

# Package ‘UniProt.ws’

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**Type** Package

**Title** R Interface to UniProt Web Services

**Version** 2.46.1

**Description** The Universal Protein Resource (UniProt) is a comprehensive resource for protein sequence and annotation data. This package provides a collection of functions for retrieving, processing, and re-packaging UniProt web services. The package makes use of UniProt's modernized REST API and allows mapping of identifiers across different databases.

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**Imports** AnnotationDbi, BiocFileCache, BiocBaseUtils, httr, httpcache, jsonlite, progress, rjsoncons

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**License** Artistic-2.0

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mapping-and-querying *Mapping identifiers with the UniProt API*

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## Description

These functions are the main workhorses for mapping identifiers from one database to another. They make use of the latest UniProt API (seen at <https://www.uniprot.org/help/api>).

## Usage

```
mapUniProt(
  from = "UniProtKB_AC-ID",
  to = "UniRef90",
  columns = character(0L),
  query,
  verbose = FALSE,
  debug = FALSE,
  paginate = TRUE,
  pageSize = 500L
)
queryUniProt(
  query = character(0L),
  fields = c("accession", "id"),
  collapse = " OR ",
  n = Inf,
  pageSize = 25L
)
allToKeys(fromName = "UniProtKB_AC-ID")
allFromKeys()
returnFields()
```

## Arguments

from	character(1) The identifier type to map from, by default "UniProtKB_AC-ID", short for UniProt accession identifiers. See a list of all 'from' type identifiers with <code>allFromKeys</code> .
to	character(1) The target mapping identifier, by default "UniRef90". It can be any one of those returned by <code>allToKeys</code> from the appropriate <code>fromName</code> argument.
columns, fields	character() Additional information to be retrieved from UniProt service. See a full list of possible input return fields at <a href="https://www.uniprot.org/help/return_fields">https://www.uniprot.org/help/return_fields</a> . Example fields include, "accession", "id", "gene_names", "xref_pdb", "xref_hgnc", "sequence", etc.

query	character() or named list() Typically, a string that would indicate the target accession identifiers but can also be a named list based on the available query fields. See <a href="https://www.uniprot.org/help/query-fields">https://www.uniprot.org/help/query-fields</a> for a list of query fields. The typical query might only include a character vector of UniProt accession identifiers, e.g., <code>c("A0A0C5B5G6", "A0A1B0GTW7", "A0JNW5", "A0JP26", "A0PK11", "A1A4S6")</code>
collapse	character(1) A string indicating either " OR " or " AND " for combining query clauses.
n	numeric(1) Maximum number of rows to return
fromName	character(1) A from key to use as the basis of mapping to other keys, by default, "UniProtKB_AC-ID".
verbose	logical(1) Whether the operations should provide verbose updates (default FALSE).
debug	logical(1) Whether to display the URL API endpoints, for advanced debugging (default FALSE)
paginate	logical(1) Whether to use the pagination API (i.e., "results" vs "stream") in the request responses. For performance, it is set to TRUE by default.
pageSize	integer(1) number of records per page. It corresponds to the size parameter in the API request.

### Details

Note that `mapUniProt` is used internally by the `select` method but made available for API queries with finer control. Provide values from the name column in `returnFields` as the columns input in either `mapUniProt` or `select` method.

When using `from='Gene_Name'`, you may restrict the search results to a specific organism by including e.g., `taxId=9606` in the query as a named list element. See examples below.

