

# Package ‘psygenet2r’

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**Title** psygenet2r - An R package for querying PsyGeNET and to perform comorbidity studies in psychiatric disorders

**Version** 1.22.5

**Description** Package to retrieve data from PsyGeNET database ([www.psygenet.org](http://www.psygenet.org)) and to perform comorbidity studies with PsyGeNET's and user's data.

**Depends** R (>= 3.4)

**License** MIT + file LICENSE

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DataGeNET.Psy-class    *Class DataGeNET.Psy*

---

## Description

Class DataGeNET.Psy is the basic object use in psygenet2r package. It is the main data container to using the different functions to query PsyGeNET database and generate their output. The constructors of this class are the functions psygenetGene and psygenetDisease.

## Slots

type Character containing 'gene' of 'disease'. It is used to perform the correct query to PsyGeNET.

search Character containing 'single' of 'list'. It is used to perform the correct query to PsyGeNET.

database Character containing the name of the database that will be queried. It can take the values 'MODELS' to use Comparative Toxigenomics Database, data from mouse and rat; 'GAD' to use Genetic Association Database; 'CTD' to use Comparative Toxigenomics Database, data from human; 'PsyCUR' to use Psychiatric disorders Gene association manually curated; 'CURATED' to use Human, manually curated databases (PsyCUR and CTD); or 'ALL' to use all these databases.

term Character with the term(s) to search into the database(s).

result data.frame with the obtained result

## See Also

psygenetGene, psygenetDisease, DataGeNET.Psy-methods

---

|            |   |
|------------|---|
| enrichedPD | <i>Enrichment of a user's input (genes) in PsyGeNET's diseases.</i> |
|------------|---|

---

**Description**

Test the enrichment of a given gene list on Psychiatric Disorders from PsyGeNET.

**Usage**

```
enrichedPD(gene, database = "ALL", verbose = FALSE, warnings = FALSE)
```

**Arguments**

|          |   |
|----------|---|
| gene     | Name or vector of names (that can be both code or uml) to specific genes from PsyGeNET.   |
| database | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |
| verbose  | By default FALSE. Change it to TRUE to get a on-time log from the function.   |
| warnings | By default TRUE. Change it to FALSE to not see the warnings.  |

**Value**

A data.frame with the enrichment at each Psychiatric Disorder

**Examples**

```
enrichedPD(c("ADCY2", "AKAP13", "ANK3"), "ALL")
```

---

|         |   |
|---------|---|
| extract | <i>Raw data from DataGeNET.Psy and JaccardIndexPsy.</i> |
|---------|---|

---

**Description**

Obtain the raw data from a PsyGeNET's query stored in a DataGeNET.Psy object or the raw data with all the Jaccard Index for the disease of interest of an JaccardIndexPsy object.

**Usage**

```
extract(object, ...)

## S4 method for signature 'DataGeNET.Psy'
extract(object)

## S4 method for signature 'JaccardIndexPsy'
extract(object, order.cl = "pval", ...)
```

**Arguments**

|          |  |
|----------|--|
| object   | Object of class DataGeNET.Psy or JaccardIndexPsy       |
| ...      | NO USED  |
| order.cl | Order resulting data.frame by the name of this column. |

**Value**

A data.frame containing the raw result from PsyGeNET or a data.frame with the result Jaccard Index for each disease.

A data.frame containing the raw result from PsyGeNET

A data.frame with the result Jaccard Index for each disease.

**Functions**

- extract,DataGeNET.Psy-method: Extract function for DataGeNET.Psy
- extract,JaccardIndexPsy-method: Extract function for JaccardIndexPsy

**Examples**

```
data(qr)
extract(qr)[1:2, ] # get internat data.frame
## Not run:
#Being x an JaccardIndexPsy
extract(x)

## End(Not run)
```

---

|                  |  |
|------------------|--|
| extractSentences | <i>Method to obtain the sentences that support a gene-disease association from a DataGeNET.Psy object.</i> |
|------------------|--|

---

**Description**

PsyGeNET contains a list of sentences that support a gene-disease association from public literature. The internal table of a DataGeNET.Psy object contains this information. The method extractSentences allows to extract those sentences that support a gene-disease association given a DataGeNET.Psy object and a disorder of interest.

