

# Package ‘clusterProfiler’

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**Type** Package

**Title** statistical analysis and visualization of functional profiles  
for genes and gene clusters

**Version** 3.99.1

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**Description** This package implements methods to analyze and visualize  
functional profiles (GO and KEGG) of gene and gene clusters.

**Depends** R (>= 3.4.0)

**Imports** AnnotationDbi, downloader, DOSE (>= 3.13.1), dplyr, enrichplot  
(>= 1.9.3), GO.db, GOSemSim, magrittr, methods, plyr, qvalue,  
rlang, rvcheck, stats, tidyr, utils

**Suggests** AnnotationHub, knitr, org.Hs.eg.db, prettydoc, ReactomePA,  
testthat

**VignetteBuilder** knitr

**ByteCompile** true

**License** Artistic-2.0

**URL** <https://yulab-smu.top/biomedical-knowledge-mining-book/>

**BugReports** <https://github.com/GuangchuangYu/clusterProfiler/issues>

**biocViews** Annotation, Clustering, GeneSetEnrichment, GO, KEGG,  
MultipleComparison, Pathways, Reactome, Visualization

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 Giovanni Dall'Olio [ctb] (formula interface of compareCluster)

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clusterProfiler-package

*statistical analysis and visualization of functional profiles for genes  
and gene clusters*

---

### Description

The package implements methods to analyze and visualize functional profiles of gene and gene clusters.

---

bitr

*bitr*

---

### Description

Biological Id TRanslator

### Usage

```
bitr(geneID, fromType, toType, OrgDb, drop = TRUE)
```

### Arguments

geneID	input gene id
fromType	input id type
toType	output id type
OrgDb	annotation db
drop	drop NA or not

### Value

data.frame

### Author(s)

Guangchuang Yu

---

bitr_kegg	<i>bitr_kegg</i>
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---

**Description**

convert biological ID using KEGG API

**Usage**

```
bitr_kegg(geneID, fromType, toType, organism, drop = TRUE)
```

**Arguments**

geneID	input gene id
fromType	input id type
toType	output id type
organism	supported organism, can be search using search_kegg_organism function
drop	drop NA or not

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

browseKEGG	<i>browseKEGG</i>
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---

**Description**

open KEGG pathway with web browser

**Usage**

```
browseKEGG(x, pathID)
```

**Arguments**

x	an instance of enrichResult or gseaResult
pathID	pathway ID

**Value**

url

**Author(s)**

Guangchuang Yu

---

buildGOMap	<i>buildGOMap</i>
------------	-------------------

---

**Description**

building GO mapping files

**Usage**

```
buildGOMap(gomap)
```

**Arguments**

gomap            data.frame with two columns of GO and gene ID

**Details**

provided by a data.frame of GO (column 1) and gene (column 2) direct annotation this function will building gene to GO and GO to gene mapping, with directly and indirectly (ancestor GO term) annotation.

**Value**

data.frame, GO annotation with indirect annotation

**Author(s)**

Yu Guangchuang

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compareCluster	<i>Compare gene clusters functional profile</i>
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### Description

Given a list of gene set, this function will compute profiles of each gene cluster.

### Usage

```
compareCluster(geneClusters, fun = "enrichGO", data = "", ...)
```

### Arguments

geneClusters	a list of entrez gene id. Alternatively, a formula of type <code>Entrez~group</code>
fun	One of "groupGO", "enrichGO", "enrichKEGG", "enrichDO" or "enrichPathway".
data	if geneClusters is a formula, the data from which the clusters must be extracted.
...	Other arguments.

### Value

A clusterProfResult instance.

### Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

### See Also

[compareClusterResult-class](#), [groupGO](#) [enrichGO](#)

### Examples

```
## Not run:
data(gcSample)
xx <- compareCluster(gcSample, fun="enrichKEGG",
                    organism="hsa", pvalueCutoff=0.05)
as.data.frame(xx)
# plot(xx, type="dot", caption="KEGG Enrichment Comparison")

## formula interface
mydf <- data.frame(Entrez=c('1', '100', '1000', '100101467',
                          '100127206', '100128071'),
                  group = c('A', 'A', 'A', 'B', 'B', 'B'),
                  othergroup = c('good', 'good', 'bad', 'bad', 'good', 'bad'))
xx.formula <- compareCluster(Entrez~group, data=mydf,
                            fun='groupGO', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula)
```

```
## formula interface with more than one grouping variable
xx.formula.twogroups <- compareCluster(Entrez~group+othergroup, data=mydf,
                                       fun='groupG0', OrgDb='org.Hs.eg.db')
as.data.frame(xx.formula.twogroups)

## End(Not run)
```

---

 DataSet

*Datasets gcSample contains a sample of gene clusters.*


---

### Description

Datasets gcSample contains a sample of gene clusters.

