

# Package ‘gDRimport’

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**Type** Package

**Title** Package for handling the import of dose-response data

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**Description** The package is a part of the gDR suite. It helps to prepare raw drug response data for downstream processing. It mainly contains helper functions for importing/loading/validating dose-response data provided in different file formats.

**License** Artistic-2.0

**LazyLoad** yes

**Depends** R (>= 4.2)

**Imports** assertthat, BumpyMatrix, checkmate, CoreGx, PharmacoGx, data.table, futile.logger, gDRutils (>= 1.7.1), magrittr, methods, MultiAssayExperiment, readxl, rio, S4Vectors, stats, stringi, SummarizedExperiment, tibble, tools, utils, XML, yaml, openxlsx

**Suggests** BiocStyle, gDRtestData (>= 1.7.1), gDRstyle (>= 1.7.1), knitr, purrr, qs, testthat

**URL** <https://github.com/gdrplatform/gDRimport>,  
<https://gdrplatform.github.io/gDRimport/>

**BugReports** <https://github.com/gdrplatform/gDRimport/issues>

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gDRimport-package	<i>gDRimport: Package for handling the import of dose-response data</i>
-------------------	---

---

## Description

The package is a part of the gDR suite. It helps to prepare raw drug response data for downstream processing. It mainly contains helper functions for importing/loading/validating dose-response data provided in different file formats.

## Value

package help page

**Note**

To learn more about functions start with `help(package = "gDRimport")`

**Author(s)**

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- Marc Hafner ([ORCID](#))
- Sergiu Mocanu
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- Allison Vuong
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**See Also**

Useful links:

- <https://github.com/gdrplatform/gDRimport>
- <https://gdrplatform.github.io/gDRimport/>
- Report bugs at <https://github.com/gdrplatform/gDRimport/issues>

---

`.check_against_single_template_sheet`

*Evaluate if template file with single sheet is present, if the name of the sheet is correct and if it can be fixed*

---

**Description**

get sheets for given set of XLS files

**Usage**

```
.check_against_single_template_sheet(ts)
```

**Arguments**

`ts` list with template sheets info

**Value**

logical flag

---

.check\_file\_structure *Check the structure of raw data*

---

### **Description**

Check the structure of raw data

### **Usage**

```
.check_file_structure(  
  df,  
  filename,  
  sheet_name,  
  readout_offset,  
  n_row,  
  n_col,  
  bcode_idx,  
  bcode_col  
)
```

### **Value**

NULL invisibly.

---

.createPseudoData *Add in pseudo-data for duration and cell reference division time*

---

### **Description**

Add in pseudo-data for duration and cell reference division time

### **Usage**

```
.createPseudoData(dt)
```

### **Value**

data.table

---

`.extractDoseResponse` *Get dose and viability readouts and melt into large data table*

---

**Description**

Get dose and viability readouts and melt into large data table

**Usage**

```
.extractDoseResponse(pset)
```

**Value**

data.table with dose-response data

---

`.extract_or_create_assay`

*Extracts an assay from a SummarizedExperiment object or creates a new one if it does not exist*

---

**Description**

This function takes a SummarizedExperiment object and an assay name as input. If the specified assay already exists in the SummarizedExperiment object, it is returned. Otherwise, a new assay with the specified name is created and added to the SummarizedExperiment object. The new assay is initialized with NA values. This is useful for when multiple Summarized Experiments in a given MAE do not have the same assays. And it is necessary to have the same assays in all Summarized Experiments in order to convert the MAE to a PSet.

**Usage**

```
.extract_or_create_assay(SE, assay_name)
```

**Arguments**

SE	A SummarizedExperiment object
assay_name	A character string specifying the name of the assay to extract or create

**Value**

A SummarizedExperiment object with the specified assay

---

.fill\_empty\_wells      *Correct plates with not fully filled readout values*

---

### Description

Correct plates with not fully filled readout values

### Usage

```
.fill_empty_wells(  
  df,  
  plate_rows,  
  data_rows,  
  exp_row,  
  exp_col,  
  numeric_regex = "^\\d+$"  
)
```

### Value

data.table with corrected plates data

---

.get\_plate\_size      *Get plate size*

---

### Description

Get plate size

### Usage

```
.get_plate_size(df)
```

### Details

All plate sizes assume 1.5x nrows = ncolumns.

