

# Package ‘dbparser’

March 17, 2023

**Title** Drugs Databases Parser

**Version** 2.0.0

**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

**Date/Publication** 2023-03-17 08:30:02 UTC

## R topics documented:

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

---

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

---

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

---

**Description**

returns drug node valid options.

**Usage**

drug\_node\_options()

**Value**

list of drug valid 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 = drug_node_options(),
  parse_salts = TRUE,
  parse_products = TRUE,
  references_options = references_node_options(),
  cett_options = cett_nodes_options()
)
```

### 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 = drug_node_options())
parse_salts	<b>boolean</b> , parse salts info (default = TRUE)
parse_products	<b>boolean</b> , parse products info (default = TRUE)
references_options	<b>character vector</b> , list of sub references related nodes names options to parse (default = references_node_options())
cett_options	<b>character vector</b> , list of sub cett related nodes names options to parse (default = cett_nodes_options())

### Value

dvector

---

references\_node\_options

*returns references node valid options.*

---

### Description

returns references node valid options.

**Usage**

```
references_node_options()
```

**Value**

list of references valid options

---

```
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, [3](#)

## \* **utility**

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

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

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

[parseDrugBank, 3](#)

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

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