

# Package: metapr2 (via r-universe)

July 15, 2024

**Title** Eukaryotic 18S rRNA metabarcode database

**Version** 2.1.1

**Description** Provides an interface to the metaPR2 database (current version = 1.0) which contains eukaryotic 18S rRNA metabarcodes. Many options for selecting samples are provided. Data can be displayed as maps, barplots, treemaps. Data can be searched and downloaded. See <https://pr2-database.org> for more information.

**License** MIT

**Encoding** UTF-8

**LazyData** true

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.2

**Imports** Biostings, blaster (>= 1.0.4), bslib, dplyr, DT, forcats, ggforce, ggplot2, leaflet, leaflet.minicharts, lubridate, markdown, patchwork, phyloseq, pkgload, plotly, pryr, purrr, qs, rio, scrypt, shiny, shinycssloaders, shinydisconnect, shinylogs, shinymanager, shinyvalidate, shinyWidgets, stringr, tidyr, treemapify, viridis

**Depends** R (>= 2.10)

**Suggests** testthat (>= 3.0.0)

**Config/testthat/edition** 3

**Remotes** manutammen/blaster

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

**RemoteUrl** <https://github.com/pr2database/metapr2-shiny>

**RemoteRef** HEAD

**RemoteSha** 90d13e3a11eda1529c11e895f78838ec82496694

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`run_app`*Launch metapr2 shiny app*

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**Description**

Launch metapr2 shiny app

**Usage**

```
run_app()
```

**Examples**

```
# Starts shiny application

## Not run:
metapr2::run_app()

## End(Not run)
```

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