

Package ‘dbparser’

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Title 'DrugBank' Database XML Parser

Version 1.0.1

Description This tool is for parsing the 'DrugBank' XML database <<http://drugbank.ca/>>. The parsed data are then returned in a proper 'R' dataframe with the ability to save them in a given database.

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Encoding UTF-8

LazyData true

Imports DBI, dplyr, ggplot2, odbc, purrr, tibble, tidyr, tools, XML

RoxygenNote 6.1.0

Suggests knitr, rmarkdown, testthat

VignetteBuilder knitr

URL <https://dainanahan.github.io/dbparser/index.html>

BugReports <https://github.com/Dainanahan/dbparser/issues>

NeedsCompilation no

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close_db	<i>Close open drug bank sql database</i>
----------	--

Description

close_db closes connection to pre-given database.

Usage

```
close_db()
```

Details

This function closes connection to pre-given database.

Examples

```
close_db()
```

dbparser

dbparser: A package for reading and parsing drug bank xml with the option to save it in a given db.

Description

dbparser package provides three categories of important functions: database related methods, xml db reader and drug bank elements parsers.

database functions

To open a connection to given database in order to store parsed drug bank elements database

xml db reader functions

Reads drug bank xml database and build drug elements full tree in database

parsers functions

Each parser function is responsible of parsing certain drug element and returning its dataframe with the ability to save it in a predefined database.

get_drugbank_exported_date

Return uploaded drugbank database exported date

Description

get_drugbank_exported_date returns uploaded drugbank database exported date.

Usage

```
get_drugbank_exported_date()
```

Value

drugbank exported date

Examples

```
get_drugbank_exported_date()
```

`get_drugbank_metadata` *Return uploaded drugbank database metadata*

Description

`get_drugbank_metadata` returns uploaded drugbank database version and exported date.

Usage

`get_drugbank_metadata()`

Value

drugbank metadata

Examples

`get_drugbank_metadata()`

`get_drugbank_version` *Return uploaded drugbank database version*

Description

`get_drugbank_version` returns uploaded drugbank database version.

Usage

`get_drugbank_version()`

Value

drugbank version

Examples

`get_drugbank_version()`

get_xml_db_rows	<i>Reads drug bank xml database and set it in memory.</i>
-----------------	---

Description

get_xml_db_rows sets drug bank db xml full tree in memory

Usage

```
get_xml_db_rows(xml_db_name)
```

Arguments

xml_db_name string, full path for the drug bank xml or zip file.

Details

This functions reads drug bank xml database and sets the full tree save it in a predefined database via [open_db](#) method. It takes one single optional argument to in memory directly without returning it. It must be called one before using parser functions, and once it is called If [get_xml_db_rows](#) is called before for any reason, so no need to call it again.

Value

TRUE when sets the db tree in memory to be used by parser methods and FALSE otherwise

Examples

```
get_xml_db_rows("db_full_path")  
get_xml_db_rows(xml_db_name = "db_full_path")
```

open_db	<i>Establish connection to given data base</i>
---------	--

Description

open_db opens connection to given database.

Usage

```
open_db(driver, server, output_database, trusted_connection = TRUE)
```

Arguments

driver odbc object to define database driver.
server string, indicated the db server name.
output_database string, the database name to be used, it has to be created before using it
trusted_connection boolean, is the connection secure

Details

This function establishes connection to given database to store, *optionally*, the parsed drug bank elements.

Value

sets the open connection in memory to be used by other functions

Examples

```
open_db(xml_db_name = "drugbank.xml", driver = "SQL Server",  
server = "MOHAMMED\\SQL2016", output_database = "drugbank2")
```

parse_drug	<i>Extracts the main drug elements and return data as tibble.</i>
------------	---

Description

parse_drug returns tibble of drugs main elements.

Usage

```
parse_drug(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the main element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug main node attributes tibble

Examples

```
parse_drug()  
parse_drug(TRUE)  
parse_drug(save_table = FALSE)
```

parse_drug_affected_organisms

Extracts the drug affected organisms element and return data as tibble.

Description

parse_drug_affected_organisms returns tibble of drug affected organisms elements.

Usage

```
parse_drug_affected_organisms(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the affected organisms element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug affected organisms node attributes tibble

Examples

```
parse_drug_affected_organisms()  
parse_drug_affected_organisms(TRUE)  
parse_drug_affected_organisms(save_table = FALSE)
```

parse_drug_ahfs_codes *Extracts the drug ahfs codes element and return data as tibble.*

Description

parse_drug_ahfs_codes returns tibble of drug ahfs codes elements.

Usage

```
parse_drug_ahfs_codes(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the ahfs codes element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug ahfs codes node attributes tibble

Examples

```
parse_drug_ahfs_codes()  
parse_drug_ahfs_codes(TRUE)  
parse_drug_ahfs_codes(save_table = FALSE)
```

parse_drug_all *Extracts the all drug elements and return data as list of dataframes.*

Description

parse_drug_all returns list of dataframes of drugs elements.

Usage

```
parse_drug_all(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts all element of drug nodes in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

all drug elements dataframes

Examples

```
parse_drug_all()  
parse_drug_all(TRUE)  
parse_drug_all(save_table = FALSE)
```

parse_drug_articles *Extracts the drug articles element and return data as tibble.*

Description

parse_drug_articles returns tibble of drug articles elements.

