

Package ‘geneRequest’

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Type Package
Title NCBI Query for Gene Annotation.
Version 1.0
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Author Frederic Commo
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Description Retrieve gene annotations from NCBI, given a HUGO symbol or an entrezgene id, using web requests.
License GPL
Imports XML

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geneRequest-package	<i>NCBI Query for Gene Annotation.</i>
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Description

Retrieve gene annotations from NCBI, given a HUGO symbol or an entrezgene id, using web requests.

Details

Package: geneRequest
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Version: 1.0
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License: GPL
1

This function simply constructs an appropriate link to query the NCBI databases. Information is extracted from The xml file returned.

Author(s)

Frederic Commo <frederic.commo@gustaveroussy.fr>

Examples

```
geneRequest("ercc1")  
geneRequest(2067)
```

geneRequest

Gene annotations via Web Queries

Description

This function simply constructs an appropriate link to query the NCBI databases. Information is extracted from The xml file returned.

Usage

```
geneRequest(geneId, DB = "gene", bySymb = TRUE, 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.
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

Examples

```
# Simple query using symbol or entrezgeneId
geneRequest("ercc1")
geneRequest(2067, bySymb=FALSE)

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

hg19*HG19 chromosomes length*

Description

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

Format

The format is: chr "inst/extdata/hg19.rda"

Source

[UCSC](#)

Examples

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

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