### Value

- `mapUniProtA` data.frame of returned results
- `allToKeysA` sorted character vector of possible "To" keytypes based on the given "From" type
- `allFromKeysA` sorted character vector of possible "From" keytypes
- `returnFieldsA` data.frame of entries for the columns input in `mapUniProt`; see 'name' column

### Author(s)

Marcel Ramos

### Examples

```
mapUniProt(
  from="UniProtKB_AC-ID",
  to='RefSeq_Protein',
  query=c('P13368', 'Q9UM73', 'P97793', 'Q17192')
)

mapUniProt(
  from='GeneID', to='UniProtKB', query=c('1', '2', '3', '9', '10')
)

mapUniProt(
```

```

    from = "UniProtKB_AC-ID",
    to = "UniProtKB",
    columns = c("accession", "id"),
    query = list(organism_id = 10090, ids = c('Q7TPG8', 'P63318'))
  )

  ## restrict 'from = Gene_Name' result to taxId 9606
  mapUniProt(
    from = "Gene_Name",
    to = "UniProtKB-Swiss-Prot",
    columns = c("accession", "id"),
    query = list(taxId = 9606, ids = 'TP53')
  )

  mapUniProt(
    from = "UniProtKB_AC-ID", to = "UniProtKB",
    query = c("P31946", "P62258"),
    columns = c("accession", "id", "xref_pdb", "xref_hgnc", "sequence")
  )

  queryUniProt(
    query = c("accession:A5YMT3", "organism_id:9606"),
    fields = c("accession", "id", "reviewed"),
    collapse = " AND "
  )

  allToKeys(fromName = "UniRef100")

  head(allFromKeys())

  head(returnFields())

```

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UniProt.ws-objects      *UniProt.ws objects and their related methods and functions*

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## Description

UniProt.ws is the base class for interacting with the Uniprot web services from Bioconductor.

In much the same way as an AnnotationDb object allows access to select for many other annotation packages, UniProt.ws is meant to allow usage of select methods and other supporting methods to enable the easy extraction of data from the Uniprot web services.

select, columns and keys are used together to extract data via an UniProt.ws object.

columns shows which kinds of data can be returned for the UniProt.ws object.

keytypes allows the user to discover which keytypes can be passed in to select or keys via the keytype argument.

keys returns keys for the database contained in the UniProt.ws object. By default it will return the primary keys for the database, which are UniProtKB keys, but if used with the keytype argument, it will return the keys from that keytype.

select will retrieve the data as a data.frame based on parameters for selected keys and columns and keytype arguments.

The `UniProt.ws` will be loaded whenever you load the `UniProt.ws` package. This object will be set up to retrieve information from *Homo sapiens* by default, but this value can be changed to any of the species supported by Uniprot. The `species` and `taxId` methods allow users to see what species is currently being accessed, and `taxId<-` allows them to change this value.

`species` shows the genus and species label currently attached to the `UniProt.ws` objects database.

`taxId` shows the NCBI taxonomy ID currently attached to the `AnnotationDb` objects database. Using the equivalently names `replace` method (`taxId<-`) allows the user to change the taxon ID, and the species represented along with it.

`availableUniprotSpecies` is a helper function to list out the available Species along with their official taxonomy IDs that are available by Uniprot. Because there are so many species represented at UniProt, there is also a `pattern` argument that can be used to restrict the range of things returned to be only those whose species names match the search term. Please remember when using this argument that the Genus is always capitalized and the species never is.

`lookupUniprotSpeciesFromTaxId` is another helper that will look up the species of any tax ID that is supported by Uniprot.

## Usage

```
columns(x)
keytypes(x)
select(x, keys, columns, keytype, ...)
species(object)
taxId(x)

availableUniprotSpecies(pattern)
lookupUniprotSpeciesFromTaxId(taxId)
UniProt.ws(taxId, ...)
```

## Arguments

<code>x</code>	the <code>UniProt.ws</code> object.
<code>object</code>	the <code>UniProt.ws</code> object.
<code>keys</code>	the keys to select records for from the database. All possible keys are returned by using the <code>keys</code> method.
<code>columns</code>	the columns or kinds of things that can be retrieved from the database. As with <code>keys</code> , all possible columns are returned by using the <code>columns</code> method.
<code>keytype</code>	the keytype that matches the keys used. For the <code>select</code> methods, this is used to indicate the kind of ID being used with the <code>keys</code> argument. For the <code>keys</code> method this is used to indicate which kind of keys are desired from <code>keys</code>
<code>pattern</code>	A string passed in to limit the results
<code>taxId</code>	a taxonomy id
<code>...</code>	other arguments

## Value

`keys`, `columns`, `keytypes`, `species` and `lookupUniprotSpeciesFromTaxId` each return a character vector of possible values.

