

# Package ‘bedbaser’

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**Title** A BEDbase client

**Version** 0.99.23

**Description** A client for BEDbase. bedbaser provides access to the API at [api.bedbase.org](https://api.bedbase.org). It also includes convenience functions to import BED files into GRanges objects and BEDsets into GRangesLists.

**URL** <https://github.com/waldronlab/bedbaser>

**BugReports** <https://github.com/waldronlab/bedbaser/issues>

**biocViews** Software, DataImport, ThirdPartyClient

**License** Artistic License 2.0

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## Contents

bedbaser-package . . . . .	2
bb_beds_in_bedset . . . . .	3
bb_bed_text_search . . . . .	3
bb_example . . . . .	4
bb_list_beds . . . . .	5
bb_list_bedsets . . . . .	5
bb_metadata . . . . .	6
bb_save . . . . .	7
bb_to_granges . . . . .	7
bb_to_grangeslist . . . . .	8
BEDbase . . . . .	9
BEDbase-class . . . . .	10
getCache,BEDbase-method . . . . .	10
operations,BEDbase-method . . . . .	11
schemas,BEDbase-method . . . . .	12
setCache,BEDbase-method . . . . .	12
tags,BEDbase-method . . . . .	13
<b>Index</b>	<b>14</b>

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bedbaser-package      *bedbaser: A BEDbase client*

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## Description

A client for BEDbase. bedbaser provides access to the API at [api.bedbase.org](http://api.bedbase.org). It also includes convenience functions to import BED files into GRanges objects and BEDsets into GRangesLists.

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## See Also

Useful links:

- <https://github.com/waldronlab/bedbaser>
- Report bugs at <https://github.com/waldronlab/bedbaser/issues>

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bb\_beds\_in\_bedset      *Get BEDs associated with BEDset*

---

**Description**

Return a tibble of BED files in BEDset given its id.

**Usage**

```
bb_beds_in_bedset(bedbase, bedset_id)
```

**Arguments**

bedbase	BEDbase() object
bedset_id	integer(1) BEDset record identifier

**Value**

tibble of BED files in BEDset

**Examples**

```
bedbase <- BEDbase()
ex_bedset <- bb_example(bedbase, "bedset")
bb_beds_in_bedset(bedbase, ex_bedset$id)
```

---

bb\_bed\_text\_search      *Search BED files by text*

---

**Description**

Return all available BED files ranked by relevance to the keywords. Uses the [bedhost API](#) default of 10 records and an initial offset of 0.

**Usage**

```
bb_bed_text_search(bedbase, query, limit = 10, offset = 0)
```

**Arguments**

bedbase	BEDbase() object
query	character() keywords to search
limit	integer(1) (default 10) maximum number of results
offset	integer(1) (default 0) page offset of results

**Value**

tibble of results

**Examples**

```
bedbase <- BEDbase()
bb_bed_text_search(bedbase, "hg38")
```

---

bb\_example

*Get the example BED file or BEDset with metadata*

---

**Description**

Get the example BED file or BEDset available through [bedhost](#). Useful for an initial exploration of bedbaser with an example BED file and BEDset in BEDbase.

**Usage**

```
bb_example(bedbase, rec_type = c("bed", "bedset"))
```

**Arguments**

bedbase	BEDbase() object
rec_type	character(1) bed or bedset

**Value**

list() bed files or bedsets

**Examples**

```
bedbase <- BEDbase()
ex_bed <- bb_example(bedbase, "bed")
str(ex_bed)
ex_bedset <- bb_example(bedbase, "bedset")
str(ex_bedset)
```

---

bb_list_beds	<i>List BEDs</i>
--------------	------------------

---

**Description**

List BED files available through [bedhost](#). By default uses the bedhost default of 1000 records and an initial offset of 0.

**Usage**

```
bb_list_beds(bedbase, genome = NULL, bed_type = NULL, limit = 1000, offset = 0)
```

**Arguments**

bedbase	BEDbase() object
genome	character(1) (default NULL) genome keyword
bed_type	character(1) (default NULL) bed file type
limit	integer(1) (default 1000) maximum records
offset	integer(1) (default 0) page token of records

**Value**

[tibble](#) of BED records

**Examples**

```
bedbase <- BEDbase()
bb_list_beds(bedbase)
```

---

bb_list_bedsets	<i>List BEDsets</i>
-----------------	---------------------

---

**Description**

List BEDsets available through [bedhost](#). By default uses the bedhost default of 1000 records and an initial offset of 0.

