

# Package ‘rbhl’

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**Title** Interface to the 'Biodiversity' 'Heritage' Library

**Description** Interface to 'Biodiversity' 'Heritage' Library ('BHL') (<<http://www.biodiversitylibrary.org/>>) 'API' (<<http://www.biodiversitylibrary.org/api2/docs/docs.html>>). 'BHL' is a repository of 'digitized' literature on 'biodiversity' studies, including 'floras', research papers, and more.

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**Author** Scott Chamberlain [aut, cre]

**Maintainer** Scott Chamberlain <[myrmecocystus@gmail.com](mailto:myrmecocystus@gmail.com)>

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---

 rbhl-package

*R interface to the Biodiversity Heritage Library API.*


---

## Description

R interface to the Biodiversity Heritage Library API.

**Details**

You need an API key to use the Biodiversity Heritage Library API. Get your BHL API key at <http://www.biodiversitylibrary.org/getapikey.aspx>. Put your API key in your .Rprofile file using e.g., `options(BioHerLibKey = "YOURBHLAPIKEY")`, and the functions within this package will be able to use your API key without you having to enter it every time you run a search.

See [rbhl-defunct](#) for defunct functions.

**Author(s)**

Scott Chamberlain <[myrmecocystus@gmail.com](mailto:myrmecocystus@gmail.com)>

---

bhl_authorsearch	<i>Return a list of authors that match (fully or partially) the specified search string.</i>
------------------	--

---

**Description**

The names searched are those contained in MARC 100a, 110a, 111a, 700a, 710a, and 711a library records.

**Usage**

```
bhl_authorsearch(name = NULL, as = "table", key = NULL, ...)
```

**Arguments**

name	full or partial name of the author for which to search (last name listed first, i.e. 'Darwin, Charles') (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that <code>as="table"</code> can give different data format back depending on the function - for example, sometimes a <code>data.frame</code> and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as <code>BHL_KEY</code> or from .Rprofile as <code>bhl_key</code> .
...	Curl options passed on to <code>curl::HttpClient()</code>

**Examples**

```
## Not run:
bhl_authorsearch(name='dimmock')
bhl_authorsearch(name='Jones')

## End(Not run)
```

---

bhl\_bioherlib                      *Search BHL across many API methods.*

---

## Description

Search BHL across many API methods.

## Usage

```
bhl_bioherlib(method = "GetPageMetadata", pageid = NULL, ocr = FALSE,
              names = FALSE, as = "table", key = NULL, ...)
```

## Arguments

method	The API method to use.
pageid	The identifier of an individual page in a scanned book.
ocr	return ocr text of the page (logical). Default: FALSE
names	return the names that appear on the page (logical). Default: FALSE
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

## Examples

```
## Not run:
bhl_bioherlib(method='GetPageMetadata', pageid=1328690, ocr=TRUE,
              names=TRUE)
bhl_bioherlib(method='GetPageMetadata', pageid=1328690, ocr=TRUE,
              names=TRUE, as="xml")
bhl_bioherlib(method='GetPageMetadata', pageid=1328690, ocr=TRUE,
              names=TRUE, as="list")

## End(Not run)
```

---

bhl\_booksearch                      *Search for titles and items in BHL.*

---

## Description

Search criteria includes title, author last name, volume, edition, year of publication, subject, language code, and collection identifier. Valid language codes and collection identifiers can be obtained from the `getlanguages` and `getcollections` functions. If year of publication is specified, it should be a 4-digit year. To execute a search, you must supply at least a title, author last name, or collection identifier.

