

# Package ‘brendaDb’

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**Title** The BRENDA Enzyme Database

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**Description** R interface for importing and analyzing enzyme information from the BRENDA database.

**License** MIT + file LICENSE

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**Author** Yi Zhou [aut, cre] (<<https://orcid.org/0000-0003-0969-3993>>)

**Maintainer** Yi Zhou <y1.zhou@uga.edu>

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brendaDb-package	<i>brendaDb: the BRENDA enzyme database.</i>
------------------	----------------------------------------------

---

## Description

brendaDb provides an R interface to download, clean and extract enzyme information from the BRENDA database.

## Details

The main aims of brendaDb include:

- Read text file downloaded from BRENDA into an R tibble
- Retrieve information for specific enzymes
- Query enzymes using their synonyms, gene symbols, etc.
- Query enzyme information for specific **BioCyc** pathways

To learn more about brendaDb, please refer to the vignette. `browseVignettes(package = "brendaDb")`

**Author(s)**

**Maintainer:** Yi Zhou <yi.zhou@uga.edu> ([ORCID](#))

**See Also**

Useful links:

- <https://github.com/y1zhou/brendaDb>
- Report bugs at <https://github.com/y1zhou/brendaDb/issues>

---

acronyms

*Information fields and their corresponding acronyms.*

---

**Description**

The RData file is generated by reading the entire BRENDA text file with `ReadBrenda()`, and getting unique values in the `field` column. The acronyms are extracted by the regex `^[A-Z_05]+`.

**Usage**

```
data(acronyms)
```

**Format**

A data.frame with 40 rows and 2 columns.

- `field`: field names in the BRENDA text file (all uppercase letters separated by underscores). This could be used in the `fields` argument of the `QueryBrenda()` function.
- `acronym`: acronyms used by the BRENDA file to indicate the fields.

---

CleanECNumber

*Remove deleted and transferred EC numbers.*

---

**Description**

Some EC numbers have comments wrapped in parentheses. Most of them are deleted (in this case we remove them) entries or transferred (in this case we point to the new entry) entries.

**Usage**

```
CleanECNumber(df)
```

**Arguments**

`df` A tibble generated by `ReadBrenda()`.

**Value**

A tibble with deleted and transferred entries moved to the bottom, with columns:

- ID being the deleted/transferred ID,
- field being "TRANSFERRED\_DELETED", and
- description being the information included in the original ID column.

**Examples**

```
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",  
                           package = "brendaDb"))  
brendaDb::CleanECNumber(df)
```

---

ConfigBPCores

*Configure the number of cores used by BiocParallel.*

---

**Description**

Configure the number of cores used by BiocParallel.

**Usage**

```
ConfigBPCores(n.core = 0)
```

**Arguments**

n.core            Integer specifying the number of cores to use. Default is 0, which would result in using all available cores.

**Value**

The back-end of type bpparamClass.

**Examples**

```
brendaDb::ConfigBPCores(2)
```

---

DownloadBrenda	<i>Download and unzip the BRENDA text file.</i>
----------------	-------------------------------------------------

---

**Description**

By default, the function downloads a zipped BRENDA text file to a local cache directory, and extracts a `brenda_download.txt` file.

**Usage**

```
DownloadBrenda(force.download = FALSE)
```

**Arguments**

`force.download` Boolean value. If TRUE, ignore the cache and force re-download of the BRENDA text file. Default is FALSE.

**Value**

A string of the path to the downloaded BRENDA text file.

**Examples**

```
## Not run: DownloadBrenda()
```

---

ExtractField	<i>Extract a specific field from a <code>brenda.entries</code> object.</i>
--------------	----------------------------------------------------------------------------

---

**Description**

Retrieve one field from all the `brenda.entry` objects. A column of EC numbers will be added to distinguish different enzymes.

**Usage**

```
ExtractField(res, field, entries = NULL)
```

**Arguments**

`res` A `brenda.entries` object from [QueryBrenda\(\)](#).

`field` A string indicating the field to extract. Nested fields should be separated by \$, e.g. `parameters$ph.optimum`.

