

# Package ‘genbankr’

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**Title** Parsing GenBank files into semantically useful objects

**Description** Reads Genbank files.

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**Depends** methods

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cds,GenBankRecord-method

*Annotation extraction api*

---

## Description

Accessor functions shared with the larger Bioconductor ecosystem.

## Usage

```
## S4 method for signature 'GenBankRecord'
cds(x)
```

```
## S4 method for signature 'GenBankRecord'
exons(x)
```

```
## S4 method for signature 'GenBankRecord'
genes(x)
```

```
## S4 method for signature 'GenBankRecord'
transcripts(x)
```

```
## S4 method for signature 'GenBankRecord'
getSeq(x, ...)
```

```
## S4 method for signature 'GenBankFile'
getSeq(x, ...)
```

```
## S4 method for signature 'GBAccession'
getSeq(x, ...)
```

```
## S4 method for signature 'GenBankRecord'
cdsBy(x, by = c("tx", "gene"))
```

```
## S4 method for signature 'GenBankRecord'
exonsBy(x, by = c("tx", "gene"))
```

```
## S4 method for signature 'GenBankRecord'
isCircular(x)
```

```
## S4 method for signature 'GenBankRecord'
seqinfo(x)
```

**Arguments**

x                    The object containing the annotations  
...                   unused.  
by                   character. Factor to group the resulting GRanges by.

**Value**

The expected types, GenomicRanges for most functions, a DNASTringSet for getSeq

**Examples**

```
gb = readGenBank(system.file("sample.gbk", package="genbankr"))  
cds(gb)  
exons(gb)  
genes(gb)
```

---

GBAccession-class      *GBAccession ID class*

---

**Description**

A class representing the (versioned) GenBank accession

**Usage**

```
GBAccession(id)
```

**Arguments**

id                    A versioned GenBank Accession id

**Value**

a GBAccession object.

**Examples**

```
id = GBAccession("U49845.1")  
## Not run: gb = readGenBank(id)
```

---

gbk-specific-api      *genbankr specific api*

---

## Description

Accessor functions specific to genbankr objects.

## Usage

```
accession(x, ...)

## S4 method for signature 'GenBankRecord'
accession(x)

definition(x, ...)

## S4 method for signature 'GenBankRecord'
definition(x)

locus(x, ...)

## S4 method for signature 'GenBankRecord'
locus(x)

vers(x, ...)

## S4 method for signature 'GenBankRecord'
vers(x)

sources(x, ...)

## S4 method for signature 'GenBankRecord'
sources(x)
```

## Arguments

x	A genbank annotation object
...	unused.

## Value

Character vectors for accession and vers

## Examples

```
gb = readGenBank(system.file("sample.gbk", package="genbankr"))
accession(gb)
vers(gb)
```

---

GenBankFile-class      *GenBank File*

---

**Description**

A resource class for use within the rtracklayer framework

Create a GenBankFile object.

**Usage**

```
GenBankFile(fil)
```

**Arguments**

`fil`                      character. Path to the genbank file

**Value**

A GenBankFile object

**Examples**

```
fil = GenBankFile(system.file("sample.gbk", package="genbankr"))
gb = import(fil)
```

---

GenBankRecord-class      *GenBank data objects*

---

**Description**

These objects represent GenBank annotations

**Examples**

```
gb = readGenBank(system.file("sample.gbk", package="genbankr"))
gb
```

---

```
import, GenBankFile, ANY, ANY-method
      Import genbank file
```

---

**Description**

Import a genbank file using the rtracklayer API.

**Usage**

```
## S4 method for signature 'GenBankFile,ANY,ANY'
import(con, format, text, ...)
```

**Arguments**

con	See import docs.
format	See import docs.
text	See import docs.
...	Arguments passed to readGenBank

**Value**

A GenBankRecord object.

---

```
intergenic      Extract intergenic regions from processed GenBank annotations
```

---

**Description**

Extract the intergenic regions from a set of GenBank annotations.

