# Package: rgbio (via r-universe)

October 7, 2026

**Title** High-Performance GenBank I/O using 'gb-io'

**Version** 0.4.0

**Description** Interfaces with the 'gb-io' Rust crate to provide fast reading and writing of GenBank files. Supports parsing of sequences, features, and metadata into R-friendly data structures.

**License** MIT + file LICENSE

**Encoding** UTF-8

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**Config/rextendr/version** 0.4.2

**SystemRequirements** Cargo (Rust's package manager), rustc >= 1.65.0, xz

**Depends** R (>= 4.2)

**Suggests** Biostrings, GenomicRanges, IRanges, S4Vectors, tibble, knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**Config/pak/sysreqs** xz-utils libclang-dev

**Repository** https://richardstoeckl.r-universe.dev

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**RemoteRef** v0.4.0

**RemoteSha** b96a0a9f89d571692fe9e1388d2274c03f19b49d

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## read_gbk *Read a GenBank file*

### Description

Reads one or more GenBank records and returns selected components in either Bioconductor, tidy, or base format.

### Usage

```
read_gbk(
  file,
  format = "bioconductor",
  sequences = TRUE,
  features = TRUE,
  metadata = TRUE,
  records = NULL,
  validate = TRUE
)
```

### Arguments

| | |
|---|---|
| file | Character path to a GenBank file. |
| format | Output format. One of "bioconductor", "tidy", or "base". |
| sequences | Logical; include sequence data. |
| features | Logical; include feature annotations. |
| metadata | Logical; include record metadata. |
| records | Integer indices or character accession/name selectors. |
| validate | Logical; validate parsed records. |

### Value

A variable object based on selected components. Returns either a single object or a named list with sequences, features, and/or metadata.

## read_genbank *Read a GenBank file*

### Description

Deprecated compatibility wrapper for read_gbk().

### Usage

```
read_genbank(file)
```

### Arguments

| | |
|---|---|
| file | Path to a GenBank file. |

### Value

Parsed records in legacy list format.

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## write_gbk *Write GenBank records*

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### Description

Writes GenBank records from sequence, feature, and metadata components.

### Usage

```
write_gbk(
  file,
  sequences,
  features = NULL,
  metadata = NULL,
  append = FALSE,
  validate = TRUE,
  line_width = 80
)
```

### Arguments

| | |
|---|---|
| file | Character path to output file. |
| sequences | DNAStringSet or named character vector. |
| features | GRanges with type and qualifiers in mcols(), or tidy feature table with columns type, start, end, strand, qualifiers. |
| metadata | DataFrame, data.frame, or list with record metadata. |
| append | Logical; append to file. |
| validate | Logical; validate inputs. |
| line_width | Integer sequence line width. |

### Value

Logical TRUE on success.

`write_genbank` *Write a GenBank file*

## Description

Deprecated compatibility wrapper for `write_gbk()`.

## Usage

```
write_genbank(file, sequence, features, metadata = list())
```

## Arguments

| | |
|---|---|
| `file` | Path to output file. |
| `sequence` | Sequence string. |
| `features` | Feature table with columns key, location, qualifiers. |
| `metadata` | Metadata list. |

## Value

Logical TRUE on success.

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