### Value

charvec with plate dims

`.removeNegatives`      *Remove negative viabilities*

---

**Description**

Remove negative viabilities

**Usage**

```
.removeNegatives(dataset)
```

**Value**

data.table with positive values in column ReadoutValue

---

`.standardize_untreated_values`  
*Standardize untreated values to ignore cases*

---

**Description**

Standardize untreated values to ignore cases

**Usage**

```
.standardize_untreated_values(df)
```

**Value**

data.table with standardized untreated values

---

`are_template_sheets_valid`  
*are template sheet valid?*

---

**Description**

are template sheet valid?

**Usage**

```
are_template_sheets_valid(ts)
```

**Arguments**

ts                    list with (per file) template sheets

**Value**

logical flag

**See Also**

get\_xl\_sheets

---

check\_metadata\_against\_spaces  
*Check metadata against spaces*

---

**Description**

Check metadata against spaces

**Usage**

```
check_metadata_against_spaces(corrected_names, df_name)
```

**Arguments**

corrected\_names

a charvec with corrected colnames of df

df\_name

a name of data.table (" " by default)

**Value**

a charvec with corrected colnames of df

---

check\_metadata\_field\_names  
*Check metadata field names*

---

**Description**

Check metadata field names

**Usage**

```
check_metadata_field_names(corrected_names, df_name)
```

**Arguments**

corrected\_names

a charvec with corrected colnames of df

df\_name

a name of data.table (" " by default)

**Value**

a charvec with corrected colnames of df

---

check\_metadata\_headers

*Check whether metadata headers are correct and make fixes if needed*

---

### Description

Check whether metadata headers are correct and make fixes if needed

### Usage

```
check_metadata_headers(corrected_names, df_name)
```

### Arguments

corrected\_names            a charvec with corrected colnames of df  
df\_name                    a name of data.table ("" by default)

### Value

a charvec with corrected colnames of df

---

check\_metadata\_names    *check\_metadata\_names*

---

### Description

Check whether all metadata names are correct

### Usage

```
check_metadata_names(col_df, df_name = "", df_type = NULL)
```

### Arguments

col\_df                    a character with colnames of df  
df\_name                    a name of data.table ("" by default)  
df\_type                    a type of a data.table (NULL by default)

### Value

a charvec with corrected colnames of df

### Examples

```
td <- get_test_data()
m_file <- manifest_path(td)
m_data <- read_excel_to_dt(m_file)
result <- check_metadata_names(col_df = colnames(m_data))
```

---

 check\_metadata\_req\_col\_names

*Check metadata for required column names*


---

**Description**

Check metadata for required column names

**Usage**

```
check_metadata_req_col_names(col_df, df_name, df_type)
```

**Arguments**

col_df	a charvec with corrected colnames of df
df_name	a name of data.table (" " by default)
df_type	a type of a data.table (NULL by default)

**Value**

NULL invisibly.

---

convert\_LEVEL5\_prism\_to\_gDR\_input

*Load, convert and process the level 5 PRISM data into a gDR input*


---

**Description**

Load, convert and process the level 5 PRISM data into a gDR input

**Usage**

```
convert_LEVEL5_prism_to_gDR_input(
  prism_data_path,
  meta_data_path,
  readout_min = 1.03
)
```

**Arguments**

prism_data_path	path to PRISM LEVEL5 csv file with data
meta_data_path	path to metadata file describing all cancer models/cell lines which are referenced by a dataset contained within the DepMap portal
readout_min	minimum ReadoutValue

**Value**

data.table object with input data for gDR pipeline

**Examples**

```
prism_data <- system.file("testdata/prism_sa.csv", package = "gDRimport")
prism_meta <- system.file("testdata/prism_model.csv", package = "gDRimport")
convert_LEVEL5_prism_to_gDR_input(prism_data, prism_meta)
```

---

```
convert_LEVEL6_prism_to_gDR_input
```

*Load, convert and process the level 6 PRISM data into a gDR input*

---

**Description**

Load, convert and process the level 6 PRISM data into a gDR input

**Usage**

```
convert_LEVEL6_prism_to_gDR_input(
  prism_data_path,
  cell_line_data_path,
  treatment_data_path,
  meta_data_path,
  readout_min = 1.03
)
```

