

# Package: bedrockbio (via r-universe)

July 28, 2026

**Title** Open-Access Computational Biology Datasets

**Version** 2.0.0

**Description** Efficiently access the 'Bedrock Bio' library of open-access computational biology datasets. Lazily query datasets backed by 'DuckDB' and 'Apache Iceberg', with support for predicate pushdown and column projection to the cloud storage backend. This enables quick, iterative access to otherwise massive, unwieldy datasets without downloading them in full. See <<https://bedrock.bio>> for available datasets and documentation.

**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 (>= 4.2)

**Imports** curl, DBI, dbplyr, dplyr, duckdb, jsonlite

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

**Config/testthat/edition** 3

**OS\_type** unix

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Config/pak/sysreqs** libicu-dev libssl-dev

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

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

**RemoteRef** v2.0.0

**RemoteSha** 5b2e43628012d945a34d0fa725a448d9c476c1e2

**RemoteSubdir** r

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|                    |                                                                               |
|--------------------|-------------------------------------------------------------------------------|
| describe_namespace | <i>Describe a namespace: its name, citation, license, context, and tables</i> |
|--------------------|-------------------------------------------------------------------------------|

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Description

Describe a namespace: its name, citation, license, context, and tables

Usage

describe\_namespace(name)

Arguments

|      |                       |
|------|-----------------------|
| name | Namespace identifier. |
|------|-----------------------|

Value

A named list with name, citation, license, context, and tables (fully-qualified table identifiers). Use describe\_table() for per-table details.

Examples

```
## Not run:
library(bedrockbio)
describe_namespace("ukb_ppp")$tables

## End(Not run)
```

---

|                |                                                               |
|----------------|---------------------------------------------------------------|
| describe_table | <i>Describe a table: its context, columns, and partitions</i> |
|----------------|---------------------------------------------------------------|

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**Description**

Describe a table: its context, columns, and partitions

**Usage**

```
describe_table(name)
```

**Arguments**

|      |                   |
|------|-------------------|
| name | Table identifier. |
|------|-------------------|

**Value**

A named list with name, context, columns (each with name, type, description, nullable), and partitions (a named list of partition column to values and default). Filter on partition columns for fastest reads.

**Examples**

```
## Not run:  
library(bedrockbio)  
describe_table("ukb_ppp.pqtls")$name  
  
## End(Not run)
```

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|                 |                                                 |
|-----------------|-------------------------------------------------|
| list_namespaces | <i>List available namespaces (data sources)</i> |
|-----------------|-------------------------------------------------|

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**Description**

List available namespaces (data sources)

**Usage**

```
list_namespaces()
```

**Value**

A character vector of namespace identifiers.

**Examples**

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

## End(Not run)
```

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|             |                                                                    |
|-------------|--------------------------------------------------------------------|
| list_tables | <i>List available tables, optionally filtered to one namespace</i> |
|-------------|--------------------------------------------------------------------|

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**Description**

List available tables, optionally filtered to one namespace

**Usage**

```
list_tables(namespace = NULL)
```

**Arguments**

namespace      If given, return only that namespace's tables; otherwise all tables.

**Value**

A character vector of fully-qualified table identifiers.

**Examples**

```
## Not run:
library(bedrockbio)
list_tables("ukb_ppp")

## End(Not run)
```

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|            |                             |
|------------|-----------------------------|
| load_table | <i>Lazily query a table</i> |
|------------|-----------------------------|

---

**Description**

Lazily query a table

**Usage**

```
load_table(name)
```

**Arguments**

|      |                   |
|------|-------------------|
| name | Table identifier. |
|------|-------------------|

**Value**

A lazy tbl backed by DuckDB, compatible with dplyr verbs. Filter on partition columns (see `describe_table()`) for fastest reads.

**Examples**

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

load_table("dbSNP.vcf") |>
  filter(assembly == "GRCh38", chromosome == "22") |>
  select(rsid, position, ref_allele, alt_allele) |>
  head(5) |>
  collect()

## End(Not run)
```

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