Datasets kegg\_species contains kegg species information

Datasets DE\_GSE8057 contains differential expressed genes obtained from GSE8057 dataset

---

 download\_KEGG

*download\_KEGG*


---

### Description

download the latest version of KEGG pathway/module

### Usage

```
download_KEGG(species, keggType = "KEGG", keyType = "kegg")
```

### Arguments

species	species
keggType	one of 'KEGG' or 'MKEGG'
keyType	supported keyType, see bitr_kegg

### Value

list

### Author(s)

Guangchuang Yu

dropGO                      *dropGO*

---

**Description**

drop GO term of specific level or specific terms (mostly too general).

**Usage**

```
dropGO(x, level = NULL, term = NULL)
```

**Arguments**

x	an instance of 'enrichResult' or 'compareClusterResult'
level	GO level
term	GO term

**Value**

modified version of x

**Author(s)**

Guangchuang Yu

---

enrichDAVID                      *enrichDAVID*

---

**Description**

enrichment analysis by DAVID

**Usage**

```
enrichDAVID(  
  gene,  
  idType = "ENTREZ_GENE_ID",  
  universe,  
  minGSSize = 10,  
  maxGSSize = 500,  
  annotation = "GOTERM_BP_FAT",  
  pvalueCutoff = 0.05,  
  pAdjustMethod = "BH",  
  qvalueCutoff = 0.2,  
  species = NA,  
  david.user  
)
```



**Arguments**

gene	input gene
idType	id type
universe	background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
minGSSize	minimal size of genes annotated for testing
maxGSSize	maximal size of genes annotated for testing
annotation	david annotation
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
qvalueCutoff	qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
species	species
david.user	david user

**Value**

A enrichResult instance

**Author(s)**

Guangchuang Yu

---

enricher	<i>enricher</i>
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---

**Description**

A universal enrichment analyzer

**Usage**

```
enricher(
  gene,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  TERM2GENE,
  TERM2NAME = NA
)
```

**Arguments**

gene	a vector of gene id
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
minGSSize	minimal size of genes annotated for testing
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
TERM2GENE	user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene
TERM2NAME	user input of TERM TO NAME mapping, a data.frame of 2 column with term and name

**Value**

A enrichResult instance

**Author(s)**

Guangchuang Yu

---

enrichGO	<i>GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.</i>
----------	---

---

**Description**

GO Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment GO categories after FDR control.

**Usage**

```
enrichGO(
  gene,
  OrgDb,
  keyType = "ENTREZID",
  ont = "MF",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  qvalueCutoff = 0.2,
```

```

    minGSSize = 10,
    maxGSSize = 500,
    readable = FALSE,
    pool = FALSE
  )

```

### Arguments

gene	a vector of entrez gene id.
OrgDb	OrgDb
keyType	keytype of input gene
ont	One of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
qvalueCutoff	qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
readable	whether mapping gene ID to gene Name
pool	If ont='ALL', whether pool 3 GO sub-ontologies

### Value

An `enrichResult` instance.

### Author(s)

Guangchuang Yu <https://guangchuangyu.github.io>

### See Also

[enrichResult-class](#), [compareCluster](#)

### Examples

```

## Not run:
  data(geneList, package = "DOSE")
  de <- names(geneList)[1:100]
  yy <- enrichGO(de, 'org.Hs.eg.db', ont="BP", pvalueCutoff=0.01)
  head(yy)

## End(Not run)

```

---

enrichKEGG	<i>KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.</i>
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---

### Description

KEGG Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG categories with FDR control.

### Usage

```
enrichKEGG(
  gene,
  organism = "hsa",
  keyType = "kegg",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2,
  use_internal_data = FALSE
)
```

### Arguments

gene	a vector of entrez gene id.
organism	supported organism listed in ' <a href="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report
pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.
use_internal_data	logical, use KEGG.db or latest online KEGG data

### Value

A enrichResult instance.