**Arguments**

prism_data_path	path to PRISM LEVEL6 csv file with collapsed log fold change data
cell_line_data_path	path to cell line info data
treatment_data_path	path to collapsed treatment info data
meta_data_path	path to metadata file describing all cancer models/cell lines which are referenced by a dataset contained within the DepMap portal
readout_min	minimum ReadoutValue

**Value**

data.table object with input data for gDR pipeline

**Examples**

```
prism_data_path <- system.file("testdata/prism_collapsed_LOGFC.csv", package = "gDRimport")
cell_line_data_path <- system.file("testdata/prism_cell_lines.csv", package = "gDRimport")
treatment_data_path <- system.file("testdata/prism_treatment.csv", package = "gDRimport")
prism_meta <- system.file("testdata/prism_model.csv", package = "gDRimport")
convert_LEVEL6_prism_to_gDR_input(prism_data_path, cell_line_data_path, treatment_data_path, prism_meta)
```

---

convert_MAE_to_PSet	<i>Convert MultiAssayExperiment to TreatmentResponseExperiment</i>
---------------------	--

---

**Description**

This function converts a `MultiAssayExperiment` generated by `gDR` into a `TreatmentResponseExperiment` for use in the `PharmacGx` package. The resulting `PharmacSet` can be used for pharmacogenomic analysis of drug response.

**Usage**

```
convert_MAE_to_PSet(mae, pset_name)
```

**Arguments**

<code>mae</code>	A <code>MultiAssayExperiment</code> object generated by <code>gDR</code> .
<code>pset_name</code>	A character string specifying the name of the resulting <code>PharmacSet</code> object.

**Value**

A `PharmacSet` object.

**Examples**

```
# Convert a MultiAssayExperiment object to a PharmacSet object
m <- 20
n <- 10
rnames <- LETTERS[1:m]
cnames <- letters[1:n]
ref_gr_value <- matrix(runif(m * n), nrow = m, ncol = n, dimnames = list(rnames, cnames))
se <- SummarizedExperiment::SummarizedExperiment(assays = list(RefGRvalue = ref_gr_value),
                                                rowData = S4Vectors::DataFrame(rnames),
                                                colData = S4Vectors::DataFrame(cnames))
mae <- MultiAssayExperiment::MultiAssayExperiment(experiments = list("single-agent" = se))
convert_MAE_to_PSet(mae, "my_pset")
```

---

convert_pset_to_df	<i>Convert a PharmacSet to a data.table that is prepare for input into gDR pipeline</i>
--------------------	---

---

**Description**

Convert a `PharmacSet` to a `data.table` that is prepare for input into `gDR` pipeline

**Usage**

```
convert_pset_to_df(pharmacoset, run_parallel = TRUE, workers = 2L)
```

**Arguments**

pharmacoset      Pharmacoset object  
run\_parallel      logical, TRUE (default) if to run functions in Parallel, FALSE to run in serial  
workers           integer, number of workers defaults to 2L if run\_parallel is TRUE

**Value**

data.table of Pharmacoset's dose response data with column names aligned with gDR standard

**Author(s)**

Jermiah Joseph – collaboration with BHKLab

**Examples**

```
pset <- suppressMessages(getPSet(  
  "Tavor_2020",  
  psetDir = system.file("extdata/pset", package = "gDRimport"),  
  use_local_PSets_list = TRUE  
))  
dt <- convert_pset_to_df(pset)  
gDRutils::reset_env_identifiers()
```

---

correct\_template\_sheets

*Correct names of the template sheets (if required)*

---

**Description**

Correct names of the template sheets (if required)

**Usage**

```
correct_template_sheets(tfiles)
```

**Arguments**

tfiles            charvec with paths to template files

**Value**

charvec with paths to corrected sheet names

---

detect\_file\_format     *Detect format of results data*

---

**Description**

Detect format of results data

**Usage**

```
detect_file_format(results_file)
```

**Arguments**

results\_file     path to results data

**Value**

string of the detected file format

**Examples**

```
td2 <- get_test_Tecan_data()
detect_file_format(td2$r_files[1])
```

---

enhance\_raw\_edited\_EnVision\_df  
*Enhance raw edited EnVision data.table*

---

**Description**

Enhance raw edited EnVision data.table

**Usage**

```
enhance_raw_edited_EnVision_df(df, barcode_col, headers)
```

**Arguments**

df                     raw data.table  
barcode\_col           column number for barcode data  
headers                list with the headers

