

# Package ‘dbparser’

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**Title** 'DrugBank' Database XML Parser

**Version** 1.0.0

**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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**VignetteBuilder** knitr

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**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.

**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**

nothing but sets the db tree in memory to be used by parser methods

**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 data frame.</i>
------------	---

---

**Description**

parse\_drug returns data frame 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 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 main node attributes data frame

**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 data frame.*

---

**Description**

parse\_drug\_affected\_organisms returns data frame 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 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 affected organisms node attributes date frame

**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 data frame.*

---

### Description

parse\_drug\_ahfs\_codes returns data frame 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 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 ahfs codes node attributes date frame

### 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 data frame.*

---

**Description**

parse\_drug\_articles returns data frame 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 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 articles node attributes data frame

## 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 data frame.*

---

### Description

parse\_drug\_books returns data frame 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 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 books node attributes date frame

### 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_carriers_links` 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 functions 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 date 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 data frame.*

---

### Description

parse\_drug\_categories returns data frame 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 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 categories node attributes date frame

**Examples**

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

---

parse\_drug\_classifications

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

---

**Description**

parse\_drug\_classifications returns data frame of drug classifications elements.

**Usage**

```
parse_drug_classifications(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_classifications()  
parse_drug_classifications(TRUE)  
parse_drug_classifications(save_table = FALSE)
```

---

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

---

**Description**

parse\_drug\_dosages returns data frame 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 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 dosages node attributes data frame

**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 data frame.*

---

### Description

parse\_drug\_experimental\_properties returns data frame 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 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 experimental properties node attributes data frame

**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 data frame.*

---

**Description**

parse\_drug\_external\_identifiers returns data frame 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 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 external identifiers node attributes date frame

**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 data frame.*

---

**Description**

`parse_drug_external_links` returns data frame 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 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 external links node attributes date frame

## 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 data frame.*

---

## Description

parse\_drug\_food\_interactions returns data frame 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 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 food interactions node attributes data frame

## 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 data frame.*

---

**Description**

parse\_drug\_groups returns data frame 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 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_groups()  
parse_drug_groups(TRUE)  
parse_drug_groups(save_table = FALSE)
```

---

parse\_drug\_interactions      *Extracts the drug interactions element and return data as data frame.*

---

**Description**

parse\_drug\_interactions returns data frame 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 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 interactions node attributes date frame

**Examples**

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

---

parse\_drug\_links      *Extracts the drug links element and return data as data frame.*

---

**Description**

parse\_drug\_links returns data frame 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 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 links node attributes date frame

## 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 data 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 data frame.*

---

### Description

parse\_drug\_mixtures returns data frame 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 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 mixtures node attributes date frame

### 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 data frame.*

---

### Description

parse\_drug\_packagers returns data frame 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 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 packagers node attributes date frame

**Examples**

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

---

parse\_drug\_patents      *Extracts the drug patents element and return data as data frame.*

---

**Description**

parse\_drug\_patents returns data frame 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 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 patents node attributes date frame



## Examples

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

---

parse_drug_pathway	<i>Extracts the drug pathway element and return data as data frame.</i>
--------------------	---

---

## 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 data 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 data frame.*

---

**Description**

parse\_drug\_pdb\_entries returns data frame 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 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 pdb entries node attributes date frame

**Examples**

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

---

parse_drug_prices	<i>Extracts the drug prices element and return data as data frame.</i>
-------------------	--

---

**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 data frame.*

---

## Description

parse\_drug\_products returns data frame 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 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 products node attributes data frame

## 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 date frame

**Examples**

```
parse_drug_reactions_enzymes()  
parse_drug_reactions_enzymes(TRUE)  
parse_drug_reactions_enzymes(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 data frame.*

---

## Description

parse\_drug\_snp\_adverse\_drug\_reactions returns data frame 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 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 snp adverse drug reactions node attributes date frame

## 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 data frame.*

---

### Description

parse\_drug\_snp\_effects returns data frame 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 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 snp effects node attributes data frame

### 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 data frame.*

---

### Description

parse\_drug\_synonyms returns data frame 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 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 synonyms node attributes data frame

**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 data 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 data 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 date 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 data 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 date 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 date 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 date 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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