Usage

```
parse_drug_articles(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the articles element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug articles node attributes tibble

Examples

```
parse_drug_articles()  
parse_drug_articles(TRUE)  
parse_drug_articles(save_table = FALSE)
```

parse_drug_atc_codes *Extracts the drug atc codes element and return data as data frame.*

Description

parse_drug_atc_codes returns data frame of drug atc codes elements.

Usage

```
parse_drug_atc_codes(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the atc codes element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug atc_codes node attributes data frame

Examples

```
parse_drug_atc_codes()  
parse_drug_atc_codes(TRUE)  
parse_drug_atc_codes(save_table = FALSE)
```

parse_drug_books *Extracts the drug books element and return data as tibble.*

Description

parse_drug_books returns tibble of drug books elements.

Usage

```
parse_drug_books(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the books element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug books node attributes tibble

Examples

```
parse_drug_books()  
parse_drug_books(TRUE)  
parse_drug_books(save_table = FALSE)
```

parse_drug_carriers *Extracts the drug carriers element and return data as data frame.*

Description

parse_drug_carriers returns data frame of drug carriers elements.

Usage

```
parse_drug_carriers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers node attributes date frame

Examples

```
parse_drug_carriers()  
parse_drug_carriers(TRUE)  
parse_drug_carriers(save_table = FALSE)
```

parse_drug_carriers_actions

Extracts the drug carriers actions element and return data as data frame.

Description

parse_drug_carriers_actions returns data frame of drug carriers actions elements.

Usage

```
parse_drug_carriers_actions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers actions element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers actions node attributes date frame

Examples

```
parse_drug_carriers_actions()  
parse_drug_carriers_actions(TRUE)  
parse_drug_carriers_actions(save_table = FALSE)
```

parse_drug_carriers_articles

Extracts the drug carriers articles element and return data as data frame.

Description

parse_drug_carriers_articles returns data frame of drug carriers articles elements.

Usage

```
parse_drug_carriers_articles(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers articles element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers_articles node attributes date frame

Examples

```
parse_drug_carriers_articles()  
parse_drug_carriers_articles(TRUE)  
parse_drug_carriers_articles(save_table = FALSE)
```

`parse_drug_carriers_links`*Extracts the drug carriers links element and return data as data frame.*

Description

`parse_drug_groups` returns data frame of drug carriers links elements.

Usage

```
parse_drug_carriers_links(save_table = FALSE)
```

Arguments

`save_table` boolean, save table in database if true.

Details

This functions extracts the carriers links element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers_links node attributes data frame

Examples

```
parse_drug_carriers_links()  
parse_drug_carriers_links(TRUE)  
parse_drug_carriers_links(save_table = FALSE)
```

`parse_drug_carriers_polypeptides`*Extracts the drug carriers polypeptides element and return data as data frame.*

Description

`carriers_polypeptides` returns data frame of drug carriers polypeptides elements.

Usage

```
parse_drug_carriers_polypeptides(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This function extracts the carriers polypeptides element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers polypeptides node attributes data frame

Examples

```
parse_drug_carriers_polypeptides()  
parse_drug_carriers_polypeptides(TRUE)  
parse_drug_carriers_polypeptides(save_table = FALSE)
```

parse_drug_carriers_polypeptides_external_identifiers

Extracts the drug carriers polypeptides external identifiers element and return data as data frame.

Description

parse_drug_carriers_polypeptides_external_identifiers returns data frame of drug carriers polypeptides external identifiers elements.

Usage

```
parse_drug_carriers_polypeptides_external_identifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers polypeptides external identifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers polypeptides external identifiers node attributes date frame

Examples

```
parse_drug_carriers_polypeptides_external_identifiers()  
parse_drug_carriers_polypeptides_external_identifiers(TRUE)  
parse_drug_carriers_polypeptides_external_identifiers(save_table = FALSE)
```

parse_drug_carriers_polypeptides_go_classifiers

Extracts the drug carriers polypeptides go classifiers element and return data as data frame.

Description

parse_drug_carriers_polypeptides_go_classifiers returns data frame of drug carriers polypeptides go classifiers elements.

Usage

```
parse_drug_carriers_polypeptides_go_classifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers polypeptides go classifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers polypeptides go classifiers node attributes date frame

Examples

```
parse_drug_carriers_polypeptides_go_classifiers()
parse_drug_carriers_polypeptides_go_classifiers(TRUE)
parse_drug_carriers_polypeptides_go_classifiers(save_table = FALSE)
```

```
parse_drug_carriers_polypeptides_pfams
```

Extracts the drug carriers polypeptides pfams element and return data as data frame.

Description

parse_drug_carriers_polypeptides_pfams returns data frame of drug carriers polypeptides pfams elements.

Usage

```
parse_drug_carriers_polypeptides_pfams(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers polypeptides pfams element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers polypeptides pfams node attributes date frame

Examples

```
parse_drug_carriers_polypeptides_pfams()
parse_drug_carriers_polypeptides_pfams(TRUE)
parse_drug_carriers_polypeptides_pfams(save_table = FALSE)
```

parse_drug_carriers_polypeptides_synonyms

Extracts the drug carriers polypeptides synonyms element and return data as data frame.

