

# UniProtKeywords

July 9, 2025

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UniProtKeywords

*Release and source information*

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## Description

Release and source information

## Usage

UniProtKeywords

## Examples

UniProtKeywords

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kw\_ancestors

*Ancestor keyword terms*

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## Description

Ancestor keyword terms

## Usage

data(kw\_ancestors)

## Value

A list of ancestor keywords.

## Examples

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

---

`kw_children`*child keyword terms*

---

**Description**

child keyword terms

**Usage**

```
data(kw_children)
```

**Value**

A list of child keywords.

**Examples**

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

---

`kw_offspring`*Offspring keyword terms*

---

**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]
```

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|          |                      |
|----------|----------------------|
| kw_terms | <i>Keyword terms</i> |
|----------|----------------------|

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**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*

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### 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*

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## Description

Print the UniProtKeywords object

## Usage

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

**Arguments**

|     |                          |
|-----|--------------------------|
| x   | A UniProtKeyword object. |
| ... | Other arguments          |

**Examples**

```
UniProtKeywords
```

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