

Package: bedrockbio (via r-universe)

February 6, 2026

Title Open-Access Computational Biology Datasets

Version 1.1.0

Description Efficiently access a curated library of open-access computational biology datasets. Datasets support predicate pushdown and projection to the cloud storage backend, enabling quick, iterative access to otherwise massive, unwieldy datasets.

Language en-US

License GPL (>= 3)

URL <https://bedrock.bio>,
<https://github.com/bedrock-bio/bedrock-bio-client>

BugReports <https://github.com/bedrock-bio/bedrock-bio-client/issues>

Depends R (>= 4.3)

Imports jsonlite, tidypolars

Additional_repositories <https://r-multiverse.r-universe.dev>

Encoding UTF-8

Roxygen list(markdown = TRUE)

RoxygenNote 7.3.3

Config/pak/sysreqs libicu-dev

Repository <https://r-multiverse-staging.r-universe.dev>

Date/Publication 2026-02-06 16:53:47 UTC

RemoteUrl <https://github.com/bedrock-bio/bedrock-bio-client>

RemoteRef v1.1.0

RemoteSha c24adc9905f06fa3f57b5fe0f11693b586addfce

RemoteSubdir r

Contents

list_datasets	2
load_dataset	2

Index	4
--------------	----------

list_datasets	<i>List available datasets in the Bedrock Bio library</i>
---------------	---

Description

List available datasets in the Bedrock Bio library

Usage

```
list_datasets()
```

Value

A character vector of dataset names

Examples

```
## Not run:
library(bedrockbio)
list_datasets()

## End(Not run)
```

load_dataset	<i>Lazily read a dataset from the Bedrock Bio library</i>
--------------	---

Description

Lazily read a dataset from the Bedrock Bio library

Usage

```
load_dataset(name)
```

Arguments

name	Dataset name (e.g., "ukb_ppp/pqtls")
------	--------------------------------------

Value

A lazy tibble

Examples

```
## Not run:
library(bedrockbio)
library(dplyr)

df <- load_dataset("ukb_ppp/pqt1s") |>
  filter(
    ancestry == "EUR",
    protein == "A0FGR8"
  ) |>
  select(
    chromosome,
    position,
    effect_allele,
    other_allele,
    beta,
    neg_log_10_p_value
  ) |>
  collect()

## End(Not run)
```

Index

`list_datasets`, [2](#)

`load_dataset`, [2](#)