

# Package: dbparser (via r-universe)

December 15, 2024

**Title** Drugs Databases Parser

**Version** 2.0.3

**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** canvasXpress, knitr, rmarkdown, testthat, tidyr

**VignetteBuilder** knitr

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

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

**Depends** R (>= 3.5)

**Config/pak/sysreqs** libxml2-dev

**Repository** <https://ropensci.r-universe.dev>

**RemoteUrl** <https://github.com/ropensci/dbparser>

**RemoteRef** master

**RemoteSha** 39d9a078503c734a74d5f0fdc693db117e94b40f

## Contents

cett_nodes_options . . . . .	2
drug_node_options . . . . .	2
parseDrugBank . . . . .	3
references_node_options . . . . .	4
show_dvobject_metadata . . . . .	4

<b>Index</b>	<b>5</b>
--------------	----------

---

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

---

**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\(\)](#)

---

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

---

**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\(\)](#)

---

parseDrugBank	<i>parseDrugBank</i>
---------------	----------------------

---

## 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\(\)](#)

---

references\_node\_options

*returns references node valid options.*

---

**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\(\)](#)

---

show\_dvobject\_metadata

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

---

**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

# Index

## \* **parsers**

- cett\_nodes\_options, [2](#)
- drug\_node\_options, [2](#)
- parseDrugBank, [3](#)
- references\_node\_options, [4](#)

## \* **utility**

- show\_dvobject\_metadata, [4](#)

[cett\\_nodes\\_options](#), [2](#), [2](#), [3](#), [4](#)

[drug\\_node\\_options](#), [2](#), [2](#), [3](#), [4](#)

[parseDrugBank](#), [2](#), [3](#), [4](#)

[references\\_node\\_options](#), [2](#), [3](#), [4](#)

[show\\_dvobject\\_metadata](#), [4](#)