Description

parse_drug_carriers_polypeptides_synonyms returns data frame of drug carriers polypeptides synonyms elements.

Usage

```
parse_drug_carriers_polypeptides_synonyms(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers polypeptides synonyms element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers polypeptides synonyms node attributes date frame

Examples

```
parse_drug_carriers_polypeptides_synonyms()  
parse_drug_carriers_polypeptides_synonyms(TRUE)  
parse_drug_carriers_polypeptides_synonyms(save_table = FALSE)
```

parse_drug_carriers_textbooks

Extracts the drug carriers textbooks element and return data as data frame.

Description

parse_drug_carriers_textbooks returns data frame of drug carriers textbooks elements.

Usage

```
parse_drug_carriers_textbooks(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the carriers textbooks element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug carriers textbooks node attributes data frame

Examples

```
parse_drug_carriers_textbooks()  
parse_drug_carriers_textbooks(TRUE)  
parse_drug_carriers_textbooks(save_table = FALSE)
```

parse_drug_categories *Extracts the drug categories element and return data as tibble.*

Description

parse_drug_categories returns tibble of drug categories elements.

Usage

```
parse_drug_categories(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the categories element of drug node in drugbank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned tibble in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug categories node attributes tibble

Examples

```
parse_drug_categories()  
parse_drug_categories(TRUE)  
parse_drug_categories(save_table = FALSE)
```

parse_drug_classification

Extracts the drug classifications element and return data as data frame.

Description

parse_drug_classification returns data frame of drug classifications elements.

Usage

```
parse_drug_classification(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the classifications element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug classifications node attributes data frame

Examples

```
parse_drug_classification()  
parse_drug_classification(TRUE)  
parse_drug_classification(save_table = FALSE)
```

parse_drug_dosages	<i>Extracts the drug dosages element and return data as tibble.</i>
--------------------	---

Description

parse_drug_dosages returns tibble of drug dosages elements.

Usage

```
parse_drug_dosages(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the dosages element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug dosages node attributes tibble

Examples

```
parse_drug_dosages()  
parse_drug_dosages(TRUE)  
parse_drug_dosages(save_table = FALSE)
```

parse_drug_element	<i>Extracts the given drug elements and return data as list of dataframes.</i>
--------------------	--

Description

parse_drug_element returns list of dataframes of drugs selected elements.

Usage

```
parse_drug_element(elements_options = c("all"), save_table = FALSE)
```

Arguments

`elements_options` list, options of elements to be parsed. Default is "all"

`save_table` boolean, save table in database if true. Default is false.

Details

This functions extracts selected element of drug nodes in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

`parse_drug_element_options` can be called to know the valid options for this method

Value

list of selected drug elements dataframes

Examples

```
parse_drug_element()  
parse_drug_element(c("drug_ahfs_codes", "drug_carriers"), save_table = TRUE)  
parse_drug_element(save_table = FALSE)  
parse_drug_element(c("drug_ahfs_codes", "drug_carriers"))
```

parse_drug_element_options

Returns parse_drug_element valid options.

Description

Returns parse_drug_element valid options.

Usage

```
parse_drug_element_options()
```

Value

list of parse_drug_element valid options

Examples

```
parse_drug_element_options()
```

parse_drug_enzymes

Extracts the drug enzymes element and return data as data frame.

Description

parse_drug_enzymes returns data frame of drug enzymes elements.

Usage

```
parse_drug_enzymes(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes node attributes date frame

Examples

```
parse_drug_enzymes()  
parse_drug_enzymes(TRUE)  
parse_drug_enzymes(save_table = FALSE)
```

parse_drug_enzymes_actions

Extracts the drug enzymes actions element and return data as data frame.

Description

parse_drug_enzymes_actions returns data frame of drug enzymes actions elements.

Usage

```
parse_drug_enzymes_actions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes actions element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes actions node attributes date frame

Examples

```
parse_drug_enzymes_actions()  
parse_drug_enzymes_actions(TRUE)  
parse_drug_enzymes_actions(save_table = FALSE)
```

parse_drug_enzymes_articles

Extracts the drug enzymes articles element and return data as data frame.

Description

parse_drug_enzymes_articles returns data frame of drug enzymes articles elements.

Usage

```
parse_drug_enzymes_articles(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes articles element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes articles node attributes data frame

Examples

```
parse_drug_enzymes_articles()  
parse_drug_enzymes_articles(TRUE)  
parse_drug_enzymes_articles(save_table = FALSE)
```

parse_drug_enzymes_links

Extracts the drug enzymes links element and return data as data frame.

Description

parse_drug_enzymes_links returns data frame of drug enzymes links elements.

