

# Package: pr2database (via r-universe)

October 10, 2024

**Title** PR2 database with shiny web interface

**Version** 5.0.0

**Description** PR2 database See <https://pr2-database.org>

**License** MIT + file LICENSE

**Imports** Biostrings, blaster (>= 1.0.4), config (>= 0.3.1), dplyr, DT, forcats, ggplot2, glue, golem (>= 0.3.5), markdown, pins, pkgload, purrr, qs, rio, shiny (>= 1.7.2), shinycssloaders, shinydisconnect, shinylogs, shinyvalidate, shinyWidgets, stringr, tidyr, yaml

**Encoding** UTF-8

**LazyData** true

**RoxygenNote** 7.2.3

**URL** <https://github.com/pr2database>

**BugReports** <https://github.com/pr2database/issues>

**Suggests** spelling, testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Language** en-US

**Depends** R (>= 2.10)

**Remotes** manutammenin/blaster

**Repository** <https://pr2database.r-universe.dev>

**RemoteUrl** <https://github.com/pr2database/pr2database>

**RemoteRef** HEAD

**RemoteSha** 6830b7d629b01d43975549871d0f9ba1ed969766

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pr2\_database

*PR2 database - Eukaryotic 18S rRNA sequences.*

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## Description

The PR2 database is provided as a data frame.

This is a join between the following tables:

- pr2\_main
- pr2\_taxonomy
- pr2\_sequence
- pr2\_metadata
- pr2\_traits
- pr2\_silva
- euribo

The metadata contains different types of fields

- gb\_ : originating from the GenBank entry
- eukref\_ : annotated by the Eukref project
- pr2\_ : annotated by pr2 such latitude and longitude
- eukribo\_ : information from the EukRibo database

Description of fields: <https://pr2-database.org/documentation/pr2-fields>

## Usage

```
pr2_database()
```

## Value

A data frame

## Examples

```
# Read the whole database
my_pr2 <- pr2_database()

# Select a specific genus
pr2_ostreo <- pr2_database()
pr2_ostreo <- dplyr::filter(pr2_ostreo , genus == "Ostreococcus")
pr2_ostreo <- dplyr::select(pr2_ostreo, pr2_accession, species)
head(pr2_ostreo)
```

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`pr2_taxonomy`*PR2 database - Taxonomy.*

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**Description**

The PR2 database taxonomy is provided as a data frame with the number of sequences for each taxon

**Usage**

```
pr2_taxonomy()
```

**Value**

A data frame

**Examples**

```
# Read the whole database taxonomy
my_pr2_taxo <- pr2_taxonomy()

# Select a specific genus
my_pr2_taxo <- dplyr::filter( my_pr2_taxo , genus == "Ostreococcus")
head(my_pr2_taxo)
```

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`run_app`*Run the PR2 Shiny application*

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**Description**

Allows to interact with the PR2 database:

\* Select and visualize taxonomy \* Select and download sequences based on length and sample type

**Usage**

```
run_app(
  onStart = NULL,
  options = list(),
  enableBookmarking = NULL,
  uiPattern = "/",
  ...
)
```

**Arguments**

onStart	A function that will be called before the app is actually run. This is only needed for shinyAppObj, since in the shinyAppDir case, a global .R file can be used for this purpose.
options	Named options that should be passed to the runApp call (these can be any of the following: "port", "launch.browser", "host", "quiet", "display.mode" and "test.mode"). You can also specify width and height parameters which provide a hint to the embedding environment about the ideal height/width for the app.
enableBookmarking	Can be one of "url", "server", or "disable". The default value, NULL, will respect the setting from any previous calls to <a href="#">enableBookmarking()</a> . See <a href="#">enableBookmarking()</a> for more information on bookmarking your app.
uiPattern	A regular expression that will be applied to each GET request to determine whether the ui should be used to handle the request. Note that the entire request path must match the regular expression in order for the match to be considered successful.
...	arguments to pass to golem_opts. See <code>'?golem::get_golem_options'</code> for more details.

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