**Usage**

```
extractSentences(object, disorder, verbose)

## S4 method for signature 'DataGeNET.Psy'
extractSentences(object, disorder, verbose = FALSE)
```

**Arguments**

|          |  |
|----------|--|
| object   | Object of class DataGeNET.Psy.   |
| disorder | The disorder of interest. Only those sentences supporting a gene-disease association with this specific disorder will be extracted. Disorder must be provided by using "Disease Id" or "Disease Name". The "Disease Id" can be provided with or without the "uml" tag. Example of a "Disease Name": "schizophrenia"; Example of a "Disease Id": "umls:C0036341", that is equivalent of using "C0036341". |
| verbose  | If set to TRUE informative messages are show.  |

**Value**

A data frame showing the sentences.

**Functions**

- extractSentences, DataGeNET.Psy-method: Get sentences or evidences

**Examples**

```
data(qr)
extractSentences(qr, "Depression")
```

---

geneAttrPlot

*Ploting the relation between genes and disease-categories*

---

**Description**

Given a set of genes or a result of psygenetGene creates four types of plots showing the relation of the genes with the disease's category in psyGeNET.

**Usage**

```
geneAttrPlot(x, type = "pie", ..., verbose = FALSE)
```

**Arguments**

|         |   |
|---------|---|
| x       | Vector of genes of interest of DataGeNET.Psy resulting of psyegnetDisease.  |
| type    | Type of the drawn chart. By default it is "pie". It can takes "pie" to plot a pie chart with the number of genes for each psychiatric category, "disease category" for visualizing a barplot with the total and specific number of genes for each psychiatric disorder, "evidence index" for a barplot showing for each psychiatric disorder the number of gene-disease associations according to the Evidence index and "gene" for visualizing a barplot with the total and specific number of diseases associated to each gene. |
| ...     | (Check NOTE section) Passed to inner functions for different plots.   |
| verbose | By default FALSE. Change it to TRUE to get a on-time log from the function.   |

**Value**

A plot for a DataGeNET.Psy in terms of the panther-class.

**Note**

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, please visit [psygenet.org](http://psygenet.org). Argument ... can be filled with specific argument depending on the type of plot:

| Type             | Argument                | Color  | Description   |
|------------------|-------------------------|--------|---|
| gene             | cuiBarColor             | Purple | Determines the color of the bar for diseases                            |
| disease category | diseaseCategoryBarColor | Yellow | Determines the color of the bar for psychiatric categories              |
|                  | uniqueGenesBarColor     | Orange | Determines the color of the bar for unique genes for a disease category |
|                  | totalGenesBarColor      | Blue   | Determines the color of the bar for total genes for a disease category  |

---

 getUMLs

*Query PsyGeNET for given gene(s) and generates an DataGeNET.Psy*


---

**Description**

Given the name of one or multiple gene and retrieves their information from PsyGeNET and creates an object of type DataGeNET.Psy.

**Usage**

```
getUMLs(word, database = "ALL")
```

**Arguments**

|          |   |
|----------|---|
| word     | Disese to convert to UMLS using PsyGeNET database.  |
| database | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |

**Value**

The corresponding UMLs for the input disease/s

**Examples**

```
umls <- getUMLs( word = "depressive", database = "ALL" )
```

---

jaccardEstimation      *Calculation of the Jaccard Index between ideseases*

---

## Description

This function is able to calculate the Jacard Index between: 1. muliple disases, 2. a set og genes and multiple diseases, 3. a set of genes and multiple main psychiatric disorders and 4. multiple diseases and multiple main psychiatric disorders.