`entries` A character vector with values of EC numbers. This should be a subset of `names(res)`.

**Value**

A tibble with all columns from the tibble in the given field, and extra columns containing the EC numbers and organisms.

## Examples

```
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",
                             package = "brendaDb"))
res <- QueryBrenda(brenda = df, EC = c("1.1.1.1", "6.3.5.8"),
                  n.core = 2)
ExtractField(res, field = "molecular$stability$general.stability")
ExtractField(res, field = "structure$subunits")
```

---

ID2Enzyme

*A helper function for converting names/synonyms to EC numbers.*

---

## Description

A helper function for converting names/synonyms to EC numbers.

## Usage

```
ID2Enzyme(brenda, ids)
```

## Arguments

brenda	A tibble generated from <a href="#">ReadBrenda()</a> .
ids	A character vector of IDs to be converted.

## Details

The function goes through "RECOMMENDED\_NAME", "SYSTEMATIC\_NAME", and "SYNONYMS" in the BRENDA file, and uses regexes to look for the given IDs. Values in the three columns are kept if the regex had a hit, otherwise NA is filled. The function can take in IDs of multiple sources, e.g. `c("ADH4", "CD38", "pyruvate dehydrogenase")`. Note that using aliases instead of symbols could lead to false positives in the output table.

## Value

A tibble with columns ID, EC, and at least one of (RECOMMENDED\_NAME, SYSTEMATIC\_NAME and SYNONYMS).

## Examples

```
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",
                             package = "brendaDb"))
ID2Enzyme(df, c("CD38", "ADH4", "pyruvate dehydrogenase"))
```

---

InitBrendaDeprecatedEntry

*Create a brenda.deprecated.entry object.*

---

## Description

Some EC numbers are transferred or deleted. For these entries, return a `brenda.deprecated.entry` object and the corresponding message.

## Usage

```
InitBrendaDeprecatedEntry(EC, msg)
```

```
is.brenda.deprecated.entry(x)
```

## Arguments

EC	A string indicating EC number of the enzyme.
msg	A string of the transferred / deleted message.
x	Any object.

## Details

`is.brenda.deprecated.entry` checks if an object is a `brenda.deprecated.entry` object. If the input is a `brenda.entries` object, check all items in the list to see if they are `brenda.deprecated.entry` objects and return a boolean vector of the same length.

## Value

A `brenda.deprecated.entry` object.

A boolean vector of the same length as `x`.

## Examples

```
brendaDb::InitBrendaDeprecatedEntry("6.3.5.8", "Transferred to EC 2.6.1.85")
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",
                             package = "brendaDb"))
is.brenda.entry(QueryBrenda(df, "6.3.5.8"))
```

---

InitBrendaEntry	<i>Create a brenda.entry object.</i>
-----------------	--------------------------------------

---

### Description

The list should contain 6 sublists: nomenclature, interactions, parameters, molecular, stability, and bibliography. All sublists should be empty by default apart from EC under nomenclature.

### Usage

```
InitBrendaEntry(  
  EC,  
  protein = NA,  
  systematic.name = NA,  
  recommended.name = NA,  
  synonyms = NA,  
  reaction = NA,  
  reaction.type = NA,  
  substrate.product = NA,  
  natural.substrate.product = NA,  
  cofactor = NA,  
  metals.ions = NA,  
  inhibitors = NA,  
  activating.compound = NA,  
  km.value = NA,  
  turnover.number = NA,  
  ki.value = NA,  
  pi.value = NA,  
  ph.optimum = NA,  
  ph.range = NA,  
  temperature.optimum = NA,  
  temperature.range = NA,  
  specific.activity = NA,  
  ic50 = NA,  
  source.tissue = NA,  
  localization = NA,  
  general.stability = NA,  
  storage.stability = NA,  
  ph.stability = NA,  
  organic.solvent.stability = NA,  
  oxidation.stability = NA,  
  temperature.stability = NA,  
  purification = NA,  
  cloned = NA,  
  engineering = NA,  
  renatured = NA,  
  application = NA,  
  molecular.weight = NA,  
  subunits = NA,  
  posttranslational.modification = NA,  
  crystallization = NA,
```



```

    bibliography = NA
  )

  is.brenda.entry(x, verbose = FALSE)