Usage

```
parse_drug_enzymes_links(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes links element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes links node attributes data frame

Examples

```
parse_drug_enzymes_links()  
parse_drug_enzymes_links(TRUE)  
parse_drug_enzymes_links(save_table = FALSE)
```

parse_drug_enzymes_polypeptides

Extracts the drug enzymes polypeptides element and return data as data frame.

Description

parse_drug_enzymes_polypeptides returns data frame of drug enzymes polypeptides elements.

Usage

```
parse_drug_enzymes_polypeptides(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes polypeptides element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes polypeptides node attributes date frame

Examples

```
parse_drug_enzymes_polypeptides()  
parse_drug_enzymes_polypeptides(TRUE)  
parse_drug_enzymes_polypeptides(save_table = FALSE)
```

parse_drug_enzymes_polypeptides_external_identifiers

Extracts the drug enzymes polypeptides external identifiers element and return data as data frame.

Description

parse_drug_enzymes_polypeptides_external_identifiers returns data frame of drug enzymes polypeptides external identifiers elements.

Usage

```
parse_drug_enzymes_polypeptides_external_identifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes polypeptides external identifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes polypeptides external identifiers node attributes date frame

Examples

```
parse_drug_enzymes_polypeptides_external_identifiers()  
parse_drug_enzymes_polypeptides_external_identifiers(TRUE)  
parse_drug_enzymes_polypeptides_external_identifiers(save_table = FALSE)
```

```
parse_drug_enzymes_polypeptides_go_classifiers
```

Extracts the drug groups element and return data as data frame.

Description

parse_drug_enzymes_polypeptides_go_classifiers returns data frame of drug enzymes polypeptides go classifiers elements.

Usage

```
parse_drug_enzymes_polypeptides_go_classifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes polypeptides go classifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes polypeptides go classifiers node attributes data frame

Examples

```
parse_drug_enzymes_polypeptides_go_classifiers()  
parse_drug_enzymes_polypeptides_go_classifiers(TRUE)  
parse_drug_enzymes_polypeptides_go_classifiers(save_table = FALSE)
```

parse_drug_enzymes_polypeptides_pfams

Extracts the drug enzymes polypeptides pfams element and return data as data frame.

Description

parse_drug_enzymes_polypeptides_pfams returns data frame of drug enzymes polypeptides pfams elements.

Usage

```
parse_drug_enzymes_polypeptides_pfams(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes polypeptides pfams element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug groups node attributes date frame

Examples

```
parse_drug_enzymes_polypeptides_pfams()  
parse_drug_enzymes_polypeptides_pfams(TRUE)  
parse_drug_enzymes_polypeptides_pfams(save_table = FALSE)
```

`parse_drug_enzymes_polypeptides_synonyms`

Extracts the drug enzymes polypeptides synonyms element and return data as data frame.

Description

`parse_drug_enzymes_polypeptides_synonyms` returns data frame of drug enzymes polypeptides synonyms elements.

Usage

```
parse_drug_enzymes_polypeptides_synonyms(save_table = FALSE)
```

Arguments

`save_table` boolean, save table in database if true.

Details

This functions extracts the enzymes polypeptides synonyms element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes polypeptides synonyms node attributes date frame

Examples

```
parse_drug_enzymes_polypeptides_synonyms()  
parse_drug_enzymes_polypeptides_synonyms(TRUE)  
parse_drug_enzymes_polypeptides_synonyms(save_table = FALSE)
```

parse_drug_enzymes_textbooks

Extracts the drug enzymes textbooks element and return data as data frame.

Description

parse_drug_enzymes_textbooks returns data frame of drug enzymes textbooks elements.

Usage

```
parse_drug_enzymes_textbooks(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the enzymes textbooks element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug enzymes textbooks node attributes data frame

Examples

```
parse_drug_enzymes_textbooks()  
parse_drug_enzymes_textbooks(TRUE)  
parse_drug_enzymes_textbooks(save_table = FALSE)
```

parse_drug_experimental_properties

Extracts the drug experimental properties element and return data as tibble.

Description

parse_drug_experimental_properties returns tibble of drug experimental properties elements.

Usage

```
parse_drug_experimental_properties(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the experimental properties element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug experimental properties node attributes tibble

Examples

```
parse_drug_experimental_properties()  
parse_drug_experimental_properties(TRUE)  
parse_drug_experimental_properties(save_table = FALSE)
```

```
parse_drug_external_identifiers
```

Extracts the drug external identifiers element and return data as tibble.

Description

parse_drug_external_identifiers returns tibble of external identifiers groups elements.

Usage

```
parse_drug_external_identifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the external identifiers element of drug node in drugbank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned tibble in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug external identifiers node attributes tibble

Examples

```
parse_drug_external_identifiers()  
parse_drug_external_identifiers(TRUE)  
parse_drug_external_identifiers(save_table = FALSE)
```

`parse_drug_external_links`

Extracts the drug external links element and return data as tibble.

Description

`parse_drug_external_links` returns tibble of drug external links elements.

Usage

```
parse_drug_external_links(save_table = FALSE)
```

Arguments

`save_table` boolean, save table in database if true.