## Usage

```
jaccardEstimation(  
  pDisease,  
  sDisease,  
  database = "ALL",  
  nboot = 100,  
  ncores = 1,  
  verbose = FALSE  
)
```

## Arguments

|          |  |
|----------|--|
| pDisease | vector of diseases, vector of genes, vector of main psychiatric disorder.  |
| sDisease | vector of diseases, vector of genes, vector of main psychiatric disorder. Only necessary when comparing genes vs. diseases, genes vs. main psychiatric disorders or diseases vs. main psychiatric disorders. To compare multiple diseases only use pDisease. |
| database | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases.     |
| nboot    | Number of iterations sued to compute the pvalue associted to the calculated Jaccard Index (default 100).   |
| ncores   | Number of cores used to calculate the pvalue associated to the computed Jaccard Index (default 1).   |
| verbose  | By default FALSE. Change it to TRUE to get a on-time log from the function.  |

## Details

Warning: The main psychiatric disorders are understood as a single set of genes composed by the genes of all the diseases that the main psychiatric disorder cotains.

## Value

An object of class JaccardIndexPsy with the computed calculation of the JaccardIndex.

## Examples

```
ji <- jaccardEstimation( c( "COMT", "CLOCK", "DRD3" ), "umls:C0005586", "ALL" )
```

---

JaccardIndexPsy-class *Class JaccardIndexPsy*

---

### Description

Class JaccardIndexPsy is the result of the process to look for a Jaccard Index between multiple diseases in psygenet2r package.

### Slots

nit Number of iterations to calculate the estimated Jaccard index  
 type Slot to save type of query (disease-disease, gene-disease)  
 table data.frame containing the result table of Jaccard indexes  
 i1 [internal use] vector with names of first component  
 i2 [internal use] vector with names of second component

### See Also

psygenetGene, psygenetDisease, JaccardIndexPsy-methods

### Examples

```
ji <- jaccardEstimation( c( "COMT", "CLOCK", "DRD3" ), "umls:C0005586", "ALL" )
```

---

ndisease *Getter from DataGeNET.Psy.*

---

### Description

Obtain the number of unique diseases in a DataGeNET.Psy.

### Usage

```
ndisease(object)

## S4 method for signature 'DataGeNET.Psy'
ndisease(object)
```

### Arguments

object Object of class DataGeNET.Psy.

### Value

The number of unique diseases

### Functions

- ndisease, DataGeNET.Psy-method: Get number of diseases

**Examples**

```
data(qr)
ndisease(qr)
```

---

|       |                                   |
|-------|-----------------------------------|
| ngene | <i>Getter from DataGeNET.Psy.</i> |
|-------|-----------------------------------|

---

**Description**

Obtain the number of unique genes in a DataGeNET.Psy.

**Usage**

```
ngene(object)

## S4 method for signature 'DataGeNET.Psy'
ngene(object)
```

**Arguments**

object            Object of class DataGeNET.Psy.

**Value**

The number of unique genes  
The number of unique genes

**Functions**

- ngene, DataGeNET.Psy-method: Get number of genes

**Examples**

```
data(qr)
ngene(qr)
```

---

|                |   |
|----------------|---|
| pantherGraphic | <i>Query PsyGeNET for given genes and creates a representation in base of their panther-class</i> |
|----------------|---|

---

**Description**

Given a vector of genes of interest (or using a DataGeNET.Psy object), this function creates a representation of a the panther-class these genes belongs to.

**Usage**

```
pantherGraphic(x, database = "ALL", evidenceIndex, verbose = FALSE)
```

**Arguments**

|               |   |
|---------------|---|
| x             | Vector of genes of interest of DataGeNET.Psy resulting of psyegnetDisease.  |
| database      | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |
| evidenceIndex | threshold to take into account a gene in the analysis   |
| verbose       | By default FALSE. Change it to TRUE to get a on-time log from the function.   |

**Value**

A plot for a DataGeNET.Psy in terms of the panther-class.

**Examples**

```
d.alch <- pantherGraphic( c( "COMT", "CLOCK", "DRD3" ), "ALL" )
```

---

plot,DataGeNET.Psy,ANY-method

*Plots the content of a DataGeNET.Psy object*

---

**Description**

This functions llows to create a variety of plots for DataGeNET.Psy and JaccardIndexPsy objects.