```

### Arguments

EC	A string indicating EC number of the enzyme.
protein	The description string of a PR field.
systematic.name	The description string of a SN field.
recommended.name	The description string of a RN field.
synonyms	The description string of a SY field.
reaction	The description string of a RE field.
reaction.type	The description string of a RT field.
substrate.product	The description string of a SP field.
natural.substrate.product	The description string of a NSP field.
cofactor	The description string of a CF field.
metals.ions	The description string of a ME field.
inhibitors	The description string of a IN field.
activating.compound	The description string of a AC field.
km.value	The description string of a KM field.
turnover.number	The description string of a TN field.
ki.value	The description string of a KI field.
pi.value	The description string of a PI field.
ph.optimum	The description string of a PHO field.
ph.range	The description string of a PHR field.
temperature.optimum	The description string of a TO field.
temperature.range	The description string of a TR field.
specific.activity	The description string of a SA field.
ic50	The description string of a IC50 field.
source.tissue	The description string of a ST field.
localization	The description string of a LO field.
general.stability	The description string of a GS field.
storage.stability	The description string of a SS field.
ph.stability	The description string of a PHS field.

<code>organic.solvent.stability</code>	The description string of a OSS field.
<code>oxidation.stability</code>	The description string of a OS field.
<code>temperature.stability</code>	The description string of a TS field.
<code>purification</code>	The description string of a PU field.
<code>cloned</code>	The description string of a CL field.
<code>engineering</code>	The description string of a EN field.
<code>renatured</code>	The description string of a REN field.
<code>application</code>	The description string of a AP field.
<code>molecular.weight</code>	The description string of a MW field.
<code>subunits</code>	The description string of a SU field.
<code>posttranslational.modification</code>	The description string of a PM field.
<code>crystallization</code>	The description string of a CR field.
<code>bibliography</code>	The description string of a RF field.
<code>x</code>	Any object.
<code>verbose</code>	Boolean value default to FALSE. If TRUE, prints message when all elements are <code>brenda.entries</code> .

### Details

`is.brenda.entry` checks if an object is a `brenda.entry` object. If the input is a `brenda.entries` object, check all items in the list to see if they are `brenda.entry` objects and return a boolean vector of the same length.

### Value

A `brenda.entry` object with all fields other than `nomenclature$ec` being NA.

A boolean vector of the same length as `x`.

### Examples

```
brendaDb:::InitBrendaEntry("1.1.1.100")
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",
                             package = "brendaDb"))
is.brenda.entry(QueryBrenda(df, "6.3.5.8"))
```

---

ParseGeneric	<i>Generic parser for a description string.</i>
--------------	-------------------------------------------------

---

### Description

Descriptions are generally structured as the following:

- Protein information is included in '#'...#',
- Literature citations are in '<...>',
- Commentaries in '(...)', and
- field-special information in '...'

This function separates these fields into different columns.

### Usage

```
ParseGeneric(description, acronym)
```

### Arguments

description	A description string from one of the entries.
acronym	The acronym of the field. Can be found with <a href="#">ShowFields()</a> .

### Details

The description column contains values extracted by BRENDA in each field.

The fieldInfo column contains different information in different fields:

- In a SYNONYMS entry, it is either the source of the identifier, or part of the description (a false positive).
- In KM\_VALUE, TURNOVER\_NUMBER entries, it's the corresponding substrate.

### Value

A tibble with columns: proteinID, description, fieldInfo, commentary, and refID

---

ParseNoDescription	<i>Generic parser for a description string without extracted values.</i>
--------------------	--------------------------------------------------------------------------

---

### Description

This parser works for fields `storage.stability`, `general.stability`, `oxidation.stability`, `cloned`, `purification`, `crystallization` and `renatured`.

These fields in BRENDA don't have extracted values - the commentary itself is the extracted value.

