UniProtKeywords

November 6, 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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