Details

This functions extracts the external links element of drug node in drugbank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned tibble in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug external links node attributes tibble

Examples

```
parse_drug_external_links()
parse_drug_external_links(TRUE)
parse_drug_external_links(save_table = FALSE)
```

parse_drug_food_interactions

Extracts the drug food interactions element and return data as tibble.

Description

parse_drug_food_interactions returns tibble of drug food interactions elements.

Usage

```
parse_drug_food_interactions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the food interactions element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug food interactions node attributes tibble

Examples

```
parse_drug_food_interactions()
parse_drug_food_interactions(TRUE)
parse_drug_food_interactions(save_table = FALSE)
```

parse_drug_groups *Extracts the drug groups element and return data as tibble.*

Description

parse_drug_groups returns tibble of drug groups elements.

Usage

```
parse_drug_groups(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the groups element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug groups node attributes tibble

Examples

```
parse_drug_groups()  
parse_drug_groups(TRUE)  
parse_drug_groups(save_table = FALSE)
```

parse_drug_interactions *Extracts the drug interactions element and return data as tibble.*

Description

parse_drug_interactions returns tibble of drug interactions elements.

Usage

```
parse_drug_interactions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the interactions element of drug node in drugbank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned tibble in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug interactions node attributes tibble

Examples

```
parse_drug_interactions()
parse_drug_interactions(TRUE)
parse_drug_interactions(save_table = FALSE)
```

parse_drug_international_brands

Extracts the drug international brands and return data as tibble.

Description

parse_drug_international_brands returns tibble of drug products elements.

Usage

```
parse_drug_international_brands(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the international brands element of drug node in drugbank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned tibble in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug international brands node attributes tibble

Examples

```
parse_drug_international_brands()  
parse_drug_international_brands(TRUE)  
parse_drug_international_brands(save_table = FALSE)
```

parse_drug_links	<i>Extracts the drug links element and return data as tibble.</i>
------------------	---

Description

parse_drug_links returns tibble of drug links elements.

Usage

```
parse_drug_links(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the links element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug links node attributes tibble

Examples

```
parse_drug_links()  
parse_drug_links(TRUE)  
parse_drug_links(save_table = FALSE)
```

parse_drug_manufacturers *Extracts the drug manufacturers element and return data as data frame.*

Description

parse_drug_manufacturers returns data frame of drug manufacturers elements.

Usage

```
parse_drug_manufacturers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the manufacturers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug manufacturers node attributes date frame

Examples

```
parse_drug_manufacturers()  
parse_drug_manufacturers(TRUE)  
parse_drug_manufacturers(save_table = FALSE)
```

parse_drug_mixtures *Extracts the drug mixtures element and return data as tibble.*

Description

parse_drug_mixtures returns tibble of drug mixtures elements.

Usage

```
parse_drug_mixtures(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the mixtures element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug mixtures node attributes tibble

Examples

```
parse_drug_mixtures()  
parse_drug_mixtures(TRUE)  
parse_drug_mixtures(save_table = FALSE)
```

parse_drug_packagers *Extracts the drug packagers element and return data as tibble.*

Description

parse_drug_packagers returns tibble of drug packagers elements.

Usage

```
parse_drug_packagers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the packagers element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug packagers node attributes tibble

Examples

```
parse_drug_packagers()  
parse_drug_packagers(TRUE)  
parse_drug_packagers(save_table = FALSE)
```

parse_drug_patents	<i>Extracts the drug patents element and return data as tibble.</i>
--------------------	---

Description

parse_drug_patents returns tibble of drug patents elements.

Usage

```
parse_drug_patents(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the patents element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug patents node attributes tibble

Examples

```
parse_drug_patents()  
parse_drug_patents(TRUE)  
parse_drug_patents(save_table = FALSE)
```

parse_drug_pathway *Extracts the drug pathway element and return data as data frame.*

Description

parse_drug_pathway returns data frame of drug pathway elements.

Usage

```
parse_drug_pathway(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the groups element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug pathway node attributes data frame

Examples

```
parse_drug_pathway()  
parse_drug_pathway(TRUE)  
parse_drug_pathway(save_table = FALSE)
```

parse_drug_pathway_drugs *Extracts the drug pathway drugs element and return data as data frame.*

Description

parse_drug_pathway_drugs returns data frame of drug pathway drugs elements.

Usage

```
parse_drug_pathway_drugs(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the pathway drugs element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug pathway drugs node attributes date frame

Examples

```
parse_drug_pathway_drugs()  
parse_drug_pathway_drugs(TRUE)  
parse_drug_pathway_drugs(save_table = FALSE)
```

parse_drug_pathway_enzyme

Extracts the drug pathway enzyme element and return data as data frame.

Description

parse_drug_pathway_enzyme returns data frame of drug pathway enzyme elements.

Usage

```
parse_drug_pathway_enzyme(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the pathway enzyme element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug pathway enzyme node attributes data frame

Examples

```
parse_drug_pathway_enzyme()  
parse_drug_pathway_enzyme(TRUE)  
parse_drug_pathway_enzyme(save_table = FALSE)
```

parse_drug_pdb_entries

Extracts the drug pdb entries element and return data as tibble.

