

Package: dbparser (via r-universe)

November 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'.

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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://epiverse-connect.r-universe.dev>

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

RemoteRef HEAD

RemoteSha 39d9a078503c734a74d5f0fdc693db117e94b40f

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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>
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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	string , full path for the DrugBank xml or zip file.
drug_options	character vector , 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	boolean , parse salts info (default = FALSE)
parse_products	boolean , parse products info (default = FALSE)
references_options	character vector , list of sub references related nodes names options to parse (default = NULL). Check references_node_options() for all available options.
cett_options	character vector , 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

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