**Usage**

```
bb_list_bedsets(bedbase, query = NULL, limit = 1000, offset = 0)
```

**Arguments**

bedbase	BEDbase() object
query	character() (default NULL) keyword
limit	integer(1) (default 1000) maximum records
offset	integer(1) (default 0) page token of records

**Value**

[tibble](#) of BEDset records

**Examples**

```
bedbase <- BEDbase()
bb_list_bedsets(bedbase)
```

---

**bb\_metadata**
*Get metadata for a BED file or BEDset*


---

**Description**

Get metadata for a BED file or BEDset given its id. Abort if not found or id is not not 32 characters.

**Usage**

```
bb_metadata(bedbase, id, full = FALSE)
```

**Arguments**

bedbase	BEDbase() object
id	integer(1) record or object identifier
full	logical(1) (default FALSE) include full record with stats, files, and metadata

**Value**

list() metadata

**Examples**

```
bedbase <- BEDbase()

ex_bed <- bb_example(bedbase, "bed")
bb_metadata(bedbase, ex_bed$id)

ex_bedset <- bb_example(bedbase, "bedset")
bb_metadata(bedbase, ex_bedset$id)
```

---

bb_save	<i>Save a BED file or BEDset to a path given an id</i>
---------	--

---

### Description

Save a BED file or a BEDset to a local path. If the path does not exist, `bb_save()` will abort.

### Usage

```
bb_save(bedbase, bed_or_bedset_id, path, file_type = "bed", quietly = TRUE)
```

### Arguments

bedbase	BEDbase() object
bed_or_bedset_id	integer(1) BED or BEDset record identifier
path	character(1) directory to save file
file_type	character(1) (default "bed") bed, bigbed, etc.
quietly	logical(1) (default TRUE) display messages

### Value

An invisible NULL

### Examples

```
bedbase <- BEDbase()
ex_bed <- bb_example(bedbase, "bed")
bb_save(bedbase, ex_bed$id, tempdir())
```

---

bb_to_granges	<i>Create a GRanges object given a BED id</i>
---------------	---

---

### Description

Create a GRanges object given a BED id. Columns and types are generated for broad and narrow peak files. Known columns and types can be passed as a named vector through `extra_cols`. Otherwise, `bb_to_granges()` attempts to determine the column type and substitute dummy column names.

**Usage**

```
bb_to_granges(
  bedbase,
  bed_id,
  file_type = "bed",
  extra_cols = NULL,
  quietly = TRUE
)
```

**Arguments**

bedbase	BEDbase() object
bed_id	integer(1) BED record identifier
file_type	character(1) bed or bigbed
extra_cols	character() (default NULL) extra column names to construct GRanges objects
quietly	logical(1) (default TRUE) display messages

**Value**

[GRanges](#)

**Examples**

```
bedbase <- BEDbase()
ex_bed <- bb_example(bedbase, "bed")
bb_to_granges(bedbase, ex_bed$id)
```

---

bb_to_grangeslist	<i>Create a GRangesList object given a BEDset id</i>
-------------------	--

---

**Description**

Create a GRangesList object given a BEDset id

**Usage**

```
bb_to_grangeslist(bedbase, bedset_id, quietly = TRUE)
```

**Arguments**

bedbase	BEDbase() object
bedset_id	integer(1) BEDset record identifier
quietly	logical(1) (default TRUE) display messages

**Value**

GRangesList

**Examples**

```
bedbase <- BEDbase()
bb_to_grangeslist(bedbase, "lola_hg38_ucsc_features")
```

BEDbase

*An R client for BEDbase***Description**

bedbaser exposes the [bedhost API](#) and includes convenience functions for common tasks, such as to import a BED file by id into a GRanges object and a BEDset by its id into a GRangesList.

**Usage**

```
BEDbase(cache_path, quietly = FALSE)

getCache(x, cache_type = c("bedfiles", "bedsets"))

setCache(x, cache_path, quietly = TRUE)
```

**Arguments**

cache_path	character(1)
quietly	logical(1) (default TRUE) display messages
x	BEDbase() object
cache_type	character(1) bedfiles or bedsets

**Details**

BEDbase() creates a cache similar to that of the [Geniml BBClient's cache](#).

