UniProtKeywords

February 25, 2026

UniProtKeywords	*Release and source information*

Description

Release and source information

Usage

```
UniProtKeywords
```

Examples

```
UniProtKeywords
```

---

kw_ancestors	*Ancestor keyword terms*

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   *Parents keyword terms*

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

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

x	A `UniProtKeyword` object.
...	Other arguments

Examples

```
UniProtKeywords
```

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