### Usage

```
ParseNoDescription(description, acronym)
```

**Arguments**

description     A description string from one of the entries.  
 acronym         The acronym of the field. Can be found with [ShowFields\(\)](#).

**Value**

A tibble with columns: proteinID, description and refID.

---

ParseProtein     *Parse a "PROTEIN" entry.*

---

**Description**

Expand the string into a tibble.

**Usage**

```
ParseProtein(description)
```

**Arguments**

description     The description string in a "PROTEIN" entry.

**Value**

A tibble with five columns: proteinID, description, uniprot, commentary and reference. The description column is the source organism.

**Examples**

```
x <- paste0(
  "PR\t#1# Cavia porcellus (#1# SULT1A2 <1,2,6,7>) <1,2,6,7>\n",
  "PR\t#2# Mus musculus <11,18,19>\n")
brendaDb:::ParseProtein(x)
```

---

ParseProteinNum     *Parse protein information strings or reference strings.*

---

**Description**

Given a string like "#1,45,72#", parse into a character vector of c("1", "45", "72"). Consecutive commas are collapsed into one, and spaces are treated as commas.

**Usage**

```
ParseProteinNum(x, type)
```

**Arguments**

x                    A string in the format of "#1#" or "#1,2,3#" or "<1,3>".  
 type                Either "protein" or "reference".

**Value**

A string, or a vector of strings of protein numbers.

**Examples**

```
brendaDb:::ParseProteinNum("#1,2,3#", "protein")
# [1] "1,2,3"
brendaDb:::ParseProteinNum("<123>", "reference")
# [1] "123"
```

---

ParseReaction	<i>Parser for the description strings of certain reaction-related fields.</i>
---------------	-------------------------------------------------------------------------------

---

**Description**

This parser works for the fields `substrate.product` and `natural.substrate.product`.

**Usage**

```
ParseReaction(description, acronym)
```

**Arguments**

description        A description string from one of the entries.  
 acronym            The acronym of the field. Can be found with [ShowFields\(\)](#).

**Details**

The reversibility of the reactions are wrapped in `;`; substrates and products are separated by `=`; commentaries on substrates are wrapped in `()`, and commentaries on products are wrapped in `||`.

**Value**

A tibble with columns: `proteinID`, `substrate`, `product`, `commentarySubstrate`, `commentaryProduct`, `fieldInfo` and `refID`

ParseRecommendedName *Parse a "RECOMMENDED\_NAME" entry into a string.*

---

**Description**

Remove useless characters in the description.

**Usage**

```
ParseRecommendedName(description)
```

**Arguments**

description     The description string in a "RECOMMENDED\_NAME" entry.

**Value**

A string to fill into the recommended.name field in brenda.nomenclature.

**Examples**

```
x <- "RN\tD-arabinose 1-dehydrogenase (NAD+)"  
brendaDb:::ParseRecommendedName(x)
```

---

ParseReference     *Parse a "REFERENCE" entry.*

---

**Description**

Expand the string into a tibble.

**Usage**

```
ParseReference(description)
```

**Arguments**

description     The description string in a "REFERENCE" entry.

**Value**

A tibble with three columns: refID, title and pubmed.

**Examples**

```
x <- paste0(
  "RF\t<1> Talbot, B.G.; Thirion, J.P.: Purification\n\t",
  "and properties of two distinct groups of ADH isozymes from Chinese\n\t",
  "hamster liver. Biochem. Genet. (1981) 19, 813-829. {Pubmed:6794566}\n",
  "RF\t<12> Woronick, C.L.: Alcohol dehydrogenase from human liver. Methods\n\t",
  "Enzymol. (1975) 41B, 369-374. {Pubmed:236461} (c,review)\n",
  "RF\t<10> Herrera, E.; Zorzano, A... {Pubmed:} (c,review)\n")
brendaDb::ParseReference(x)
```

---

ParseSystematicName    *Parse a "SYSTEMATIC\_NAME" entry into a string.*

---

**Description**

Remove useless characters in the description.