**Value**

data.table derived from EnVision data

---

fix\_typos\_with\_reference

*Fix typos using reference data*

---

### Description

Fix typos using reference data Evaluate given list of ids and try to update them

### Usage

```
fix_typos_with_reference(
  data,
  ref,
  method = c("exact", "grepl", "adist"),
  fix_underscores = FALSE
)
```

### Arguments

data	list of charvec(s) or charvec with data
ref	charvec with reference data
method	charvec type of the method to be used 'exact' is used to find identical entries from 'ref' in the data (after corrections and uppercase'ing) 'grepl' is used to find entries from 'ref' that might be somehow pre- or post- fixed
fix_underscores	logical flag fix the issues with underscores in data identifiers?

### Value

list or charvec with corrected data

---

gdr\_test\_data-class    *gDR Test Data object*

---

### Description

Object class gdr\_test\_data is build by function [get\\_test\\_data\(\)](#)

### Value

object class gdr\_test\_data with primary test data

**Slots**

manifest\_path character, path to manifest file  
 result\_path character, path(s) to results file  
 template\_path character, path(s) to data.table with template data  
 ref\_m\_df character, data.table with manifest data  
 ref\_r1\_r2 character, path to reference file with raw data for treated & untreated  
 ref\_r1 character, path to reference file with raw data for treated  
 ref\_t1\_t2 character, path to reference template file with treated & untreated data  
 ref\_t1 character, path to reference template file with treated data

---

getPSet	<i>Get PharmacoSet</i>
---------	------------------------

---

**Description**

Get PharmacoSet

**Usage**

```

getPSet(
  pset_name,
  psetDir = getwd(),
  canonical = FALSE,
  timeout = 600,
  use_local_PSets_list = FALSE
)

```

**Arguments**

pset_name	string with the name of the PharmacoSet
psetDir	string with the temporary directory for the PharmacoSet
canonical	logical flag indicating if the PSet canonical
timeout	maximum number of seconds allowed for PSet download
use_local_PSets_list	logical flag if PSets list should be used from local. If FALSE PSets list will be taken from web.

**Value**

PharmacoSet object

**Examples**

```

suppressMessages(getPSet(
  "Tavor_2020",
  psetDir = system.file("extdata/pset", package = "gDRimport"),
  use_local_PSets_list = TRUE
))

```

---

```
get_df_from_raw_edited_EnVision_df
```

*Get final results (as a data.table) from raw edited EnVision data.table*

---

### Description

Get final results (as a data.table) from raw edited EnVision data.table

### Usage

```
get_df_from_raw_edited_EnVision_df(
  df,
  barcode_idx,
  barcode_col,
  n_row,
  n_col,
  fname,
  sheet_name,
  headers
)
```

### Arguments

df	raw data.table
barcode_idx	numeric vector with barcode indices
barcode_col	column number for barcode data
n_row	number of rows
n_col	number of columns
fname	file name
sheet_name	name of the Excel sheet
headers	list with the headers

### Value

data.table derived from EnVision data

---

```
get_df_from_raw_unedited_EnVision_df
```

*Get final results (as a data.table) from raw unedited EnVision data.table*

---

### Description

Get final results (as a data.table) from raw unedited EnVision data.table

### Usage

```
get_df_from_raw_unedited_EnVision_df(df, n_row, n_col, barcode_col)
```

**Arguments**

df	raw data.table
n_row	number of rows
n_col	number of columns
barcode_col	column number for barcode data

**Value**

data.table derived from EnVision data

---

get\_EnVision\_properties

*Get properties of EnVision data*

---

**Description**

This function return properties of EnVision data

**Usage**

```
get_EnVision_properties(results.list, fname)
```

**Arguments**

results.list	list with EnVision data
fname	name of the input file

**Value**

list with EnVision propertiesa

---

get\_excel\_sheet\_names *get Excel sheets names for a charvec of files for non-Excel files return 0*

