PANTHER.db

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PANTHER.db-objects *PANTHER.db objects and their related methods and functions*

Description

In much the same way as an AnnotationDb object allows access to select for many other annotation packages, PANTHER.db is meant to allow usage of select methods and other supporting methods to enable the easy extraction of data from the PANTHER gene ontology.

select, columns and keys are used together to extract data via an PANTHER.db object.

columns shows which kinds of data can be returned for the PANTHER.db 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 PANTHER.db object. By default it will return the primary keys for the database, which are FAMILY_ID 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.

pthOrganisms shows the organism label currently attached to the PANTHER.db objects database. The organism supported by PANTHER.db is currently restricted to the organisms supported by the main annotation packages in Bioconductor.

The PANTHER.db object will be loaded whenever you load the PANTHER.db package. This object will be set up to return information on PANTHER ontology terms and accessions based on all available organisms. The pthOrganisms<- method can be used to restrict queries to a specific organism and resetPthOrganisms can be used to remove the organism restriction.

availablePthOrganisms is a helper function to list out the available Species currently supported by the PANTHER.db package along with their official taxonomy IDs that are available by Uniprot.

The PANTHER Protein Class ontology was adapted from the PANTHER/X molecular function ontology, and includes commonly used classes of protein functions, many of which are not covered by GO molecular function. traverseClassTree can be used to traverse the tree structure of the PANTHER Protein Class ontology.

Usage

```
columns(x)
keytypes(x)
keys(x, keytype,...)
select(x, keys, columns, keytype, ...)
pthOrganisms(x)
availablePthOrganisms(x)
resetPthOrganisms(x)
traverseClassTree(x,query,scope)
```

Arguments

x	the PANTHER.db object.
keys	the keys to select records for from the database. All possible keys are returned by using the keys method.
columns	the columns or kinds of things that can be retrieved from the database. As with keys, all possible columns are returned by using the columns method.
keytype	the keytype that matches the keys used. For the select methods, this is used to indicate the kind of ID being used with the keys argument. For the keys method this is used to indicate which kind of keys are desired from keys
query	character vector of valid PANTHER class identifiers e.g. PC00000
scope	character CHILD, PARENT, ANCESTOR or OFFSPRING to define the scope of the PANTHER class identifiers returned.
...	other arguments

Value

keys,columns,keytypes, traverseClassTree and pthOrganisms each return a character vector of possible values.

select and availablePthOrganisms each return a data.frame.

Author(s)

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See Also

select

Examples

```
## look at the object
PANTHER.db

## get the current organism
pthOrganisms(PANTHER.db)
```

```
## list the possible key types
keytypes(PANTHER.db)

## list the columns that can be retreived
columns(PANTHER.db)

## list all possible keys of type entrez gene ID.
head(keys(PANTHER.db))


## use select to extract some data
 keys <- c("E1C9F4","O14618")
 cols <- c("FAMILY_ID","SPECIES","FAMILY_TERM")
 kt <- "UNIPROT"
 select(PANTHER.db, keys, cols, kt)
```

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