Package ‘babelgene’

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Type Package

Title Gene Orthologs for Model Organisms in a Tidy Data Format

Version 22.9


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URL https://igordot.github.io/babelgene/

BugReports https://github.com/igordot/babelgene/issues

Depends R (>= 3.4)

Imports dplyr, methods, rlang

Suggests covr, knitr, rmarkdown, testthat (>= 3.0.0)

VignetteBuilder knitr

Config/testthat/edition 3

Encoding UTF-8

RoxygenNote 7.2.1

NeedsCompilation no

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Repository CRAN

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orthologs Retrieve gene orthologs/homologs

Description


Usage

orthologs(genes, species, human = TRUE, min_support = 3, top = TRUE)

Arguments

genes A vector of gene symbols or Entrez/Ensembl IDs.
species Species name, such as Mus musculus or mouse (see species() for options).
human A logical scalar indicating if the input genes are human. If TRUE, the input genes are human. If FALSE, the input genes correspond to the non-human species and the output will be the human equivalents.
min_support Minimum number of supporting source databases. Gene pairs available in this package are supported by 2 to 12 databases (the maximum varies depending on the species).
top For each gene, output only the match with the highest support level if there are multiple hits.

Value

A data frame of gene pairs (human and given species).

References


Examples

orthologs(genes = "TP53", species = "mouse", human = TRUE)
orthologs(genes = c("Ptprc", "Cd34"), species = "mouse", human = FALSE)
species

Retrieve the available species

Description
List the species with available human orthologs.

Usage
species(species = NULL)

Arguments

species Species name, such as Mus musculus or mouse. If specified, will return results for the given species only.

Value
A data frame of the available species.

Examples

species()
species("Mus musculus")
species("mouse")
species("rat")
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