Description

parse_drug_pdb_entries returns tibble of drug pdb entries elements.

Usage

```
parse_drug_pdb_entries(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the pdb entries element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug pdb entries node attributes tibble

Examples

```
parse_drug_pdb_entries()  
parse_drug_pdb_entries(TRUE)  
parse_drug_pdb_entries(save_table = FALSE)
```

parse_drug_prices *Extracts the drug prices element and return data as data frame.*

Description

parse_drug_prices returns data frame of drug prices elements.

Usage

```
parse_drug_prices(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the prices element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug prices node attributes date frame

Examples

```
parse_drug_prices()  
parse_drug_prices(TRUE)  
parse_drug_prices(save_table = FALSE)
```

parse_drug_products *Extracts the drug products element and return data as tibble.*

Description

parse_drug_products returns tibble of drug products elements.

Usage

```
parse_drug_products(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the products element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug products node attributes tibble

Examples

```
parse_drug_products()  
parse_drug_products(TRUE)  
parse_drug_products(save_table = FALSE)
```

parse_drug_reactions *Extracts the drug reactions element and return data as data frame.*

Description

parse_drug_reactions returns data frame of drug reactions elements.

Usage

```
parse_drug_reactions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the groups element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug reactions node attributes date frame

Examples

```
parse_drug_reactions()  
parse_drug_reactions(TRUE)  
parse_drug_reactions(save_table = FALSE)
```

parse_drug_reactions_enzymes

Extracts the drug reactions enzymes element and return data as data frame.

Description

parse_drug_reactions_enzymes returns data frame of drug reactions enzymes elements.

Usage

```
parse_drug_reactions_enzymes(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the reactions enzymes element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug reactions enzymes node attributes data frame

Examples

```
parse_drug_reactions_enzymes()  
parse_drug_reactions_enzymes(TRUE)  
parse_drug_reactions_enzymes(save_table = FALSE)
```

parse_drug_salts *Extracts the drug salts and return data as tibble.*

Description

parse_drug_salts returns tibble of drug products elements.

Usage

```
parse_drug_salts(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the salts element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug salts node attributes tibble

Examples

```
parse_drug_salts()  
parse_drug_salts(TRUE)  
parse_drug_salts(save_table = FALSE)
```

parse_drug_sequences *Extracts the drug sequences element and return data as data frame.*

Description

parse_drug_sequences returns data frame of drug sequences elements.

Usage

```
parse_drug_sequences(save_table = FALSE)
```


Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the sequences element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug sequences node attributes date frame

Examples

```
parse_drug_sequences()  
parse_drug_sequences(TRUE)  
parse_drug_sequences(save_table = FALSE)
```

parse_drug_snp_adverse_drug_reactions

Extracts the drug snp adverse drug reactions element and return data as tibble.

Description

parse_drug_snp_adverse_drug_reactions returns tibble of drug snp adverse drug reactions elements.

Usage

```
parse_drug_snp_adverse_drug_reactions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the groups element of drug node in drugbank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned tibble in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug_snp_adverse_drug_reactions_node_attributes_tibble

Examples

```
parse_drug_snp_adverse_drug_reactions()  
parse_drug_snp_adverse_drug_reactions(TRUE)  
parse_drug_snp_adverse_drug_reactions(save_table = FALSE)
```

parse_drug_snp_effects

Extracts the drug_snp_effects element and return data as tibble.

Description

parse_drug_snp_effects returns tibble of snp effects groups elements.

Usage

```
parse_drug_snp_effects(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the snp effects element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug_snp_effects_node_attributes_tibble

Examples

```
parse_drug_snp_effects()  
parse_drug_snp_effects(TRUE)  
parse_drug_snp_effects(save_table = FALSE)
```

parse_drug_synonyms *Extracts the drug synonyms element and return data as tibble.*

Description

parse_drug_synonyms returns tibble of drug synonyms elements.

Usage

```
parse_drug_synonyms(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the synonyms element of drug node in drugbank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned tibble in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug synonyms node attributes tibble

Examples

```
parse_drug_synonyms()  
parse_drug_synonyms(TRUE)  
parse_drug_synonyms(save_table = FALSE)
```

parse_drug_targets *Extracts the drug targets element and return data as data frame.*

Description

parse_drug_targets returns data frame of drug targets elements.

Usage

```
parse_drug_targets(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the target element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug target node attributes data frame

Examples

```
parse_drug_targets()  
parse_drug_targets(TRUE)  
parse_drug_targets(save_table = FALSE)
```

parse_drug_targets_actions

Extracts the drug targets actions element and return data as data frame.

Description

parse_drug_targets_actions returns data frame of drug targets actions elements.

