

# Package ‘UniProtKeywords’

December 10, 2025

**Type** Package

**Title** Keywords from UniProt Database

**Version** 0.99.7

**Date** 2023-09-23

**Depends** R (>= 4.0.0)

**Imports** utils

**Suggests** knitr, rmarkdown, markdown, testthat

**biocViews** AnnotationData, Organism, Homo\_sapiens

**Description** UniProt database provides a list of controlled vocabulary represented as keywords for genes or proteins. This is useful for summarizing gene functions in a compact way. This package provides data of keywords hierarchy and gene-keyword relations.

**VignetteBuilder** knitr

**URL** <https://github.com/jokergoo/UniProtKeywords>,  
<https://www.uniprot.org/keywords/>

**BugReports** <https://github.com/jokergoo/UniProtKeywords/issues>

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**NeedsCompilation** no

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

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**Author** Zuguang Gu [aut, cre] (ORCID: <<https://orcid.org/0000-0002-7395-8709>>)

**Maintainer** Zuguang Gu <z.gu@dkfz.de>

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|              |                               |
|--------------|-------------------------------|
| kw_ancestors | <i>Ancestor keyword terms</i> |
|--------------|-------------------------------|

---

Description

Ancestor keyword terms

Usage

data(kw\_ancestors)

Value

A list of ancestor keywords.

Examples

```
data(kw_ancestors)
kw_ancestors[1:2]
```

---

|             |                            |
|-------------|----------------------------|
| kw_children | <i>child keyword terms</i> |
|-------------|----------------------------|

---

Description

child keyword terms

Usage

data(kw\_children)

Value

A list of child keywords.

**Examples**

```
data(kw_children)
kw_children[1:2]
```

---

|              |                                |
|--------------|--------------------------------|
| kw_offspring | <i>Offspring keyword terms</i> |
|--------------|--------------------------------|

---

**Description**

Offspring keyword terms

**Usage**

```
data(kw_offspring)
```

**Value**

A list of offspring keywords.

**Examples**

```
data(kw_offspring)
kw_offspring[1:2]
```

---

|            |                              |
|------------|------------------------------|
| kw_parents | <i>Parents keyword terms</i> |
|------------|------------------------------|

---

**Description**

Parents keyword terms

**Usage**

```
data(kw_parents)
```

**Value**

A list of parent keywords.

**Examples**

```
data(kw_parents)
kw_parents[1:2]
```

---

`kw_terms`*Keyword terms*

---

**Description**

Keyword terms

**Usage**

```
data(kw_terms)
```

**Details**

Data is from [https://ftp.uniprot.org/pub/databases/uniprot/current\\_release/knowledgebase/complete/docs/keywlist.txt](https://ftp.uniprot.org/pub/databases/uniprot/current_release/knowledgebase/complete/docs/keywlist.txt)

Last updated: 2023-03-22.

**Value**

A list of keyword terms. Each keyword term has the following elements:

- Identifier
- Accession
- Description
- Synonyms
- Gene\_ontology
- Hierarchy
- WWW\_site
- Category

**Examples**

```
data(kw_terms)
kw_terms[[1]]
```

---

load\_keyword\_genesets *Load keyword genesets for a specific species*


---

**Description**

Load keyword genesets for a specific species

**Usage**

```
load_keyword_genesets(taxon_id = 9606, category = NULL, as_table = FALSE)
```

**Arguments**

|          |                                                                                                                                                                                                                                                                     |
|----------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| taxon_id | The taxon ID. To make it more flexible, you can also provide the Latin name or the normal name of the species.                                                                                                                                                      |
| category | Category of keywords. There are the following categories: "Biological process", "Cellular component", "Coding sequence diversity", "Developmental stage", "Disease", "Domain", "Ligand", "Molecular function", "Post-translational modification", "Technical term". |
| as_table | If true, the returned value will be a two-column data frame.                                                                                                                                                                                                        |

**Details**

Following are the supported species (with more than 1000 genes annotated):

- "10090": *Mus musculus* / house mouse
- "10116": *Rattus norvegicus* / Norway rat
- "208964": *Pseudomonas aeruginosa* PAO1 / strain, g-proteobacteria
- "224308": *Bacillus subtilis* subsp. *subtilis* str. 168 / strain, firmicutes
- "237561": *Candida albicans* SC5314 / strain, budding yeasts
- "243232": *Methanocaldococcus jannaschii* DSM 2661 / strain, euryarchaeotes
- "284812": *Schizosaccharomyces pombe* 972h- / strain, ascomycete fungi
- "3702": *Arabidopsis thaliana* / thale cress
- "39947": *Oryza sativa* Japonica Group / (Japanese rice), monocots
- "44689": *Dictyostelium discoideum* / species, cellular slime molds
- "559292": *Saccharomyces cerevisiae* S288C / strain, budding yeasts
- "6239": *Caenorhabditis elegans* / species, nematodes
- "623": *Shigella flexneri* / species, enterobacteria
- "7227": *Drosophila melanogaster* / (fruit fly), species, flies
- "7955": *Danio rerio* / (zebrafish), species, bony fishes
- "83332": *Mycobacterium tuberculosis* H37Rv / strain, high G+C Gram-positive bacteria
- "83333": *Escherichia coli* K-12 / strain, enterobacteria

- "83334": Escherichia coli O157:H7 / serotype, enterobacteria
- "8355": Xenopus laevis / (African clawed frog), species, frogs & toads
- "8364": Xenopus tropicalis / (tropical clawed frog), species, frogs & toads
- "9031": Gallus gallus / (chicken), species, birds
- "9601": Pongo abelii / (Sumatran orangutan), species, primates
- "9606": Homo sapiens / human
- "9823": Sus scrofa / (pig), species, even-toed ungulates
- "9913": Bos taurus / cattle
- "99287": Salmonella enterica subsp. enterica serovar Typhimurium str. LT2 / strain, enterobacteria

### Value

If `as_table` is set to `FALSE`, it returns a list of gene sets where Entrez IDs are the gene IDs. If `as_table` is set to `TRUE`, it returns a two-column data frame.

### Examples

```
lt = load_keyword_genesets(9606)
lt[3:4]
tb = load_keyword_genesets(9606, as_table = TRUE)
head(tb)
# load_keyword_genesets("mouse")
```

---

```
print.UniProtKeywords_info
      Print the UniProtKeywords object
```

---

### Description

Print the UniProtKeywords object

### Usage

```
## S3 method for class 'UniProtKeywords_info'
print(x, ...)
```

### Arguments

|                  |                          |
|------------------|--------------------------|
| <code>x</code>   | A UniProtKeyword object. |
| <code>...</code> | Other arguments          |

### Examples

```
UniProtKeywords
```

---

|                 |                                       |
|-----------------|---------------------------------------|
| UniProtKeywords | <i>Release and source information</i> |
|-----------------|---------------------------------------|

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**Description**

Release and source information

**Usage**

UniProtKeywords

**Examples**

UniProtKeywords

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