## Usage

```
bhl_booksearch(title = NULL, lname = NULL, volume = NULL,
               edition = NULL, year = NULL, collectionid = NULL, language = NULL,
               as = "table", key = NULL, ...)
```

## Arguments

title	string to search for in the title (character)
lname	last name to search for (character)
volume	volume to search for (numeric)
edition	edition to search for (character)
year	year to search for, four characters, e.g. 1970 (numeric)
collectionid	collection identifier to search for (numeric)
language	language to search for (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that <code>as="table"</code> can give different data format back depending on the function - for example, sometimes a <code>data.frame</code> and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your <code>.Renvi</code> on as <code>BHL_KEY</code> or from <code>.Rprofile</code> as <code>bhl_key</code> .
...	Curl options passed on to <code>curl::HttpClient()</code>

## Note

Use `bhl_getcollections()` or `bhl_getlanguages()` to get acceptable terms

## Examples

```
## Not run:
bhl_booksearch(title='Selborne', lname='White', volume=2, edition='new',
               year=1825, collectionid=4, language='eng')
bhl_booksearch(title='evolution', year=2000, as='json')
bhl_booksearch('evolution', year=2000, as='xml')
```

```
bhl_booksearch('evolution', year=2000, as="list")
## End(Not run)
```

---

bhl_getauthorparts	<i>Return a list of parts (articles, chapters, etc) associated with a given BHL author identifier. Unless the identifier for a particular BHL author record is known in advance, this method should be used in combination with the AuthorSearch method.</i>
--------------------	--

---

### Description

Note: haven't seen examples for this function that work yet...

### Usage

```
bhl_getauthorparts(creatorid, as = "table", key = NULL, ...)
```

### Arguments

creatorid	BHL identifier for a particular author (numeric)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

### Examples

```
## Not run:
# bhl_getauthorparts(147)
# bhl_getauthorparts(39120, as='json')
# bhl_getauthorparts(39120, as='xml')
# bhl_getauthorparts(39120, as='list')

## End(Not run)
```

---

bhl\_getauthortitles     *Return a list of titles associated with a given BHL author identifier.*

---

### Description

Unless the identifier for a particular BHL author record is known in advance, this method should be used in combination with the AuthorSearch method.

### Usage

```
bhl_getauthortitles(creatorid, as = "table", key = NULL, ...)
```

### Arguments

creatorid	BHL identifier for a particular author (numeric)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

### Examples

```
## Not run:
bhl_getauthortitles(1970)
bhl_getauthortitles(1970, as='json')
bhl_getauthortitles(1970, as='xml')
bhl_getauthortitles(1970, as='list')

## End(Not run)
```

---

bhl\_getcollections     *Get a list of collections which are used to group titles and items. A single collection may contain either titles or items, but not both.*

---

### Description

Get a list of collections which are used to group titles and items. A single collection may contain either titles or items, but not both.

### Usage

```
bhl_getcollections(as = "table", key = NULL, ...)
```

**Arguments**

as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getcollections()
bhl_getcollections(as = 'list')
bhl_getcollections(as = 'json')
bhl_getcollections(as = 'xml')

## End(Not run)
```

---

bhl\_getinstitutions    *GetInstitutions data*

---

**Description**

GetInstitutions data

**Usage**

```
bhl_getinstitutions(as = "table", key = NULL, ...)
```

**Arguments**

as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Details**

Get a list of institutions which have contributed to BHL in some way. These institutions may fill roles such as contributors, rights holders, and scanning institutions.



**Examples**

```
## Not run:
bhl_getinstitutions()

## End(Not run)
```

---

```
bhl_getitembyidentifier
```

*Find and return metadata about an item or items that match a specific identifier.*

---

**Description**

If you know the Internet Archive identifier for an item, use this method to look up the equivalent item in BHL.

**Usage**

```
bhl_getitembyidentifier(type = NULL, value = NULL, as = "table",
  key = NULL, ...)
```

**Arguments**

type	the type of identifier (barcode or ia) (character)
value	the identifier value (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi')
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi',
  as='json')
bhl_getitembyidentifier(type='ia', value='animalkingdomarr03cuvi',
  as='xml')

## End(Not run)
```

---

bhl\_getitemmetadata *Return metadata about an item.*

---

## Description

You may choose to include a list of the item's pages.