Usage

```
parse_drug_targets_actions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets actions element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug targets actions node attributes date frame

Examples

```
parse_drug_targets_actions()
parse_drug_targets_actions(TRUE)
parse_drug_targets_actions(save_table = FALSE)
```

parse_drug_targets_articles

Extracts the drug targets articles element and return data as data frame.

Description

parse_drug_targets_articles returns data frame of drug targets articles elements.

Usage

```
parse_drug_targets_articles(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets articles element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets articles node attributes date frame

Examples

```
parse_drug_targets_articles()
parse_drug_targets_articles(TRUE)
parse_drug_targets_articles(save_table = FALSE)
```

parse_drug_targets_links

Extracts the drug targets links element and return data as data frame.

Description

parse_drug_targets_links returns data frame of drug targets links elements.

Usage

```
parse_drug_targets_links(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets links element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets_links node attributes data frame

Examples

```
parse_drug_targets_links()  
parse_drug_targets_links(TRUE)  
parse_drug_targets_links(save_table = FALSE)
```

parse_drug_targets_polypeptides

Extracts the drug targets polypeptides element and return data as data frame.

Description

parse_drug_targets_polypeptides returns data frame of drug targets polypeptides elements.

Usage

```
parse_drug_targets_polypeptides(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets polypeptides element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets polypeptides node attributes data frame

Examples

```
parse_drug_targets_polypeptides()  
parse_drug_targets_polypeptides(TRUE)  
parse_drug_targets_polypeptides(save_table = FALSE)
```

parse_drug_targets_polypeptides_external_identifiers

Extracts the drug targets polypeptides external identifiers element and return data as data frame.

Description

parse_drug_targets_polypeptides_external_identifiers returns data frame of drug targets polypeptides external identifiers elements.

Usage

```
parse_drug_targets_polypeptides_external_identifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets polypeptides external identifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets polypeptides external identifiers node attributes date frame

Examples

```
parse_drug_targets_polypeptides_external_identifiers()  
parse_drug_targets_polypeptides_external_identifiers(TRUE)  
parse_drug_targets_polypeptides_external_identifiers(save_table = FALSE)
```

parse_drug_targets_polypeptides_go_classifiers

Extracts the drug targets polypeptides go classifiers element and return data as data frame.

Description

parse_drug_targets_polypeptides_go_classifiers returns data frame of drug targets polypeptides go classifiers elements.

Usage

```
parse_drug_targets_polypeptides_go_classifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets polypeptides go classifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets polypeptides go classifiers node attributes date frame

Examples

```
parse_drug_targets_polypeptides_go_classifiers()  
parse_drug_targets_polypeptides_go_classifiers(TRUE)  
parse_drug_targets_polypeptides_go_classifiers(save_table = FALSE)
```

parse_drug_targets_polypeptides_pfams

Extracts the drug targets polypeptides pfams element and return data as data frame.

Description

parse_drug_targets_polypeptides_pfams returns data frame of drug targets polypeptides pfams elements.

Usage

```
parse_drug_targets_polypeptides_pfams(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets polypeptides pfams element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets polypeptides pfams node attributes data frame

Examples

```
parse_drug_targets_polypeptides_pfams()  
parse_drug_targets_polypeptides_pfams(TRUE)  
parse_drug_targets_polypeptides_pfams(save_table = FALSE)
```

parse_drug_targets_polypeptides_synonyms

Extracts the drug targets polypeptides synonyms element and return data as data frame.

Description

parse_drug_targets_polypeptides_synonyms returns data frame of drug targets polypeptides synonyms elements.

Usage

```
parse_drug_targets_polypeptides_synonyms(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets polypeptides synonyms element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets polypeptides synonyms node attributes date frame

Examples

```
parse_drug_targets_polypeptides_synonyms()  
parse_drug_targets_polypeptides_synonyms(TRUE)  
parse_drug_targets_polypeptides_synonyms(save_table = FALSE)
```

parse_drug_targets_textbooks

Extracts the drug targets textbooks element and return data as data frame.

Description

parse_drug_targets_textbooks returns data frame of drug targets textbooks elements.

Usage

```
parse_drug_targets_textbooks(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the targets textbooks element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug targets textbooks node attributes data frame

Examples

```
parse_drug_targets_textbooks()  
parse_drug_targets_textbooks(TRUE)  
parse_drug_targets_textbooks(save_table = FALSE)
```

parse_drug_transporters

Extracts the drug transporters element and return data as data frame.

Description

parse_drug_transporters returns data frame of drug transporters elements.

Usage

```
parse_drug_transporters(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters node attributes data frame

Examples

```
parse_drug_transporters()  
parse_drug_transporters(TRUE)  
parse_drug_transporters(save_table = FALSE)
```

parse_drug_transporters_actions

Extracts the drug transporters actions element and return data as data frame.

Description

parse_drug_transporters_actions returns data frame of drug transporters actions elements.

