneSets : chr "05016"\$ disease : chr "Huntington'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: 0x7e09e1f0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 22 obs. of 2 variables:\$ Sample: chr [1:22] "GSM217766" "GSM217767" "GSM217768" "GSM217769"\$ Group : chr [1:22] "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': 22 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

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE8762>

Examples

```
data(GSE8762)
```

GSE9348

Gene Expression Omnibus (GEO) Data Set Id: GSE9348

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348>

Usage

```
data(GSE9348)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE9348"@ lab : chr "CRC research lab"@ contact : chr "hong.yi@sgh.com.sg;fbap8570@yahoo.com"@ title : chr "Expression data from healthy controls and early stage CRC patient's tumor"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348"@ pubMedIds : chr "20143136"@ 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: 0x6239b018> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 82 obs. of 2 variables:\$ Sample: chr [1:82] "GSM237984" "GSM237985" "GSM237986" "GSM237987"\$ Group : chr [1:82] "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': 82 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

Details

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348>

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9348>

Examples

```
data(GSE9348)
```

GSE9476

Gene Expression Omnibus (GEO) Data Set Id: GSE9476

Description

For detailed description visit: <http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9476>

Usage

```
data(GSE9476)
```

Format

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experiment-Data :Formal class 'MIAME' [package "Biobase"] with 13 slots@ name : chr "GSE9476"@ lab : chr "Stirewalt Lab"@ contact : chr "dstirewa@fhcrc.org"@ title : chr "Abnormal Expression Changes in AML"@ abstract : chr ""@ url : chr "http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9476"@ pubMedIds : chr "17910043"@ 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: 0x6a5d4cd0> ..@ phenoData :Formal class 'AnnotatedDataFrame' [package "Biobase"] with 4 slots@ varMetadata : 'data.frame': 2 obs. of 1 variable:\$ labelDescription: chr [1:2] "GEO Sample ID" "Control/Disease status"@ data : 'data.frame': 63 obs. of 2 variables:\$ Sample: chr [1:63] "GSM239170" "GSM239323" "GSM239324" "GSM239326"\$ Group : chr [1:63] "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': 63 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

Details

The sample, GSM240433, was excluded during Quality Control.

Source

<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE9476>

Examples

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data(GSE9476)
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