**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

**See Also**

[enrichResult-class](#), [compareCluster](#)

**Examples**

```
data(geneList, package='DOSE')
de <- names(geneList)[1:100]
yy <- enrichKEGG(de, pvalueCutoff=0.01)
head(yy)
```

---

enrichMKEGG

*KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.*

---

**Description**

KEGG Module Enrichment Analysis of a gene set. Given a vector of genes, this function will return the enrichment KEGG Module categories with FDR control.

**Usage**

```
enrichMKEGG(
  gene,
  organism = "hsa",
  keyType = "kegg",
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  universe,
  minGSSize = 10,
  maxGSSize = 500,
  qvalueCutoff = 0.2
)
```

**Arguments**

gene	a vector of entrez gene id.
organism	supported organism listed in ' <a href="http://www.genome.jp/kegg/catalog/org_list.html">http://www.genome.jp/kegg/catalog/org_list.html</a> '
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
pvalueCutoff	adjusted pvalue cutoff on enrichment tests to report

pAdjustMethod	one of "holm", "hochberg", "hommel", "bonferroni", "BH", "BY", "fdr", "none"
universe	background genes. If missing, the all genes listed in the database (eg TERM2GENE table) will be used as background.
minGSSize	minimal size of genes annotated by Ontology term for testing.
maxGSSize	maximal size of genes annotated for testing
qvalueCutoff	qvalue cutoff on enrichment tests to report as significant. Tests must pass i) pvalueCutoff on unadjusted pvalues, ii) pvalueCutoff on adjusted pvalues and iii) qvalueCutoff on qvalues to be reported.

**Value**

A enrichResult instance.

---

enrichWP	<i>enrichWP</i>
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---

**Description**

ORA analysis for WikiPathways

**Usage**

```
enrichWP(gene, organism, ...)
```

**Arguments**

gene	a vector of entrez gene id
organism	supported organisms, which can be accessed via the get_wp_organisms() function
...	additional parameters, see also the parameters supported by the enricher() function

**Details**

This function performs over-representation analysis using WikiPathways

**Value**

A enrichResult instance

**Author(s)**

Guangchuang Yu

---

get_wp_organisms	<i>get_wp_organism</i>
------------------	------------------------

---

**Description**

list supported organism of WikiPathways

**Usage**

```
get_wp_organisms()
```

**Details**

This function extracts information from 'http://data.wikipathways.org/current/gmt/' and lists all supported organisms

**Value**

supported organism list

**Author(s)**

Guangchuang Yu

---

Gff2GeneTable	<i>Gff2GeneTable</i>
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---

**Description**

read GFF file and build gene information table

**Usage**

```
Gff2GeneTable(gffFile, compress = TRUE)
```

**Arguments**

gffFile	GFF file
compress	compress file or not

**Details**

given a GFF file, this function extracts information from it and save it in working directory

**Value**

file save.

**Author(s)**

Yu Guangchuang

---

`go2ont`*go2ont*

---

**Description**

convert goid to ontology (BP, CC, MF)

**Usage**`go2ont(goid)`**Arguments**`goid` a vector of GO IDs**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

`go2term`*go2term*

---

**Description**

convert goid to descriptive term

**Usage**`go2term(goid)`**Arguments**`goid` a vector of GO IDs**Value**

data.frame

**Author(s)**

Guangchuang Yu



---

`gofilter`*gofilter*

---

**Description**

filter GO enriched result at specific level

**Usage**

```
gofilter(x, level = 4)
```

**Arguments**

x	output from enrichGO or compareCluster
level	GO level

**Value**

updated object

**Author(s)**

Guangchuang Yu

---

`groupGO`

*Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at a specific level.*

---

**Description**

Functional Profile of a gene set at specific GO level. Given a vector of genes, this function will return the GO profile at a specific level.

**Usage**

```
groupGO(  
  gene,  
  OrgDb,  
  keyType = "ENTREZID",  
  ont = "CC",  
  level = 2,  
  readable = FALSE  
)
```

**Arguments**

gene	a vector of entrez gene id.
OrgDb	OrgDb
keyType	key type of input gene
ont	One of "MF", "BP", and "CC" subontologies.
level	Specific GO Level.
readable	if readable is TRUE, the gene IDs will mapping to gene symbols.

**Value**

A groupGOResult instance.

**Author(s)**

Guangchuang Yu <http://guangchuangyu.github.io>

**See Also**

[groupGOResult-class](#), [compareCluster](#)

**Examples**

```
data(gcSample)
yy <- groupGO(gcSample[[1]], 'org.Hs.eg.db', ont="BP", level=2)
head(summary(yy))
#plot(yy)
```

---

groupGOResult-class    *Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.*

---

**Description**

Class "groupGOResult" This class represents the result of functional Profiles of a set of gene at specific GO level.