Usage

```
parse_drug_transporters_actions(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters actions element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters actions node attributes date frame

Examples

```
parse_drug_transporters_actions()  
parse_drug_transporters_actions(TRUE)  
parse_drug_transporters_actions(save_table = FALSE)
```

parse_drug_transporters_articles

Extracts the drug transporters articles element and return data as data frame.

Description

`parse_drug_transporters_articles` returns data frame of drug transporters articles elements.

Usage

```
parse_drug_transporters_articles(save_table = FALSE)
```

Arguments

`save_table` boolean, save table in database if true.

Details

This functions extracts the transporters articles element of drug node in drug bank xml database with the option to save it in a predefined database via `open_db` method. It takes one single optional argument to save the returned dataframe in the database. It must be called after `get_xml_db_rows` function like any other parser function. If `get_xml_db_rows` is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters articles node attributes date frame

Examples

```
parse_drug_transporters_articles()  
parse_drug_transporters_articles(TRUE)  
parse_drug_transporters_articles(save_table = FALSE)
```

parse_drug_transporters_links

Extracts the drug transporters links element and return data as data frame.

Description

parse_drug_transporters_links returns data frame of drug transporters_inks elements.

Usage

```
parse_drug_transporters_links(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters links element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters links node attributes data frame

Examples

```
parse_drug_transporters_links()  
parse_drug_transporters_links(TRUE)  
parse_drug_transporters_links(save_table = FALSE)
```

parse_drug_transporters_polypeptides

Extracts the drug transporters polypeptides element and return data as data frame.

Description

parse_drug_transporters_polypeptides returns data frame of transporters polypeptides groups elements.

Usage

```
parse_drug_transporters_polypeptides(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters polypeptides element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters polypeptides node attributes date frame

Examples

```
parse_drug_transporters_polypeptides()  
parse_drug_transporters_polypeptides(TRUE)  
parse_drug_transporters_polypeptides(save_table = FALSE)
```

parse_drug_transporters_polypeptides_external_identifiers

Extracts the drug transporters polypeptides external identifiers element and return data as data frame.

Description

parse_drug_transporters_polypeptides_external_identifiers returns data frame of drug transporters polypeptides external identifiers elements.

Usage

```
parse_drug_transporters_polypeptides_external_identifiers(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters polypeptides external identifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters polypeptides external identifiers node attributes data frame

Examples

```
parse_drug_transporters_polypeptides_external_identifiers()  
parse_drug_transporters_polypeptides_external_identifiers(TRUE)  
parse_drug_transporters_polypeptides_external_identifiers(save_table = FALSE)
```

`parse_drug_transporters_polypeptides_go_classifiers`

Extracts the drug transporters polypeptides go classifiers element and return data as data frame.

Description

`parse_drug_transporters_polypeptides_go_classifiers` returns data frame of drug transporters polypeptides go classifiers elements.

Usage

```
parse_drug_transporters_polypeptides_go_classifiers(save_table = FALSE)
```

Arguments

`save_table` boolean, save table in database if true.

Details

This functions extracts the transporters polypeptides go classifiers element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters polypeptides go classifiers node attributes date frame

Examples

```
parse_drug_transporters_polypeptides_go_classifiers()  
parse_drug_transporters_polypeptides_go_classifiers(TRUE)  
parse_drug_transporters_polypeptides_go_classifiers(save_table = FALSE)
```

parse_drug_transporters_polypeptides_pfams

Extracts the drug transporters polypeptides pfams element and return data as data frame.

Description

parse_drug_transporters_polypeptides_pfams returns data frame of drug transporters polypeptides pfams elements.

Usage

```
parse_drug_transporters_polypeptides_pfams(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters polypeptides pfams element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters polypeptides pfams node attributes date frame

Examples

```
parse_drug_transporters_polypeptides_pfams()  
parse_drug_transporters_polypeptides_pfams(TRUE)  
parse_drug_transporters_polypeptides_pfams(save_table = FALSE)
```

`parse_drug_transporters_polypeptides_synonyms`

Extracts the drug transporters polypeptides synonyms element and return data as data frame.

Description

`parse_drug_transporters_polypeptides_synonyms` returns data frame of drug transporters polypeptides synonyms elements.

Usage

```
parse_drug_transporters_polypeptides_synonyms(save_table = FALSE)
```

Arguments

`save_table` boolean, save table in database if true.

Details

This functions extracts the transporters polypeptides synonyms element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters polypeptides synonyms node attributes date frame

Examples

```
parse_drug_transporters_polypeptides_synonyms()  
parse_drug_transporters_polypeptides_synonyms(TRUE)  
parse_drug_transporters_polypeptides_synonyms(save_table = FALSE)
```

parse_drug_transporters_textbooks

Extracts the drug transporters textbooks element and return data as data frame.

Description

parse_drug_transporters_textbooks returns data frame of drug transporters textbooks elements.

Usage

```
parse_drug_transporters_textbooks(save_table = FALSE)
```

Arguments

save_table boolean, save table in database if true.

Details

This functions extracts the transporters textbooks element of drug node in drug bank xml database with the option to save it in a predefined database via [open_db](#) method. It takes one single optional argument to save the returned dataframe in the database. It must be called after [get_xml_db_rows](#) function like any other parser function. If [get_xml_db_rows](#) is called before for any reason, so no need to call it again before calling this function.

Value

drug transporters textbooks node attributes data frame

Examples

```
parse_drug_transporters_textbooks()  
parse_drug_transporters_textbooks(TRUE)  
parse_drug_transporters_textbooks(save_table = FALSE)
```

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