

# UniProtKeywords

May 7, 2024

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UniProtKeywords	<i>Release and source information</i>
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## Description

Release and source information

## Usage

UniProtKeywords

## Examples

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kw_ancestors	<i>Ancestor keyword terms</i>
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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]
```

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`kw_children`*child keyword terms*

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**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*

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**Description**

Offspring keyword terms

**Usage**

```
data(kw_offspring)
```

**Value**

A list of offspring keywords.

**Examples**

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

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kw_parents	<i>Parents keyword terms</i>
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**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]]
```

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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")
```

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```
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**

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