

# 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

**git\_url** <https://git.bioconductor.org/packages/KEGGdzPathwaysGEO>

**git\_branch** devel

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KEGGdzPathwaysGEO-package

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

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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.

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	<i>pmid17045896</i>	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

**Details**

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

**Source**

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

**Examples**

```
data(GSE19188)
```

GSE19728

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

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

**Usage**

```
data(GSE19728)
```

**Format**

```
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 .. .. .. ..$
: int [1:3] 1 0 0 .. .. .. ..$ : 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: .. .. ..$ 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" ... .. .. ..$ 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**

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



```
'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



```
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 ..@ experimentData :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 :<envi-
ronment: 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 vari-
ables: ... ..$ 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
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': 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] 2 15 0 ... ..$ : int [1:3] 2 16 0 ... ..$ : int [1:3] 1 3 0 ... ..$ : int [1:3] 1
0 0

```

### Details

GSE5281\_HIP contains data for hippocampus samples from the data set GSE5281.

### Source

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

### Examples

```
data(GSE5281_HIP)
```

---

GSE5281\_VCX

*Gene Expression Omnibus (GEO) Data Set Id: GSE5281.  
GSE5281\_VCX contains data for Visual Cortex samples from the data  
set GSE5281.*

---

### Description

GSE5281\_VCX contains data for Visual 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_VCX)
```

**Format**

```
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 :<envi-
ronment: 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)
```

## Format

```
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=GS
.. ..@ 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
```



**Details**

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

**Source**

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

**Examples**

```
data(GSE6956AA)
```

---

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

---

**Description**

GSE6956C contains data for European-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(GSE6956C)
```

**Format**

The format is: Formal class 'ExpressionSet' [package "Biobase"] with 7 slots ..@ experimentData :Formal class 'MIAME' [package "Biobase"] with 13 slots .. ..@ name : chr "GSE6956C" .. ..@ 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=GSE6956" .. ..@ 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: 0x3f9f5cd8> ..@ 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': 16 obs. of 3 variables: .. .. ..@\$ Sample: chr [1:16] "GSM160402" "GSM160407" "GSM160409" "GSM160411" ... .. ..@\$ Group : chr [1:16] "c" "c" "c" "c" ... .. ..@\$ Block : chr [1:16] "63" "68" "70" "72" ... .. ..@ 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"



```
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 .. .\$@ experimentData :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] "feature-
Names" "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**

```
data(GSE9476)
```



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