The convenience functions are as follows

- `bedbaser::BEDbase()`: API service constructor
- `bedbaser::getCache()`: Retrieve cache
- `bedbaser::setCache()`: Set path to cache
- `bedbaser::bb_example()`: Retrieve an example BED file or BEDset
- `bedbaser::bb_metadata()`: Retrieve metadata for a BED file or BEDset
- `bedbaser::bb_list_beds()`: List all BED files
- `bedbaser::bb_list_bedsets()`: List all BEDsets

- `bedbaser::bb_beds_in_bedset()`: List BED files in BEDset
- `bedbaser::bb_bed_text_search()`: Search BED files by text
- `bedbaser::bb_to_granges()`: Create a GRanges object from a BED id
- `bedbaser::bb_to_grangeslist()`: Create a GRangesList from a BEDset id
- `bedbaser::bb_save()`: Save a BED file to a path.

**Value**

BEDbase object

**Examples**

```
bedbase <- BEDbase(cache_path = tempdir())
ex_bed <- bb_example(bedbase, "bed")
bb_metadata(bedbase, ex_bed$id)
```

---

BEDbase-class

*BEDbase class*

---

**Description**

BEDbase class

**Value**

BEDbase class instance

---

*getCache, BEDbase-method*

*Return cache path*

---

**Description**

Return cache path

**Usage**

```
## S4 method for signature 'BEDbase'
getCache(x, cache_type = c("bedfiles", "bedsets"))
```

**Arguments**

`x` BEDbase() object  
`cache_type` character(1) bedfiles or bedsets

**Value**

BiocFileCache() object of BED files

**Examples**

```
bedbase <- BEDbase(tempdir())
getCache(bedbase, "bedfiles")
```

---

operations,BEDbase-method

*Display API functions*

---

**Description**

Display functions defined through the **bedhost API** and their corresponding parameters.

**Usage**

```
## S4 method for signature 'BEDbase'
operations(x, ..., .deprecated = FALSE)
```

**Arguments**

x	BEDbase() object
...	other options
.deprecated	(default FALSE) if deprecated

**Value**

list() API endpoints

**Examples**

```
bedbase <- BEDbase()
operations(bedbase)
```

---

 schemas,BEDbase-method

*Display bedhost API schemas*


---

### Description

Display bedhost API schemas

### Usage

```
## S4 method for signature 'BEDbase'
schemas(x)
```

### Arguments

x                   BEDbase() object

### Value

list() API endpoints

### Examples

```
bedbase <- BEDbase()
schemas(bedbase)
```

---

 setCache,BEDbase-method

*Set cache along path*


---

### Description

Create a cache for BED files and BEDsets like [Geniml BBClient's cache](#).

### Usage

```
## S4 method for signature 'BEDbase'
setCache(x, cache_path, quietly = TRUE)
```

### Arguments

x                   BEDbase() object  
 cache\_path       character(1)  
 quietly           logical(1) (default TRUE) display messages

**Value**

[BiocFileCache\(\)](#) object of BED files

**Examples**

```
bedbase <- BEDbase(tempdir())
bedbase <- setCache(bedbase, "/tmp")
```

---

tags, BEDbase-method     *Display functions for a tag*

---

**Description**

Display functions available through the API associated with a tag keyword in [bedhost](#).

**Usage**

```
## S4 method for signature 'BEDbase'
tags(x, .tags, .deprecated = FALSE)
```

**Arguments**

x	BEDbase() object
.tags	character() tags for filtering operations
.deprecated	(default FALSE) if deprecated

**Value**

list() API endpoints

**Examples**

```
bedbase <- BEDbase()
unique(tags(bedbase)$tag)
tags(bedbase, "bedset")
```

# Index

## \* **internal**

- bedbaser-package, [2](#)
- .BEDbase (BEDbase-class), [10](#)
  
- bb\_bed\_text\_search, [3](#)
- bb\_beds\_in\_bedset, [3](#)
- bb\_example, [4](#)
- bb\_list\_beds, [5](#)
- bb\_list\_bedsets, [5](#)
- bb\_metadata, [6](#)
- bb\_save, [7](#)
- bb\_to\_granges, [7](#)
- bb\_to\_grangeslist, [8](#)
- BEDbase, [9](#)
- BEDbase-class, [10](#)
- bedbaser (bedbaser-package), [2](#)
- bedbaser-package, [2](#)
- BiocFileCache(), [13](#)
  
- getCache (BEDbase), [9](#)
- getCache, BEDbase-method, [10](#)
- GRanges, [8](#)
- GRangesList, [9](#)
  
- operations, BEDbase-method, [11](#)
  
- schemas, BEDbase-method, [12](#)
- setCache (BEDbase), [9](#)
- setCache, BEDbase-method, [12](#)
  
- tags, BEDbase-method, [13](#)
- tibble, [3-6](#)