`taxId` returns a numeric value that corresponds to the taxonomy ID.

`select` and `availableUniprotSpecies` each return a `data.frame`.

**Author(s)**

Marc Carlson

**See Also**

select

**Examples**

```
## Make a UniProt.ws object
up <- UniProt.ws(taxId=9606)

## look at the object
up

## get the current species
species(up)

## look up available species with their tax ids
availableUniprotSpecies("musculus")

## get the current taxId
taxId(up)

## look up the species that goes with a tax id
lookupUniprotSpeciesFromTaxId(9606)

## set the taxId to something else
taxId(up) <- 10090
up

## list the possible key types
head(keytypes(up))

## list of possible columns
head(columns(up))

## list all possible keys of type entrez gene ID
egs <- keys(up, "GeneID")

## use select to extract some data
res <- select(
  x = up,
  keys = c("22627", "22629"),
  columns = c("xref_pdb", "xref_hgnc", "sequence"),
  keytype = "GeneID"
)
res

univals <- c("A0A0C5B5G6", "A0A1B0GTW7", "A0JNW5", "A0JP26", "A0PK11")
res <- select(
  x = up,
  keys = univals,
  to = "Ensembl"
)
res
```

## Description

UniProt uses custom coding of organism names from which protein sequences they store. These taxon names are used also in the protein names (not in the UniProt IDs!). These functions help to translate those names to standard scientific (Latin) taxon names and other useful identifiers.

- `taxname2species()`: converts UniProt taxonomy names to scientific species names
- `taxname2taxid()`: converts UniProt taxonomy names to NCBI Taxonomy IDs
- `taxname2domain()`: converts UniProt taxonomy names to the following taxonomical domains: 'A' for archaea (=archaeobacteria)\ 'B' for bacteria (=prokaryota or eubacteria)\ 'E' for eukaryota (=eukarya)\ 'V' for viruses and phages (=viridae)\ 'O' for others (such as artificial sequences)\
- `updatespecfile()`: The `updatespecfile` helper function attempts to download the current version of the controlled vocabulary of species table from [UniProt controlled vocabulary of species](#). If it fails to download, an archived version of the table in (in `extdata/`) will be used.

## Usage

```
taxname2species(taxname, specfile)
taxname2taxid(taxname, specfile)
taxname2domain(taxname, specfile)
```

## Arguments

<code>taxname</code>	Character string up to 6 uppercase characters, like HUMAN, MOUSE, or AERPX. Also works for a vector of such taxon names.
<code>specfile</code>	An optional local file where <code>speclist.RData</code> is saved from UniProt.org. When <code>specfile</code> is missing, a cached file from the <code>extdata/</code> package directory is used.

## Value

Function `taxname2species` returns a character vector of scientific taxon names matching to the UniProt taxon names supplied as `taxname`.

Function `taxname2taxid` returns a numeric vector of Taxonomy IDs matching to the UniProt taxon names supplied as `taxname`.

Function `taxname2domain` returns a character vector of one letter domain symbols matching to the UniProt taxon names supplied as `taxname`.

Function `updatespecfile` is deprecated and no longer required as the `specfile` is self updating based on `BiocFileCache`'s `bfcneedsupdate` when necessary.

## Author(s)

Csaba Ortutay

## See Also

[UniProt controlled vocabulary of species](#), which defines the taxon names.

**Examples**

```
taxname2species("PIG")  
taxname2species(c("PIG", "HUMAN", "TRIHA"))
```

```
taxname2taxid("PIG")  
taxname2taxid(c("PIG", "HUMAN", "TRIHA"))
```

```
taxname2domain("PIG")  
taxname2domain(c("PIG", "HUMAN", "TRIHA"))
```



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