

# Package ‘dbparser’

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**Title** Drugs Databases Parser

**Version** 2.0.1

**Description** This tool is for parsing public drug databases such as 'DrugBank' XML database <<https://go.drugbank.com/>>.

The parsed data are then returned in a proper 'R' object called 'dvobject'.

**License** MIT + file LICENSE

**Encoding** UTF-8

**Imports** dplyr, progress, purrr, tibble, tools, XML

**RoxygenNote** 7.2.3

**Suggests** knitr, rmarkdown, testthat

**VignetteBuilder** knitr

**URL** <https://docs.ropensci.org/dbparser/>,  
<https://github.com/ropensci/dbparser/>

**BugReports** <https://github.com/ropensci/dbparser/issues>

**Depends** R (>= 3.5)

**NeedsCompilation** no

**Author** Mohammed Ali [aut, cre],  
Ali Ezzat [aut],  
Hao Zhu [rev],  
Emma Mendelsohn [rev]

**Maintainer** Mohammed Ali <moh\_fcis@yahoo.com>

**Repository** CRAN

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cett\_nodes\_options      *returns carriers, enzymes, targets and transporters node valid options.*

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**Description**

returns carriers, enzymes, targets and transporters node valid options.

**Usage**

cett\_nodes\_options()

**Value**

list of CETT valid options

**See Also**

Other parsers: [drug\\_node\\_options\(\)](#), [parseDrugBank\(\)](#), [references\\_node\\_options\(\)](#)

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drug\_node\_options      *returns drug node valid options.*

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**Description**

returns drug node valid options.

**Usage**

drug\_node\_options()

**Value**

list of drug valid options

**See Also**

Other parsers: [cett\\_nodes\\_options\(\)](#), [parseDrugBank\(\)](#), [references\\_node\\_options\(\)](#)

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parseDrugBank	<i>parseDrugBank</i>
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## Description

parses given DrugBank XML database into a dvector. dvector is a list of data.frames in which each data.frame represents a part of parsed data (i.e drugs, prices, carriers, ...)

## Usage

```
parseDrugBank(  
  db_path,  
  drug_options = NULL,  
  parse_salts = FALSE,  
  parse_products = FALSE,  
  references_options = NULL,  
  cett_options = NULL  
)
```

## Arguments

db_path	<b>string</b> , full path for the <b>DrugBank</b> xml or zip file.
drug_options	<b>character vector</b> , list of sub drug related nodes names options to parse (default = NULL). Check drug_node_options() for all available options. If its value is 'NULL' ONLY 'drug_general_information' will be placed in the returned dvector.
parse_salts	<b>boolean</b> , parse salts info (default = FALSE)
parse_products	<b>boolean</b> , parse products info (default = FALSE)
references_options	<b>character vector</b> , list of sub references related nodes names options to parse (default = NULL). Check references_node_options() for all available options.
cett_options	<b>character vector</b> , list of sub cett related nodes names options to parse (default = NULL). Check cett_nodes_options() for all available options.

## Value

dvector

## See Also

Other parsers: [cett\\_nodes\\_options\(\)](#), [drug\\_node\\_options\(\)](#), [references\\_node\\_options\(\)](#)

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references\_node\_options

*returns references node valid options.*

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**Description**

returns references node valid options.

**Usage**

references\_node\_options()

**Value**

list of references valid options

**See Also**

Other parsers: [cett\\_nodes\\_options\(\)](#), [drug\\_node\\_options\(\)](#), [parseDrugBank\(\)](#)

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show\_dvobject\_metadata

*init\_dvobject Returns data.frame with two columns (key, value) of dvobject attributes*

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**Description**

init\_dvobject Returns data.frame with two columns (key, value) of dvobject attributes

**Usage**

show\_dvobject\_metadata(dvobject)

**Arguments**

dvobject           - dvobject list to show related metadata

**Value**

data.frame

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