**Usage**

```
## S4 method for signature 'DataGeNET.Psy,ANY'
plot(
  x,
  y,
  layout = igraph::layout.fruchterman.reingold,
  type = "GDA network",
  verbose = FALSE,
  ...
)
```

**Arguments**

|         |   |
|---------|---|
| x       | Object of class DataGeNET.Psy   |
| y       | NOT USED  |
| layout  | Function to design the location of the different nodes. By default layout.fruchterman.reingold from igraph is used.   |
| type    | Type of the drawn chart. By default it is "GDA network" but it also can be "GDCA network", "GDCA heatmap", "GDA heatmap" and "publications". The first two are network representations of the second two. While the last one draws a barplot with the number of PMIDs between genes and diseases. |
| verbose | By default FALSE. If set to TRUE information on the drawing process will be shown.  |
| ...     | (Check NOTE section) Passed to inner functions for different plots.   |

**Value**

A plot for DataGeNET.Psy.

**Note**

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, please visit [psygenet.org](http://psygenet.org). Argument ... can be filled with specific argument depending on the type of plot:

| Type         | Argument        | Color   | Description  |
|--------------|-----------------|---------|--|
| GDA network  | geneColor       | Yellow  | Determines the color of the gene nodes   |
|              | diseaseColor    | Blue    | Determines the color of the disease nodes                                      |
| GDA heatmap  | highColor       | Blue    | Determines the color of the heatmap for the highest value                      |
|              | lowColor        | White   | Determines the color of the heatmap for the lowest value                       |
| GDCA network | ei0color        | Yellow  | Determines the color for those associations with evidence index 0              |
|              | eiAmbiguitcolor | Grey    | Determines the color for those associations with evidence index greater than 0 |
|              | ei1color        | Blue    | Determines the color for those associations with evidence index 1              |
| GDCA heatmap | AUDcolor        | #FF3C32 |  |
|              | BDcolor         | #FFC698 |  |
|              | DEPcolor        | #9BE75E |  |
|              | SCHZcolor       | #1F6024 |  |
|              | CUDcolor        | #5AB69C |  |
|              | SIDEPcolor      | #50B8D6 |  |
|              | CanUDcolor      | #5467C3 |  |
|              | SYPSYcolor      | #A654C3 |  |
|              | geneColor       | Orange  |  |

**Examples**

```
data(qr)
plot(qr) # for all-disease plot
plot(qr, type = 'GDCA network') # for MPI plot
```

---

plot,JaccardIndexPsy,ANY-method

*Plot the content of a JaccardIndexPsy object.*

---

**Description**

This functions llows to create a variety of plots for DataGeNET.Psy and JaccardIndexPsy objects.

**Usage**

```
## S4 method for signature 'JaccardIndexPsy,ANY'
plot(
  x,
  y,
  cutOff,
  zero.remove = TRUE,
  noTitle = FALSE,
  lowColor = "white",
```

```

    highColor = "mediumorchid4",
    verbose = FALSE,
    ...
)

```

### Arguments

|             |  |
|-------------|--|
| x           | Object of class JaccardIndexPsy.   |
| y           | NOT USED   |
| cutOff      | Number to filter the shown results.  |
| zero.remove | By default TRUE. It removes those relations with a Jaccard Index of 0.             |
| noTitle     | By default FALSE. If set to true no title will be added to the plot.               |
| lowColor    | By default "white". It can be changed to any other color.                          |
| highColor   | By default "mediumorchid4". It can be changed to any other color.                  |
| verbose     | By default FALSE. If set to TRUE information on the drawing process will be shown. |
| ...         | NOT USED   |

### Value

A plot for JaccardIndexPsy.

### Examples

```

## Not run:
#Being x an JaccardIndexPsy
qr <- plot(x)

## End(Not run)

```

---

psygenet2r

*psygenet2r: Package to query PsyGeNET database and to perform comorbidity studies*

---

### Description

psygenet2r has two categories of functions: querying functions and analysis and plotting functions.