---

**Description**

get Excel sheets names for a charvec of files for non-Excel files return 0

**Usage**

```
get_excel_sheet_names(fls)
```

**Arguments**

fls	charvec with file pathsa
-----	--------------------------

**Value**

list with one element per file with sheet names or 0 (for non-Excel file)

get\_exception\_data      *get exception data*

---

**Description**

get exception data

**Usage**

```
get_exception_data(status_code = NULL)
```

**Arguments**

status\_code      A numeric value

**Value**

A data.table row with exception data or all exceptions

**Examples**

```
get_exception_data(1)
get_exception_data()
```

---

get\_expected\_template\_sheets

*Get names of the sheets expected in templates.xlsx*

---

**Description**

Get names of the sheets expected in templates.xlsx

**Usage**

```
get_expected_template_sheets(type = c("all", "core", "optional"))
```

**Arguments**

type              charvec type of the sheets

**Value**

string with type of the sheets

---

`get_plate_info_from_template_xlsx`  
*Get plate info from template xlsx*

---

**Description**

Get plate info from template xlsx

**Usage**

`get_plate_info_from_template_xlsx(template_file, Gnumber_idx, idx)`

**Arguments**

`template_file` character, file path(s) to template(s)  
`Gnumber_idx` index with Gnumber data  
`idx` template file index

**Value**

list with plate info

---

`get_test_D300_data` *get test D300 data*

---

**Description**

get test D300 data

**Usage**

`get_test_D300_data()`

**Value**

list with with input data (manifest/template/result paths) and related reference data (qs file paths)

**Examples**

`get_test_D300_data()`

---

<code>get_test_data</code>	<i>get primary test data</i>
----------------------------	------------------------------

---

**Description**

get primary test data

**Usage**

```
get_test_data()
```

**Value**

object class "gdr\_test\_data" with with input data (manifest/template/result paths) and related reference data (qs file paths)

**Examples**

```
get_test_data()
```

---

<code>get_test_EnVision_data</code>	<i>get test EnVision data</i>
-------------------------------------	-------------------------------

---

**Description**

get test EnVision data

**Usage**

```
get_test_EnVision_data()
```

**Value**

list with with input data (manifest/template/result paths) and related reference data (.qs file paths)

**Examples**

```
get_test_EnVision_data()
```

---

*get\_test\_Tecan\_data*     *get test Tecan data*

---

**Description**

get test Tecan data

**Usage**

`get_test_Tecan_data()`

**Value**

list with with input data (manifest/template/result paths) and related reference data (qs file paths)

**Examples**

`get_test_Tecan_data()`

---

*get\_test\_tsv\_data*     *get test tsv data*

---

**Description**

get test tsv data

**Usage**

`get_test_tsv_data()`

**Value**

list with with input data (manifest/template/result paths) and related reference data (.qs file paths)

**Examples**

`get_test_tsv_data()`

---

get_xl_sheets	<i>Get Excel sheets</i>
---------------	-------------------------

---

**Description**

get sheets for given set of XLS files

**Usage**

```
get_xl_sheets(files)
```

**Arguments**

files	charvec with file paths
-------	-------------------------

**Value**

named list where names are the excel filenames and the values are the sheets within each file

---

import_D300	<i>Import D300</i>
-------------	--------------------

---

**Description**

This functions takes a D300 file and generates corresponding template files

**Usage**

```
import_D300(D300_file, metadata_file, destination_path)
```

**Arguments**

D300_file	character, file path to D300 file
metadata_file	character, file path to file with mapping from D300 names to Gnumbers
destination_path	character, path to folder where template files will be generated

**Details**

For example, wells treated with 2 drugs in combination will result in 4 sheets per plate.

- Sheet 1: Drug 1
- Sheet 2: Conc of Drug 1
- Sheet 3: Drug 2
- Sheet 4: Conc of Drug 2

**Value**

Create one Excel file per plate. Each sheet in each plate file describes the drugs and corresponding concentrations of what was tested in each well.