## Usage

```
bhl_getitemmetadata(itemid = NULL, pages = TRUE, ocr = FALSE,
  parts = FALSE, as = "table", key = NULL, ...)
```

## Arguments

itemid	item id (character)
pages	return the items pages (TRUE/FALSE)
ocr	(logical) TRUE to return the ocr for the item's pages. Setting this to TRUE apparently doesn't return any actual ocr text, but leaving parameter here for now.
parts	(logical) TRUE to return the item's parts. Setting this to TRUE apparently doesn't return any parts text, but leaving parameter here for now.
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

## Examples

```
## Not run:
bhl_getitemmetadata('16800', TRUE)
bhl_getitemmetadata('16800', TRUE, as='xml')
bhl_getitemmetadata('16800', TRUE, as='json')
bhl_getitemmetadata('16800', TRUE, as='list')

# bhl_getitemmetadata(20419, pages=FALSE, parts=TRUE)

## End(Not run)
```

---

bhl\_getitempages      *Return a list of an item's pages.*

---

### Description

Return a list of an item's pages.

### Usage

```
bhl_getitempages(itemid, ocr = FALSE, as = "table", key = NULL, ...)
```

### Arguments

itemid	the item id (character)
ocr	return ocr text of the page (TRUE/FALSE)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

### Examples

```
## Not run:  
bhl_getitempages('16800')  
bhl_getitempages('16800', as='json')  
bhl_getitempages('16800', as='xml')  
  
# Return ocr text  
bhl_getitempages('16800', TRUE)  
  
## End(Not run)
```

---

bhl\_getitemparts      *Return a list of an item's parts.*

---

### Description

Return a list of an item's parts.

### Usage

```
bhl_getitemparts(itemid, as = "table", key = NULL, ...)
```

**Arguments**

itemid	the item id (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getitemparts(35600)
bhl_getitemparts(35600, 'json')
bhl_getitemparts(35600, 'xml')

## End(Not run)
```

---

bhl_getlanguages	<i>Get a list of languages in which materials in BHL have been written.</i>
------------------	---

---

**Description**

Get a list of languages in which materials in BHL have been written.

**Usage**

```
bhl_getlanguages(as = "table", key = NULL, ...)
```

**Arguments**

as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getlanguages()
bhl_getlanguages('json')
bhl_getlanguages('xml')
bhl_getlanguages('list')

## End(Not run)
```

---

bhl\_getpagemetadadata *Return metadata about a page.*

---

**Description**

You may choose to include the OCR text and a list of names found on the page.

**Usage**

```
bhl_getpagemetadadata(page = NULL, ocr = FALSE, names = FALSE,
  as = "table", key = NULL, ...)
```

**Arguments**

page	page number to get
ocr	return ocr text of the page (TRUE/FALSE)
names	return the names that appear on the page (TRUE/FALSE)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getpagemetadadata(page=1328690, ocr=TRUE)
bhl_getpagemetadadata(page=1328690, ocr=TRUE, as='json')
bhl_getpagemetadadata(page=1328690, ocr=TRUE, as='xml')
bhl_getpagemetadadata(page=1328690, ocr=TRUE, as='list')

## End(Not run)
```

---

bhl\_getpagenames      *Return a list of names that appear on a page.*

---

### Description

Return a list of names that appear on a page.

### Usage

```
bhl_getpagenames(page = NULL, as = "table", key = NULL, ...)
```

### Arguments

page	page number to get
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

### Examples

```
## Not run:
bhl_getpagenames('1328690')
bhl_getpagenames('1328690', 'json')
bhl_getpagenames('1328690', 'list')

## End(Not run)
```

---

bhl\_getpageocrtext      *Return the OCR-generated text of a page.*

---

### Description

Return the OCR-generated text of a page.

### Usage

```
bhl_getpageocrtext(page = NULL, as = "table", key = NULL, ...)
```

**Arguments**

page	page number to get
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getpageocrtext(page=1328690)
bhl_getpageocrtext(1328690, 'json')

## End(Not run)
```

---

bhl_getpartbibtex	<i>Return a citation for a part, using the BibTeX format.</i>
-------------------	---

---

**Description**

Return a citation for a part, using the BibTeX format.

