

# Package ‘babelgene’

July 22, 2025

**Type** Package

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

**Version** 22.9

**Description** Genomic analysis of model organisms frequently requires the use of databases based on human data or making comparisons to patient-derived resources. This requires harmonization of gene names into the same gene space. The 'babelgene' R package converts between human and non-human gene orthologs/homologs. 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](https://doi.org/10.1007/s00335-005-0103-2)>, Eyre et al. 2007 <[doi:10.1093/bib/bbl030](https://doi.org/10.1093/bib/bbl030)>, Seal et al. 2011 <[doi:10.1093/nar/gkq892](https://doi.org/10.1093/nar/gkq892)>).

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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 | <i>Retrieve gene orthologs/homologs</i> |
|-----------|-----------------------------------------|

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Description

Retrieve gene orthologs/homologs for a set of genes. Converts between human and non-human analogs.

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       | 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

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

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

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

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 <i>Mus musculus</i> 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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