

Package ‘webQueries’

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Type Package

Title NCBI Queries for Gene and Protein Annotations.

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Author Frederic Commo

Maintainer Frederic Commo <frederic.commo@gustaveroussy.fr>

Description Retrieve gene and protein annotations from NCBI,
given HUGO symbols or ids (entrezgene and Uniprot are supported).

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biocViews Annotation,GenomeAnnotation

Imports XML

Suggests RUnit,knitr,BiocGenerics

VignetteBuilder knitr

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webQueries-package	<i>Querying NCBI for Gene and/or Protein Annotations.</i>
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Description

Retrieve gene and protein annotations from NCBI, given HUGO symbols or official ids (entrezgene and Uniprot are supported). See note.

[xpathApply](#) is used to extract information from xml files.

Details

Package: webQueries
Type: Package
Version: 0.98.0
Date: 2015-03-15
License: Artistic-2.0

This function simply constructs an appropriate link to query the NCBI databases, using E-utilities. Information is extracted from the returned xml file.

Note

See [Introduction to the E-utilities](#) for more details.

Author(s)

Frederic Commo <frederic.commo@gustaveroussy.fr>

Examples

```
# Using HUGO symbol
geneQuery("erbb2")

# Using entrezgene id
geneQuery(2064)

# Using HUGO symbol
protQuery("erbb2")

# Using UniProt id
protQuery("P04626")
```

geneQuery

Gene annotations via Web Queries

Description

This function simply constructs an appropriate link to query the NCBI databases, using E-utilities. See note. HUGO symbols and entrezgene ids are supported. Information is extracted from the returned xml file, using [xpathApply](#) from XLM package.

Usage

```
geneQuery(geneId, DB = "gene", bySymb = TRUE, kTries = 10, verbose = TRUE)
```

Arguments

geneId : character or numeric. geneId can be either a valid HUGO symbol (not case sensitive), or an entrezgene id. See note.

DB : string. The NCBI database to query. This must be one of the NCBI databases supporting web queries.

bySymb : logical. Must be set to TRUE when a HUGO symbols is used.

kTries : numeric. The number of retries when connexion errors occur. Default is 10.

verbose : logical. If TRUE, progress is prompted.

Value

A vector of values.

Note

See [Introduction to the E-utilities](#) for more details.

Author(s)

Frederic Commo

See Also

[protQuery](#)

Examples

```
# Simple query using HUGO symbol or entrezgene id
geneQuery("erbb2")
geneQuery(2064)

# Multiple queries
ids <- c("egfr", "erbb2", "fgfr1")
annots <- lapply(ids, function(id) geneQuery(id) )
annots <- do.call(rbind, annots)
annots
```

hg19

Hg19 chromosomes length

Description

A data set containing the 24 chromosome lengths, and cumulative lengths.

Usage

```
hg19
```

Format

dataset

Details

A data set containing chromosome lengths, according to hg19 genome build.

Value

none.

Source

[UCSC](#).

References

None.

Examples

```
load(system.file("extdata", "hg19.rda", package="webQueries"))
```

protQuery	<i>Gene annotations via Web Queries</i>
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Description

This function simply constructs an appropriate link to query the NCBI databases, using E-utilities. See note. HUGO symbols and UniProt ids are supported. Information is extracted from the returned xml file, using [xpathApply](#) from XLM package.

Usage

```
protQuery(protId, DB = "protein", kTries = 10, verbose = TRUE)
```

Arguments

protId	: character or numeric. geneId can be either a valid HUGO symbol (not case sensitive), or an entrezgene id.
DB	: string. The NCBI database to query. This must be one of the NCBI databases supporting web queries.
kTries	: numeric. The number of retries when connexion errors occur. Default is 10.
verbose	: logical. If TRUE, progress in prompted.

Value

A vector of values.

Note

See [Introduction to the E-utilities](#) for more details.

Author(s)

Frederic Commo

See Also

[geneQuery](#)

Examples

```
# Simple query using HUGO symbol or UniProt id.
protQuery("erbb2")
protQuery("P04626")

# Multiple queries
ids <- c("egfr", "erbb2", "fgfr1")
annots <- lapply(ids, function(id) protQuery(id) )
annots <- do.call(rbind, annots)
annots
```

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