**Usage**

```
bhl_getpartbibtex(partid, as = "list", key = NULL, ...)
```

**Arguments**

partid	The identifier of an individual part (article, chapter, etc) (numeric)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getpartbibtex(1000)
bhl_getpartbibtex(1000, 'json')

## End(Not run)
```

---

**bhl\_getpartbyidentifier**
*Return a list of the identifiers of all unpublished items.*


---

### Description

Return a list of the identifiers of all unpublished items.

### Usage

```
bhl_getpartbyidentifier(type = NULL, value = NULL, as = "table",
  key = NULL, ...)
```

### Arguments

type	The type of identifier (doi, oclc, issn, isbn, lccn, ddc, nal, nlm, coden)
value	The identifier value
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

### Examples

```
## Not run:
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12')
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12', as='json')
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12', as='xml')
bhl_getpartbyidentifier('doi', '10.4039/Ent38406-12', as='list')

## End(Not run)
```

---

**bhl\_getpartmetadata**    *Return a list of an item's pages.*


---

### Description

Return a list of an item's pages.

### Usage

```
bhl_getpartmetadata(partid, key = NULL, ...)
```



**Arguments**

partid	The identifier of an individual part (article, chapter, etc) (numeric)
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getpartmetadata(10409)

## End(Not run)
```

---

bhl_getpartnames	<i>Return a list of scientific names associated with a part.</i>
------------------	--

---

**Description**

Return a list of scientific names associated with a part.

**Usage**

```
bhl_getpartnames(partid, as = "table", key = NULL, ...)
```

**Arguments**

partid	The identifier of an individual part (article, chapter, etc) (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getpartnames(7443)
bhl_getpartnames(7443, "xml")
bhl_getpartnames(7443, "json")
bhl_getpartnames(7443, "list")

## End(Not run)
```

---

`bhl_getsubjectparts`    *Return a list of parts (articles, chapters, etc) associated with a subject.*

---

### Description

Note: haven't seen examples for this function that work yet...

### Usage

```
bhl_getsubjectparts(subject = NULL, as = "table", key = NULL, ...)
```

### Arguments

<code>subject</code>	the full or partial subject for which to search (character)
<code>as</code>	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that <code>as="table"</code> can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
<code>key</code>	Your BHL API key, either enter, or loads from your <code>.Renvirom</code> as <code>BHL_KEY</code> or from <code>.Rprofile</code> as <code>bhl_key</code> .
<code>...</code>	Curl options passed on to <code>curl::HttpClient()</code>

### Examples

```
## Not run:
bhl_getsubjectparts('frogs')
bhl_getsubjectparts('diptera', 'xml')
bhl_getsubjectparts('diptera', 'json')

## End(Not run)
```

---

`bhl_getsubjecttitles`    *Return a list of titles associated with a subject.*

---

### Description

Return a list of titles associated with a subject.

### Usage

```
bhl_getsubjecttitles(subject = NULL, as = "table", key = NULL, ...)
```

**Arguments**

subject	the full or partial subject for which to search (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getsubjecttitles('diptera')
bhl_getsubjecttitles('diptera', 'xml')
bhl_getsubjecttitles('diptera', 'json')

## End(Not run)
```

---

bhl\_gettitlebibTex      *Return a citation for a title, using the BibTeX format.*

---

**Description**

Return a citation for a title, using the BibTeX format.

