

UniProtKeywords

February 3, 2023

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

Description

Release and source information

Usage

UniProtKeywords

Examples

UniProtKeywords

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`*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]
```

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

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: 2022-09-06.

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.
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):

- "9606": Homo sapiens / human
- "10090": Mus musculus / house mouse
- "3702": Arabidopsis thaliana / thale cress
- "10116": Rattus norvegicus / Norway rat
- "559292": Saccharomyces cerevisiae S288C / strain, budding yeasts
- "9913": Bos taurus / cattle
- "284812": Schizosaccharomyces pombe 972h- / strain, ascomycete fungi
- "224308": Bacillus subtilis subsp. subtilis str. 168 / strain, firmicutes
- "83333": Escherichia coli K-12 / strain, enterobacteria
- "44689": Dictyostelium discoideum / species, cellular slime molds

- "39947": *Oryza sativa Japonica Group* / (Japanese rice), monocots
- "6239": *Caenorhabditis elegans* / species, nematodes
- "7227": *Drosophila melanogaster* / (fruit fly), species, flies
- "8355": *Xenopus laevis* / (African clawed frog), species, frogs & toads
- "7955": *Danio rerio* / (zebrafish), species, bony fishes
- "83332": *Mycobacterium tuberculosis H37Rv* / strain, high G+C Gram-positive bacteria
- "9601": *Pongo abelii* / (Sumatran orangutan), species, primates
- "83334": *Escherichia coli O157:H7* / serotype, enterobacteria
- "9031": *Gallus gallus* / (chicken), species, birds
- "99287": *Salmonella enterica* subsp. *enterica* serovar *Typhimurium* str. *LT2* / strain, enterobacteria
- "623": *Shigella flexneri* / species, enterobacteria
- "8364": *Xenopus tropicalis* / (tropical clawed frog), species, frogs & toads
- "208964": *Pseudomonas aeruginosa PAO1* / strain, g-proteobacteria
- "243232": *Methanocaldococcus jannaschii DSM 2661* / strain, euryarchaeotes
- "9823": *Sus scrofa* / (pig), species, even-toed ungulates
- "237561": *Candida albicans SC5314* / strain, budding yeasts

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)
```

```
print.UniProtKeywords_info
```

Print the UniProtKeywords object

Description

Print the UniProtKeywords object

Usage

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

6

print.UniProtKeywords_info

Arguments

x A UniProtKeyword object.
... Other arguments

Examples

UniProtKeywords

Index

[kw_ancestors](#), [1](#)

[kw_children](#), [2](#)

[kw_offspring](#), [2](#)

[kw_parents](#), [3](#)

[kw_terms](#), [3](#)

[load_keyword_genesets](#), [4](#)

[print.UniProtKeywords_info](#), [5](#)

[UniProtKeywords](#), [1](#)