**Usage**

```
## S4 method for signature 'GenBankRecord'
intergenic(x)
```

**Arguments**

x	A GenBankRecord object
---	------------------------

**Value**

A GRanges for the intergenic regions, defined as regions not overlapping any genes defined in the annotations on either strand.

**Examples**

```
gb = readGenBank(system.file("sample.gbk", package="genbankr"))
intergenic(gb)
```

---

makeTxDbFromGenBank     *Create a TxDb from a GenBank record*

---

### Description

Create a TxDb object from a GenBankRecord.

### Usage

```
makeTxDbFromGenBank(gbr, reassign.ids = FALSE)

## S4 method for signature 'GenBankRecord'
makeTxDbFromGenBank(gbr, reassign.ids = FALSE)

## S4 method for signature 'GBAccession'
makeTxDbFromGenBank(gbr, reassign.ids = FALSE)
```

### Arguments

gbr                    A GenBankRecord or GBAccession object  
reassign.ids        logical. Passed down to makeTxDb

### Value

A TxDb object

### Examples

```
thing = readGenBank(system.file("unitTests/compjoin.gbk", package="genbankr"))
tx = makeTxDbFromGenBank(thing)
```

---

make\_gbrecord             *GenBank object constructors*

---

### Description

Constructors for GenBankRecord objects.

### Usage

```
make_gbrecord(rawgbk, verbose = FALSE)
```

### Arguments

rawgbk                list. The output of parseGenBank  
verbose               logical. Should informative messages be shown

### Value

A GenBankRecord object

**Examples**

```
prsed = parseGenBank(system.file("sample.gbk", package="genbankr"))
gb = make_gbrecord(prsed)
```

---

otherFeatures	<i>Retrieve 'other' features</i>
---------------	----------------------------------

---

**Description**

Retrieve the other features (not covered by a different accessor) from the set of annotations

**Usage**

```
otherFeatures(x)

## S4 method for signature 'GenBankRecord'
otherFeatures(x)
```

**Arguments**

x                    a GenBankRecord object

**Value**

A GRanges containing the features which don't fall into another category (ie not gene, exon, transcript, cds, or variant) annotated in the source file

**Examples**

```
gb = readGenBank(system.file("sample.gbk", package="genbankr"))
otherFeatures(gb)
```

---

parseGenBank	<i>Parse raw genbank file content</i>
--------------	---------------------------------------

---

**Description**

Parse genbank content and return a low-level list object containing each component of the file.

**Usage**

```
parseGenBank(file, text = readLines(file), partial = NA, verbose = FALSE,
  ret.anno = TRUE, ret.seq = TRUE)
```



**Arguments**

<code>file</code>	character. The file to be parsed. Ignored if <code>text</code> is specified
<code>text</code>	character. The text to be parsed.
<code>partial</code>	logical. If TRUE, features with non-exact boundaries will be included. Otherwise, non-exact features are excluded, with a warning if <code>partial</code> is NA (the default).
<code>verbose</code>	logical. Should informative messages be printed to the console as the file is being processed.
<code>ret.anno</code>	logical. Should the annotations in the GenBank file be parsed and included in the returned object. (Defaults to TRUE)
<code>ret.seq</code>	logical. Should the origin sequence (if present) in the GenBank file be included in the returned object. (Defaults to TRUE)

**Value**

if `ret.anno` is TRUE, a list containing the parsed contents of the file, suitable for passing to `make_gbrecord`. If `ret.anno` is FALSE, a `DNAStrngSet` object containing the origin sequence.

**Note**

This is a low level function not intended for common end-user use. In nearly all cases, end-users (and most developers) should call `readGenBank` or create a `GenBankFile` object and call `import` instead.

**Examples**

```
prsd = parseGenBank(system.file("sample.gbk", package="genbankr"))
```

---

<code>readGenBank</code>	<i>Read a GenBank File</i>
--------------------------	----------------------------

---

**Description**

Read a GenBank file from a local file, or retrieve and read one based on an accession number. See Details for exact behavior.

