Package ‘babelgene’

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Type Package
Title Gene Orthologs for Model Organisms in a Tidy Data Format
Version 21.4
License MIT + file LICENSE
Encoding UTF-8
URL https://igordot.github.io/babelgene/
BugReports https://github.com/igordot/babelgene/issues
Depends R (>= 3.3)
Imports dplyr, methods, rlang
Suggests covr, knitr, rmarkdown, testthat (>= 3.0.0)
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RoxygenNote 7.1.1
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orthologs

Description
Retrieve gene orthologs/homologs for a set of genes.

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: Input genes are human (or not).
- min_support: Minimum number of supporting sources.
- top: For each gene, output only the match with the highest support level.

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.

Value
A data frame of the available species.

Examples
species()