**Usage**

```
ParseSystematicName(description)
```

**Arguments**

description    The description string in a "SYSTEMATIC\_NAME" entry.

**Value**

A string to fill into the systematic.name field in brenda.nomenclature.

**Examples**

```
x <- "SN\talcohol:NAD+ oxidoreductase"
brendaDb::ParseSystematicName(x)
```

---

PrettyPrintBrendaEntry  
*Print a brenda.entry in a tree view.*

---

**Description**

Print a brenda.entry in a tree view.

**Usage**

```
PrettyPrintBrendaEntry(x, index, tail.idx, depth, full.output)
```

**Arguments**

<code>x</code>	A <code>brenda.entry</code> object.
<code>index</code>	A string of the name of the sublist.
<code>tail.idx</code>	A string showing the last element in the entry. This is for printing a different character in the tree.
<code>depth</code>	Int, showing the depth of the element.
<code>full.output</code>	A boolean default to <code>FALSE</code> . If <code>TRUE</code> , print entry even if it's empty (NA or 0 rows).

**Value**

Nothing; prints object tree-view to the terminal.

---

`print.brenda.entries` *Show the number of regular and transferred/deleted `brenda.entry` objects in the `brenda.entries` list.*

---

**Description**

Show the number of regular and transferred/deleted `brenda.entry` objects in the `brenda.entries` list.

**Usage**

```
## S3 method for class 'brenda.entries'
print(x, ..., verbose = FALSE)
```

**Arguments**

<code>x</code>	A <code>brenda.entries</code> list returned by <code>QueryBrenda()</code> .
<code>...</code>	Other arguments passed to the generic function.
<code>verbose</code>	Boolean; if <code>TRUE</code> , print tree views of <code>brenda.query</code> objects.

**Value**

Nothing; print summary information to the terminal.



---

print.brenda.entry      *Show the non-empty fields in the query result.*

---

### Description

For details, see [PrettyPrintBrendaEntry\(\)](#).

### Usage

```
## S3 method for class 'brenda.entry'
print(x, full.output = FALSE, ...)
```

### Arguments

x	A brenda.entry object (elements in the list returned by the function <a href="#">QueryBrenda()</a> ).
full.output	A boolean default to FALSE. If TRUE, include all entries even if they are empty (NA or 0 rows).
...	Other arguments passed to the generic function.

### Value

Nothing; print object information to the terminal.

---

PrintTreeHelper      *Print the tree structure with correct whitespace.*

---

### Description

Print the tree structure with correct whitespace.

### Usage

```
PrintTreeHelper(index, tail.idx, depth)
```

### Arguments

index	A string of the name of the sublist.
tail.idx	A string showing the last element in the entry. This is for printing a different character in the tree.
depth	Int, showing the depth of the element.

### Value

Nothing; prints tree structure to the terminal.

---

QueryBrenda                      *Query for multiple enzymes.*

---

### Description

Use a vector of EC numbers to retrieve information from the BRENDA tibble read in by [ReadBrenda\(\)](#). Invalid EC numbers will be removed and a message will be generated.

### Usage

```
QueryBrenda(brenda, EC, n.core = 0, fields = FALSE, ...)
```

### Arguments

brenda	A tibble containing information from BRENDA.
EC	A string of the EC number.
n.core	Integer specifying the number of cores to use. Default is 0, which would result in using all available cores.
fields	A character vector indicating fields to parse. Default is FALSE, which would be returning all fields.
...	Other parameters passed to <a href="#">QueryBrendaBase()</a> .

### Value

A list of brenda.entry objects.

### See Also

[QueryBrendaBase\(\)](#) [ConfigBPCores\(\)](#) [SelectOrganism\(\)](#)

### Examples

```
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",
                             package = "brendaDb"))
res <- QueryBrenda(brenda = df, EC = c("1.1.1.1", "1.1.1.10", "6.3.5.8"),
                  n.core = 2, organisms = "Homo sapiens")
```

---

QueryBrendaBase                      *Query for a specific enzyme.*

---

### Description

Use a EC number to retrieve information from the BRENDA tibble read in by [ReadBrenda\(\)](#).