**Usage**

```
readGenBank(file, text = readLines(file), partial = NA, ret.seq = TRUE,
  verbose = FALSE)
```

**Arguments**

<code>file</code>	character or <code>GBAccession</code> . The path to the file, or a <code>GBAccession</code> object containing Nuccore versioned accession numbers. Ignored if <code>text</code> is specified.
<code>text</code>	character. The text of the file. Defaults to text within <code>file</code>
<code>partial</code>	logical. If TRUE, features with non-exact boundaries will be included. Otherwise, non-exact features are excluded, with a warning if <code>partial</code> is NA (the default).

ret.seq	logical. Should an object containing the raw ORIGIN sequence be created and returned. Defaults to TRUE. If FALSE, the sequence slot is set to NULL. See NOTE.
verbose	logical. Should informative messages be printed to the console as the file is processed. Defaults to FALSE.

### Details

If a GBAccession object is passed to file, the rentrez package is used to attempt to fetch full GenBank records for all ids in the

Often times, GenBank files don't contain exhaustive annotations. For example, files including CDS annotations often do not have separate transcript features. Furthermore, chromosomes are not always named, particularly in organisms that have only one. The details of how genbankr handles such cases are as follows:

In files where CDSs are annotated but individual exons are not, 'approximate exons' are defined as the individual contiguous elements within each CDS. Currently, no mixing of approximate and explicitly annotated exons is performed, even in cases where, e.g., exons are not annotated for some genes with CDS annotations.

In files where transcripts are not present, 'approximate transcripts' defined by the ranges spanned by groups of exons are used. Currently, we do not support generating approximate transcripts from CDSs in files that contain actual transcript annotations, even if those annotations do not cover all genes with CDS/exon annotations.

Features (gene, cds, variant, etc) are assumed to be contained within the most recent previous source feature (chromosome/physical piece of DNA). Chromosome name for source features (seqnames in the resulting GRanges/VRanges is determined as follows:

1. The 'chromosome' attribute, as is (e.g., "chr1");
2. the 'strain' attribute, combined with auto-generated count (e.g., "VR1814:1");
3. the 'organism' attribute, combined with auto-generated count (e.g. "Human herpesvirus 5:1").

In files where no origin sequence is present, importing variation features is not currently supported, as there is no easy/ self-contained way of determining the reference in those situations and the features themselves list only alt. If variation features are present in a file without origin sequence, those features are ignored with a warning.

Currently some information about from the header of a GenBank file, primarily reference and author based information, is not captured and returned. Please contact the maintainer if you have a direct use-case for this type of information.

### Value

A GenBankRecord object containing (most, see details) of the information within file/text Or a list of GenBankRecord objects in cases where a GBAccession vector with more than one ID in it is passed to file

### Note

We have endeavored to make this parser as efficient as easily possible. On our local machines, a 19MB genbank file takes 2-3 minutes to be parsed. That said, this function is not tested and likely not suitable for processing extremely large genbank files.

The origin sequence is always parsed when calling readGenBank, because it is necessary to generate a VRanges from variant features. So currently ret.seq=FALSE will not reduce parsing time, or maximum memory usage, though it will reduce memory usage by the final GenBankRecord object.

The lower-level `parseGenBank` does not parse the sequence at all via `ret.seq=FALSE`, but variant annotations will be excluded if `make_gbrecord` is called on the resulting parsed list.

### Examples

```
gb = readGenBank(system.file("sample.gb", package="genbankr"))
```

---

variants	<i>Retrieve variantion features</i>
----------	-------------------------------------

---

### Description

Extract the annotated variants from a `GenBankRecord` object

### Usage

```
variants(x)  
  
## S4 method for signature 'GenBankRecord'  
variants(x)
```

### Arguments

x                    a `GenBankRecord` object

### Value

A `VRanges` containing the variations annotated in the source file

### Examples

```
gb = readGenBank(system.file("sample.gb", package="genbankr"))  
variants(gb)
```

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