**Usage**

```
bhl_gettitlebibTex(titleid = NULL, as = "list", key = NULL, ...)
```

**Arguments**

titleid	the identifier of an individual title (numeric)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_gettitlebibTex(1726)
bhl_gettitlebibTex(1726, 'json')

## End(Not run)
```

---

bhl\_gettitlebyidentifier

*Find and return metadata about a title or titles that match a specific identifier.*

---

### Description

Find and return metadata about a title or titles that match a specific identifier.

### Usage

```
bhl_gettitlebyidentifier(type = NULL, value = NULL, as = "table",
  key = NULL, ...)
```

### Arguments

type	the type of identifier (oclc, issn, isbn, lccn, ddc, nal, nlm, coden) character
value	the identifier value (numeric)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

### Examples

```
## Not run:
bhl_gettitlebyidentifier('oclc', 2992225)
bhl_gettitlebyidentifier('oclc', 2992225, 'json')
bhl_gettitlebyidentifier('oclc', 2992225, 'xml')

## End(Not run)
```

---

bhl\_gettitleitems

*Return a list of a title's items (books).*

---

### Description

Return a list of a title's items (books).

### Usage

```
bhl_gettitleitems(titleid, as = "table", key = NULL, ...)
```

**Arguments**

titleid	the identifier of an individual title (numeric)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_gettitleitems(1726)
bhl_gettitleitems(1726, as='xml')
bhl_gettitleitems(1726, as='list')

## End(Not run)
```

---

bhl\_gettitlemetadata *Get title metadata*

---

**Description**

Return metadata about a title. You may choose to include a list of the items (books) associated with the title.

**Usage**

```
bhl_gettitlemetadata(titleid = NA, items = FALSE, as = "list",
  key = NULL, ...)
```

**Arguments**

titleid	the identifier of an individual title (numeric)
items	(logical) TRUE or FALSE (default) to include items
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

## Examples

```
## Not run:
bhl_gettitlemetadata(1726, TRUE)
bhl_gettitlemetadata(1726, as='list')
bhl_gettitlemetadata(1726, as='xml')

## End(Not run)
```

---

bhl\_getunpublisheditems

*Return a list of the identifiers of all unpublished items.*

---

## Description

Return a list of the identifiers of all unpublished items.

## Usage

```
bhl_getunpublisheditems(as = "table", key = NULL, ...)
```

## Arguments

as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviro as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>curl::HttpClient()</code>

## Examples

```
## Not run:
bhl_getunpublisheditems()
bhl_getunpublisheditems('xml')
bhl_getunpublisheditems('json')

## End(Not run)
```

---

`bhl_getunpublishedparts`

*Return a list of the identifiers of all unpublished parts (articles, chapters, etc).*

---

**Description**

Return a list of the identifiers of all unpublished parts (articles, chapters, etc).

**Usage**

```
bhl_getunpublishedparts(as = "table", key = NULL, ...)
```

**Arguments**

<code>as</code>	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that <code>as="table"</code> can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
<code>key</code>	Your BHL API key, either enter, or loads from your <code>.Renviron</code> as <code>BHL_KEY</code> or from <code>.Rprofile</code> as <code>bhl_key</code> .
<code>...</code>	Curl options passed on to <code>curl::HttpClient()</code>

**Examples**

```
## Not run:  
bhl_getunpublishedparts()  
bhl_getunpublishedparts('json')  
bhl_getunpublishedparts('xml')  
  
## End(Not run)
```

---

`bhl_getunpublishedtitles`

*Return a list of the identifiers of all unpublished titles.*

---

**Description**

Return a list of the identifiers of all unpublished titles.