**Slots**

result GO classification result  
ontology Ontology  
level GO level  
organism one of "human", "mouse" and "yeast"  
gene Gene IDs  
readable logical flag of gene ID in symbol or not.

**Author(s)**

Guangchuang Yu <https://guangchuangyu.github.io>

**See Also**

[compareClusterResult](#) [compareCluster](#) [groupGO](#)

---

GSEA

*GSEA*

---

**Description**

a universal gene set enrichment analysis tools

**Usage**

```
GSEA(
  geneList,
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  TERM2GENE,
  TERM2NAME = NA,
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...
)
```

**Arguments**

geneList	order ranked geneList
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
eps	This parameter sets the boundary for calculating the p value.
pvalueCutoff	adjusted pvalue cutoff
pAdjustMethod	p value adjustment method
TERM2GENE	user input annotation of TERM TO GENE mapping, a data.frame of 2 column with term and gene
TERM2NAME	user input of TERM TO NAME mapping, a data.frame of 2 column with term and name

verbose	logical
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

**Value**

gseaResult object

**Author(s)**

Guangchuang Yu

---

gseGO

*gseGO*

---

**Description**

Gene Set Enrichment Analysis of Gene Ontology

**Usage**

```
gseGO(
  geneList,
  ont = "BP",
  OrgDb,
  keyType = "ENTREZID",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  seed = FALSE,
  by = "fgsea",
  ...
)
```

**Arguments**

geneList	order ranked geneList
ont	one of "BP", "MF", and "CC" subontologies, or "ALL" for all three.
OrgDb	OrgDb
keyType	keytype of gene

exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
eps	This parameter sets the boundary for calculating the p value.
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseKEGG

*gseKEGG*

---

**Description**

Gene Set Enrichment Analysis of KEGG

**Usage**

```
gseKEGG(
  geneList,
  organism = "hsa",
  keyType = "kegg",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
  pAdjustMethod = "BH",
  verbose = TRUE,
  use_internal_data = FALSE,
  seed = FALSE,
  by = "fgsea",
  ...
)
```

**Arguments**

geneList	order ranked geneList
organism	supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
eps	This parameter sets the boundary for calculating the p value.
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
use_internal_data	logical, use KEGG.db or latest online KEGG data
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

**Value**

gseaResult object

**Author(s)**

Yu Guangchuang

---

gseMKEGG

*gseMKEGG*

---

**Description**

Gene Set Enrichment Analysis of KEGG Module

**Usage**

```
gseMKEGG(
  geneList,
  organism = "hsa",
  keyType = "kegg",
  exponent = 1,
  minGSSize = 10,
  maxGSSize = 500,
  eps = 1e-10,
  pvalueCutoff = 0.05,
```

```

    pAdjustMethod = "BH",
    verbose = TRUE,
    seed = FALSE,
    by = "fgsea",
    ...
)

```

### Arguments

geneList	order ranked geneList
organism	supported organism listed in 'http://www.genome.jp/kegg/catalog/org_list.html'
keyType	one of "kegg", 'ncbi-geneid', 'ncib-proteinid' and 'uniprot'
exponent	weight of each step
minGSSize	minimal size of each geneSet for analyzing
maxGSSize	maximal size of genes annotated for testing
eps	This parameter sets the boundary for calculating the p value.
pvalueCutoff	pvalue Cutoff
pAdjustMethod	pvalue adjustment method
verbose	print message or not
seed	logical
by	one of 'fgsea' or 'DOSE'
...	other parameter

### Value

gseaResult object

### Author(s)

Yu Guangchuang

---

gseWP

*gseWP*

---

### Description

GSEA analysis for WikiPathways

### Usage

```
gseWP(geneList, organism, ...)
```

**Arguments**

geneList	ranked gene list
organism	supported organisms, which can be accessed via the <code>get_wp_organisms()</code> function
...	additional parameters, see also the parameters supported by the <code>enricher()</code> function

**Details**

This function performs GSEA using WikiPathways

**Value**

A `gseaResult` instance

**Author(s)**

Guangchuang Yu

---

hgmlist

*A list with 6980 K genes of human gut genome*

---

**Description**

All 6980 K genes were reported on "An integrated catalog of reference genes in the human gut microbiome.[J]. Nature Biotechnology, 2014."