### Usage

```
QueryBrendaBase(brenda, EC, organisms = FALSE)
```

**Arguments**

brenda	A tibble containing information from BRENDA.
EC	A string of the EC number.
organisms	A character vector indicating organisms to keep. Default is FALSE, which would keep all organisms.

**Value**

A `brenda.entry` object.

**See Also**

[ReadBrenda\(\)](#) [InitBrendaEntry\(\)](#)

**Examples**

```
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",
                             package = "brendaDb"))
brendaDb:::QueryBrendaBase(brenda = df, EC = "1.1.1.1",
                           organisms = "Homo sapiens")
```

---

ReadBrenda

*Read BRENDA text file into matrix.*

---

**Description**

For each EC entry, split the annotations into three columns:

- ID: EC number, e.g. 1.1.1.1
- field: the content of the information, e.g. protein, localization
- description: everything else

**Usage**

```
ReadBrenda(filepath, clean = TRUE)
```

**Arguments**

filepath	A string indicating the path to the text file.
clean	Boolean; if TRUE, run <a href="#">CleanECNumber()</a> after reading the file.

**Value**

A matrix containing information about the EC entries.

**Examples**

```
brenda_txt <- system.file("extdata", "brenda_download_test.txt",
                          package = "brendaDb")
df <- ReadBrenda(brenda_txt)
```

---

ReadBrendaFile	<i>Read raw BRENDA text file.</i>
----------------	-----------------------------------

---

**Description**

Read file into buffer, and load all non-empty lines. Comment lines (starting with \*) are skipped. The text file should be downloaded from [https://www.brenda-enzymes.org/download\\_brenda\\_without\\_registration.php](https://www.brenda-enzymes.org/download_brenda_without_registration.php)

**Usage**

```
ReadBrendaFile(filepath)
```

**Arguments**

filepath	A string indicating the path to the text file.
----------	------------------------------------------------

**Value**

A vector with each element being a line in the file.

---

SelectOrganism	<i>Select a subset of organisms in the brenda.query object.</i>
----------------	-----------------------------------------------------------------

---

**Description**

Select a subset of organisms in the brenda.query object.

**Usage**

```
SelectOrganism(query, org.id)
```

**Arguments**

query	A brenda.entry object from <a href="#">QueryBrendaBase()</a> .
org.id	A named character vector with values as proteinIDs.

**Value**

A subset of the given brenda.query object with the given organisms selected.

**See Also**

[QueryBrendaBase\(\)](#)

---

SeparateEntries	<i>Convert vector of lines to matrix.</i>
-----------------	-------------------------------------------

---

**Description**

For each EC entry, split the annotations into three columns:

- ID: EC number, e.g. 1.1.1.1
- field: the content of the information, e.g. protein, localization
- description: everything else

**Usage**

```
SeparateEntries(lines)
```

**Arguments**

lines            The output vector from read\_brenda\_file.

**Value**

A vector<vector> containing information about the EC entries. In R this is a list of 3 lists.

---

SeparateSubentries	<i>Preprocessing of entry description.</i>
--------------------	--------------------------------------------

---

**Description**

Separate subentries and strip unnecessary whitespace.

**Usage**

```
SeparateSubentries(description, acronym = NA)
```

**Arguments**

description    The description string of the field.  
acronym        The acronym of the field. Can be found with [ShowFields\(\)](#).

**Value**

A list of strings with each subentry as an element.

**Examples**

```
x <- "SN\talcohol:NAD+ oxidoreductase"  
brendaDb:::SeparateSubentries(x, "SN")
```

---

ShowFields

*Show all unique BRENDA fields and their corresponding acronyms.*

---

**Description**

Show all unique BRENDA fields and their corresponding acronyms.

**Usage**

```
ShowFields(df)
```

**Arguments**

df                    A data.frame with columns "field" and "description"

**Value**

A data.frame with columns "field" and "acronym".

**Examples**

```
df <- ReadBrenda(system.file("extdata", "brenda_download_test.txt",  
                             package = "brendaDb"))  
ShowFields(df)
```

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