#### querying functions

The functions to retrieve data from PsyGeNET are [psygenetDisease](#) and [psygenetGene](#). There are some other support functions like [psygenetGeneSentences](#).

#### analysis and plotting functions

The functions [extract](#) and [extractSentences](#) allows to retrieve the row data obtained from on-line resources. The functions [plot](#) and [pantherGraphic](#) draws a variety of charts to illustrate the obtained results. The function [enrichedPD](#) was built to perform enrichment studies on PsyGeNET data. Finally the function [jaccardEstimation](#) computes a Jaccard Index from a given input on PsyGeNET data.

---

|                 |   |
|-----------------|---|
| psygenetDisease | <i>Query PsyGeNET for given disease(s) and generates an DataGeNET.Psy</i> |
|-----------------|---|

---

### Description

Given the name of one or multiple diseases and retrieves their information from PsyGeNET and creates an object of type DataGeNET.Psy.

### Usage

```
psygenetDisease(
  disease,
  database = "ALL",
  evidenceIndex = c(">", 0),
  verbose = FALSE,
  warnings = TRUE
)
```

### Arguments

|               |   |
|---------------|---|
| disease       | Name or vector of names (that can be both code or uml) to specific diseases from PsyGeNET. The diseases non existing in PsyGeNET will be removed from the output.   |
| database      | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |
| evidenceIndex | A vector with two elements: 1) character with greather '>' or with lower '<' meaing greather or equal and lower or equal; 2) the evidence index cut-off to be compared. By default: c('>', 0).  |
| verbose       | By default FALSE. Change it to TRUE to get a on-time log from the function.   |
| warnings      | By default TRUE. Change it to FALSE to don't see the warnings.  |

### Value

An object of class DataGeNET.Psy

### Note

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, please visit [psygenet.org](http://psygenet.org).

### Examples

```
d.sch <- psygenetDisease( "schizophrenia", "ALL" )
```

---

psygenetDiseaseSentences

*Query PsyGeNET for given disease(s) and extract the pmids sentences that report a gene-disease association.*

---

### Description

Given a disease or a disease list, retrieves the pmids and sentences for each gene-disease association from PsyGeNET and creates an object of type DataGeNET.Psy.

### Usage

```
psygenetDiseaseSentences(diseaseList, database = "ALL", verbose = FALSE)
```

### Arguments

|             |   |
|-------------|---|
| diseaseList | Name or vector of names (that can be both code or uml) to specific diseases from PsyGeNET. The diseases non existing in PsyGeNET will be removed from the output.   |
| database    | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |
| verbose     | By default FALSE. Change it to TRUE to get a on-time log from the function.   |

### Value

An object of class DataGeNET.Psy

### Examples

```
diseasesOfInterest <- c( "Bipolar Disorder", "Depressive Disorder, Major" )
psyDisSen <- psygenetDiseaseSentences( diseaseList = diseasesOfInterest,
                                       database = "ALL" )
```

---

psygenetGene

*Query PsyGeNET for given gene(s) and generates an DataGeNET.Psy*

---

### Description

Given the name of one or multiple gene and retrieves their information from PsyGeNET and creates an object of type DataGeNET.Psy.

### Usage

```
psygenetGene(
  gene,
  database = "ALL",
  evidenceIndex = c(">", 0),
  verbose = FALSE,
  warnings = TRUE
)
```

**Arguments**

|               |   |
|---------------|---|
| gene          | Name or vector of names (that can be both code or symbol) to specific genes from PsyGeNET. The genes non existing in PsyGeNET will be removed from the output.  |
| database      | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |
| evidenceIndex | A vector with two elements: 1) character with greather '>' or with lower '<' meaing greather or equal and lower or equal; 2) the evidence index cut-off to be compared. By default: c('>', 0).  |
| verbose       | By default FALSE. Change it to TRUE to get a on-time log from the function.   |
| warnings      | By default TRUE. Change it to FALSE to not see the warnings.  |

**Value**

An object of class `DataGeNET.Psy`

**Note**

The "Evidence Index" is gotten from PsyGeNET. For more information about it and its calculation, please visit [psygenet.org](http://psygenet.org).

