

# Package ‘babelgene’

April 26, 2021

**Type** Package

**Title** Gene Orthologs for Model Organisms in a Tidy Data Format

**Version** 21.4

**Description** Genomic analysis of model organisms often requires the use of databases based on human data or making comparisons to patient-derived resources. This requires converting genes between human and non-human analogues. The babelgene R package provides predicted gene orthologs/homologs for frequently studied model organisms in an R-friendly tidy/long format. The package integrates orthology assertion predictions sourced from multiple databases as compiled by the HGNC Comparison of Orthology Predictions (HCOP) (Wright et al. 2005 <doi:10.1007/s00335-005-0103-2>, Eyre et al. 2007 <doi:10.1093/bib/bbl030>, Seal et al. 2011 <doi:10.1093/nar/gkq892>).

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**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)

**Config/testthat/edition** 3

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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orthologs                      *Retrieve gene orthologs/homologs*

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**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 <i>Mus musculus</i> or mouse (see <code>species()</code> 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**

Wright MW, Eyre TA, Lush MJ, Povey S, Bruford EA. HCOP: the HGNC comparison of orthology predictions search tool. *Mamm Genome*. 2005 Nov;16(11):827-8. doi: [10.1007/s0033500501032](https://doi.org/10.1007/s0033500501032)

Eyre TA, Wright MW, Lush MJ, Bruford EA. HCOP: a searchable database of human orthology predictions. *Brief Bioinform*. 2007 Jan;8(1):2-5. doi: [10.1093/bib/bbl030](https://doi.org/10.1093/bib/bbl030)

Seal RL, Gordon SM, Lush MJ, Wright MW, Bruford EA. genenames.org: the HGNC resources in 2011. *Nucleic Acids Res*. 2011 Jan;39:D514-9. doi: [10.1093/nar/gkq892](https://doi.org/10.1093/nar/gkq892)

**Examples**

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

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species	<i>Retrieve the available species</i>
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**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()
```

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