**Usage**

```
hgmlist
```

**Format**

A list with 6980 K genes

**Details**

```
data(hgmlist) kk <- enrichKEGG(gene = hgmlist[1:20], organism = "ko", universe = hgmlist ) dot-plot(kk)
```



---

<i>idType</i>	<i>idType</i>
---------------	---------------

---

**Description**

list ID types supported by annoDb

**Usage**

```
idType(OrgDb = "org.Hs.eg.db")
```

**Arguments**

OrgDb            annotation db

**Value**

character vector

**Author(s)**

Guangchuang Yu

---

<i>ko2name</i>	<i>ko2name</i>
----------------	----------------

---

**Description**

convert ko ID to descriptive name

**Usage**

```
ko2name(ko)
```

**Arguments**

ko                ko ID

**Value**

data.frame

**Author(s)**

guangchuang yu

merge\_result            *merge\_result*

---

**Description**

merge a list of enrichResult objects to compareClusterResult

**Usage**

```
merge_result(enrichResultList)
```

**Arguments**

enrichResultList  
a list of enrichResult objects

**Value**

a compareClusterResult instance

**Author(s)**

Guangchuang Yu

---

plotGOgraph            *plotGOgraph*

---

**Description**

plot GO graph

**Usage**

```
plotGOgraph(  
  x,  
  firstSigNodes = 10,  
  useInfo = "all",  
  sigForAll = TRUE,  
  useFullNames = TRUE,  
  ...  
)
```

**Arguments**

x	output of enrichGO or gseGO
firstSigNodes	number of significant nodes (rectangle nodes in the graph)
useInfo	additional info
sigForAll	if TRUE the score/p-value of all nodes in the DAG is shown, otherwise only score will be shown
useFullNames	logical
...	additional parameter of showSigOfNodes, please refer to topGO

**Value**

GO DAG graph

**Author(s)**

Guangchuang Yu

---

read.gmt

*read.gmt*

---

**Description**

parse gmt file to a data.frame

**Usage**

```
read.gmt(gmtfile)
```

```
read.gmt.wp(gmtfile)
```

**Arguments**

gmtfile           gmt file

**Value**

data.frame

**Author(s)**

Guangchuang Yu

search\_kegg\_organism    *search\_kegg\_organism*

---

**Description**

search kegg organism, listed in [http://www.genome.jp/kegg/catalog/org\\_list.html](http://www.genome.jp/kegg/catalog/org_list.html)

**Usage**

```
search_kegg_organism(str, by = "scientific_name", ignore.case = FALSE)
```

**Arguments**

str	string
by	one of 'kegg.code', 'scientific_name' and 'common_name'
ignore.case	TRUE or FALSE

**Value**

data.frame

**Author(s)**

Guangchuang Yu

---

simplify                    *simplify method*

---

**Description**

simplify output from enrichGO and gseGO by removing redundancy of enriched GO terms

simplify output from compareCluster by removing redundancy of enriched GO terms

**Usage**

```
## S4 method for signature 'enrichResult'  
simplify(  
  x,  
  cutoff = 0.7,  
  by = "p.adjust",  
  select_fun = min,  
  measure = "Wang",  
  semData = NULL  
)
```

```
## S4 method for signature 'gseaResult'
simplify(
  x,
  cutoff = 0.7,
  by = "p.adjust",
  select_fun = min,
  measure = "Wang",
  semData = NULL
)

## S4 method for signature 'compareClusterResult'
simplify(
  x,
  cutoff = 0.7,
  by = "p.adjust",
  select_fun = min,
  measure = "Wang",
  semData = NULL
)
```

### Arguments

x	output of enrichGO
cutoff	similarity cutoff
by	feature to select representative term, selected by 'select_fun' function
select_fun	function to select feature passed by 'by' parameter
measure	method to measure similarity
semData	GOSemSimDATA object

### Value

updated enrichResult object  
updated compareClusterResult object

### Author(s)

Guangchuang Yu  
Gwang-Jin Kim and Guangchuang Yu  
Guangchuang Yu

### References

issue #28 <https://github.com/GuangchuangYu/clusterProfiler/issues/28>  
issue #162 <https://github.com/GuangchuangYu/clusterProfiler/issues/162>

---

`uniprot_get``uniprot_get`

---

**Description**

retrieve annotation data from uniprot

**Usage**

```
uniprot_get(taxID)
```

**Arguments**

taxID            taxonomy ID

**Value**

gene table data frame

**Author(s)**

guangchuang yu

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