**Examples**

```
d.alch <- psygenetGene( "ALDH2", "ALL" )
```

---

`psygenetGeneSentences` *Query PsyGeNET for given gene(s) and extract the pmids sentences that report a gene-disease association.*

---

**Description**

Given a gene or a gene list, retrieves the pmids and sentences for each gene-disease association from PsyGeNET and creates an object of type `DataGeNET.Psy`.

**Usage**

```
psygenetGeneSentences(geneList, database = "ALL", verbose = FALSE)
```

**Arguments**

|          |   |
|----------|---|
| geneList | Name or vector of names (that can be both code or symbol) to specific genes from PsyGeNET. The genes non existing in PsyGeNET will be removed from the output.  |
| database | Name of the database that will be queried. It can take the values 'psycur15' to use data validated by experts for first release of PsyGeNET; 'psycur16' to use data validated by experts for second release of PsyGeNET; or 'ALL' to use both databases. Default 'ALL'. |
| verbose  | By default FALSE. Change it to TRUE to get a on-time log from the function.   |

**Value**

An object of class `DataGeNET.Psy`

**Examples**

```
genesOfInterest <- c("PECR", "ADH1C", "CAST", "ERAP1", "PPP2R2B",  
                    "ESR1", "GATA4", "CDH13")  
psyGeneSen <- psygenetGeneSentences( geneList = genesOfInterest,  
                                     database = "ALL")
```

---

qr

*DataGeNET.Psy obtained from querying PsyGeNET for gene '4852'.*

---

**Description**

A dataset obtained from PsyGeNET after being queried with `psygenetGene` using the term '4852' on "ALL" database.

**Usage**

```
data("qr")
```

**Format**

The format is: Formal class 'DataGeNET.Psy' [package "psygenet2r"] with 5 slots .. type : chr "gene" .. search : chr "" .. database: chr "ALL" .. term : chr "4852" .. qresult : 'data.frame'

**Value**

A `DataGeNET.Psy` object.

**Source**

<http://psygenet.org>

**Examples**

```
ngene(qr)  
ndisease(qr)
```

---

|                   |  |
|-------------------|--|
| topAnatEnrichment | <i>Enrichment of a user's input (genes) in anatomical terms (TopAnat).</i> |
|-------------------|--|

---

## Description

Test the enrichment of a given gene list on Psychiatric Disorders from PsyGeNET.

## Usage

```
topAnatEnrichment(  
  gene,  
  datatype = c("rna_seq", "affymetrix", "est", "in_situ"),  
  statistic = "fisher",  
  cutOff = 1,  
  verbose = FALSE,  
  warnings = FALSE  
)
```

## Arguments

|           |   |
|-----------|---|
| gene      | Name or vector of names (that can be both code or uml) to specific genes from PsyGeNET.   |
| datatype  | It can take the values 'rna_seq', 'affymetrix', "est" or "in situ". Default c("rna_seq", "affymetrix", "est", "in_situ").           |
| statistic | By default it is "fisher". But it can be changed to "ks", "t", "globaltest", "sum" or "ks.ties". All from <a href="#">runTest</a> . |
| cutOff    | Default 1.  |
| verbose   | By default FALSE. Change it to TRUE to get a on-time log from the function.   |
| warnings  | By default TRUE. Change it to FALSE to not see the warnings.  |

## Value

A data.frame with the enrichment results

## Examples

```
## Not run:  
topAnatEnrichment(gene=c("ADCY2", "AKAP13", "ANK3"))  
  
## End(Not run)
```

---

universe

*Vector with gene universe for Jaccard Index*

---

**Description**

Vector with all the gene names from DisGeNET database (<http://www.disgenet.org>) used as gene universe for Jaccard Index computation.

**Usage**

```
universe
```

**Format**

An object of class character of length 8947.

**Details**

```
data("universe", package = "psygenet2r")
```

**Value**

A character vector.

**Source**

<http://www.disgenet.org>

**Examples**

```
length(universe)
universe[1:10]
```

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