**Usage**

```
bhl_getunpublishedtitles(as = "table", key = NULL, ...)
```

**Arguments**

as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_getunpublishedtitles()
bhl_getunpublishedtitles('json')
bhl_getunpublishedtitles('xml')

## End(Not run)
```

---

bhl_namecount	<i>Return the number of unique names found on pages in BHL.</i>
---------------	---

---

**Description**

Names both with and without NameBank identifiers are counted.

**Usage**

```
bhl_namecount(startdate = NULL, enddate = NULL, as = "table",
  key = NULL, ...)
```

**Arguments**

startdate	start date of range between which to count names (optional)
enddate	end date of range between which to count names (optional)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Details**

**BEWARE:** this API call can take a long time. They are likely working on speeding up the service, but slow for now.



**Examples**

```
## Not run:
bhl_namecount(startdate = '12/25/2009', enddate = '12/27/2009')
bhl_namecount(startdate = '10/15/2009', enddate = '10/17/2009', as='json')

## End(Not run)
```

---

bhl_namegetdetail	<i>Get basic title, item, and page metadata for each page on which the specified name appears.</i>
-------------------	--

---

**Description**

Get basic title, item, and page metadata for each page on which the specified name appears.

**Usage**

```
bhl_namegetdetail(namebankid = NULL, name = NULL, as = "table",
  key = NULL, ...)
```

**Arguments**

namebankid	(not used if 'name' specified) NameBank identifier for a name (numeric)
name	(not used if 'namebankid' specified) a complete name string (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
# bhl_namegetdetail(namebankid = 3501464)
# bhl_namegetdetail(name = 'poa annua')

## End(Not run)
```

---

bhl_namelist	<i>List the unique names.</i>
--------------	-------------------------------

---

### Description

By using the `startrow` and `batchsize` parameters appropriately, you can pull the list all at once, or in batches (i.e. 1000 names at a time). Names both with and without NameBank identifiers are returned.

### Usage

```
bhl_namelist(startrow = NULL, batchsize = NULL, startdate = NULL,
             enddate = NULL, as = "table", key = NULL, ...)
```

### Arguments

<code>startrow</code>	first name to return (if using as an offset)
<code>batchsize</code>	number of names to return (numeric)
<code>startdate</code>	(optional) start date of range between which to count names (date)
<code>enddate</code>	(optional) end date of range between which to count names (date)
<code>as</code>	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that <code>as="table"</code> can give different data format back depending on the function - for example, sometimes a <code>data.frame</code> and sometimes a character vector.
<code>key</code>	Your BHL API key, either enter, or loads from your <code>.Renviro</code> n as <code>BHL_KEY</code> or from <code>.Rprofile</code> as <code>bhl_key</code> .
<code>...</code>	Curl options passed on to <code>curl::HttpClient()</code>

### Examples

```
## Not run:
bhl_namelist(startrow=1, batchsize=99, startdate='10/15/2009',
             enddate='10/16/2009')
bhl_namelist(startrow=1, batchsize=5, startdate='10/15/2009',
             enddate='10/31/2009', as='json')

## End(Not run)
```

---

bhl_namesearch	<i>Search for a particular name.</i>
----------------	--------------------------------------

---

**Description**

Names both with and without NameBank identifiers are returned.

**Usage**

```
bhl_namesearch(name = NULL, as = "table", key = NULL, ...)
```

**Arguments**

name	species name (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_namesearch('poa annua')
bhl_namesearch(name='helianthus annuus')
bhl_namesearch(name='helianthus annuus', as='xml')
bhl_namesearch(name='helianthus annuus', as='json')

## End(Not run)
```

---

bhl_openurl	<i>Not sure how this differs from their other API...</i>
-------------	--

---

**Description**

Not sure how this differs from their other API...

**Usage**

```
bhl_openurl(genre = NULL, title = NULL, aufirst = NULL, aulast = NULL,
  date = NULL, spage = NULL, issue = NULL, version = 0.1, as = "list",
  key = NULL, ...)
```

**Arguments**

genre	Book genre
title	Book title
aufirst	First author
aulast	Last author
date	Date of publication
spage	Start page
issue	Issue number
version	One of 0.1 or 1.0
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviron as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_openurl(
  genre="book",
  title="Manual+of+North+American+Diptera",
  aufirst="Samuel Wendell",
  aulast="Williston",
  date=1908,
  spage=16)

bhl_openurl(genre="book", title="Manual+of+North+American+Diptera",
  aufirst="Samuel Wendell", aulast="Williston", date=1908, spage=16)

bhl_openurl(genre="book", title="Manual+of+North+American+Diptera",
  aufirst="Samuel Wendell", aulast="Williston", date=1908, spage=16,
  as='xml')

## End(Not run)
```

---

bhl_partsearch	<i>Search for parts of books in BHL, such as articles, chapters, or treatments. Search criteria includes title, container (journal or book title), author, date of publication, volume, series, and issue.</i>
----------------	--

---

**Description**

To execute a search, you must supply at least a title or author.

