

Package: bedrockbio (via r-universe)

February 12, 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.r-universe.dev>

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

RemoteRef v1.1.0

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RemoteSubdir r

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

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