**Usage**

```
bhl_partsearch(title = NULL, containerTitle = NULL, author = NULL,
  date = NULL, volume = NULL, series = NULL, issue = NULL,
  as = "table", key = NULL, ...)
```

**Arguments**

title	Title of the work
containerTitle	Container title of the work
author	Author of the work
date	Date of the work
volume	Volume of the work
series	Series of the work
issue	Issue of the work
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Details**

The metadata returned by this method includes Part Identifier, Part URL, Item ID, Page ID for the start page, Genre, Title, Container Title, Publication Details, Volume, Series, Issue, Date, Page Range, Language, rights information, authors, keywords, identifiers, pages, and related parts. For more information, see the "Data Elements" section of this documentation.

**Examples**

```
## Not run:
bhl_partsearch(title='Critical approach to the definition of
  Darwinian units')
bhl_partsearch(author='Charles Darwin')

## End(Not run)
```

---

bhl_subjectsearch	<i>Return a list of subjects that match (fully or partially) the specified search string.</i>
-------------------	---

---

### Description

Return a list of subjects that match (fully or partially) the specified search string.

### Usage

```
bhl_subjectsearch(subject, as = "table", key = NULL, ...)
```

### Arguments

subject	the full or partial subject for which to search (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renvirom as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

### Examples

```
## Not run:
bhl_subjectsearch('diptera')
bhl_subjectsearch('diptera', "json")

## End(Not run)
```

---

bhl_titlesearchsimple	<i>Perform a simple title search.</i>
-----------------------	---------------------------------------

---

### Description

The full title (as specified in MARC 245a and MARC 245b library records) is searched for the specified string. Basic metadata for all full and partial matches is returned.

### Usage

```
bhl_titlesearchsimple(title = NA, as = "table", key = NULL, ...)
```

**Arguments**

title	full or partial title for which to search (character)
as	(character) Return a list ("list"), json ("json"), xml ("xml"), or parsed table ("table", default). Note that as="table" can give different data format back depending on the function - for example, sometimes a data.frame and sometimes a character vector.
key	Your BHL API key, either enter, or loads from your .Renviro as BHL_KEY or from .Rprofile as bhl_key.
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
bhl_titlesearchsimple('nematoceros')
bhl_titlesearchsimple('husbandry')

## End(Not run)
```

---

getpages

*Get many OCR-generated pages given a single item id*


---

**Description**

Get many OCR-generated pages given a single item id

**Usage**

```
getpages(itemid, key = NULL, ...)
```

**Arguments**

itemid	the item id (character). Required
key	Your BHL API key, either enter, or loads from your .Renviro as BHL_KEY or from .Rprofile as bhl_key
...	Curl options passed on to <code>crul::HttpClient()</code>

**Examples**

```
## Not run:
books <- bhl_booksearch(title='Selborne', lname='White', volume=2,
  edition='new', year=1825, collectionid=4, language='eng')
getpages(itemid = 16800)

## End(Not run)
```

---

rbhl-defunct

*Defunct functions in rbhl*

---

**Description**

These functions are gone, no longer available.

**Details**

- `bhl_getpartendnote()`: BHL removed this API method.
- `bhl_gettitleendnote()`: BHL removed this API method.

---

rbhlmethods

*Data.frame of all the BHL API methods from the BHL website.*

---

**Description**

Data.frame of all the BHL API methods from the BHL website.



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