**Examples**

```
td3 <- get_test_D300_data()[["f_96w"]]
o_path <- file.path(tempdir(), "td3")
dir.create(o_path)
import_D300(td3$d300, td3$Gnum, o_path)
list.files(o_path)
unlink(o_path, recursive = TRUE)
```

---

is_readable_v	<i>is_readable_v Check if all paths in vector are readable</i>
---------------	--

---

**Description**

is\_readable\_v Check if all paths in vector are readable

**Usage**

```
is_readable_v(paths)
```

**Arguments**

paths            a character with path(s)

**Value**

NULL invisibly.

**Examples**

```
td2 <- get_test_Tecan_data()
is_readable_v(td2$r_files)
```

---

load_data	<i>Load data</i>
-----------	------------------

---

**Description**

This functions loads and checks the data file(s)

**Usage**

```
load_data(
  manifest_file,
  df_template_files,
  results_file,
  instrument = "EnVision"
)
```

**Arguments**

manifest\_file character, file path(s) to manifest(s)  
df\_template\_files data.table, with datapaths and names of results file(s) or character with file path of templates file(s)  
results\_file data.table, with datapaths and names of results file(s) or character with file path of results file(s)  
instrument character

**Value**

a list with three data.tables for manifest/treatment and results

**Examples**

```
td <- get_test_data()
l_tbl <- load_data(manifest_path(td), template_path(td), result_path(td))
```

---

load_manifest	<i>Load manifest</i>
---------------	----------------------

---

**Description**

This functions loads and checks the manifest file(s)

**Usage**

```
load_manifest(manifest_file)
```

**Arguments**

manifest\_file character, file path(s) to manifest(s)

**Value**

list with manifest data.table and headers

**Examples**

```
td <- get_test_data()
ml <- load_manifest(manifest_path(td))
```

---

load_results	<i>Load results</i>
--------------	---------------------

---

**Description**

This functions loads and checks the results file(s)

**Usage**

```
load_results(
  df_results_files,
  instrument = "EnVision",
  headers = gDRutils::get_env_identifiers()
)
```

**Arguments**

df_results_files	data.table, with datapaths and names of results file(s) or character with file path of results file(s)
instrument	character
headers	list of headers identified in the manifest file

**Value**

data.table with results' data

**Examples**

```
td <- get_test_data()
r_df <- load_results(result_path(td))
```

---

load_results_EnVision	<i>Load EnVision results from xlsx</i>
-----------------------	--

---

**Description**

This functions loads and checks the results file(s)

**Usage**

```
load_results_EnVision(results_file, headers = gDRutils::get_env_identifiers())
```

**Arguments**

results_file	character vector containing file path(s) to results file(s)
headers	list of headers identified in the manifest

**Value**

data.table with results data

---

load_results_Tecan	<i>Load tecan results from xlsx</i>
--------------------	-------------------------------------

---

**Description**

This functions loads and checks the results file

**Usage**

```
load_results_Tecan(results_file, headers = gDRutils::get_env_identifiers())
```

**Arguments**

results_file	string, file path to a result file
headers	list of headers identified in the manifest

**Value**

data.table derived from Tecan data

---

load_results_tsv	<i>Load results from tsv</i>
------------------	------------------------------

---

**Description**

This functions loads and checks the results file(s)

**Usage**

```
load_results_tsv(results_file, headers)
```

**Arguments**

results_file	character, file path(s) to template(s)
headers	list of headers identified in the manifest

**Value**

data.table with results data

---

load_templates	<i>Load templates</i>
----------------	-----------------------

---

**Description**

This functions loads and checks the template file(s)

**Usage**

```
load_templates(df_template_files)
```

**Arguments**

df\_template\_files  
 data.table, with datapaths and names of results file(s) or character with file path of templates file(s)

**Value**

data.table with templates data

**Examples**

```
td <- get_test_data()
t_df <- load_templates(template_path(td))
```

---

load_templates_tsv	<i>Load templates from tsv</i>
--------------------	--------------------------------

---

**Description**

This functions loads and checks the template file(s)

**Usage**

```
load_templates_tsv(template_file, template_filename = NULL)
```

**Arguments**

template\_file character, file path(s) to template(s)  
 template\_filename  
 character, file name(s)

**Value**

data.table with template data

---

load_templates_xlsx	<i>Load templates from xlsx</i>
---------------------	---------------------------------

---

**Description**

This functions loads and checks the template file(s)

**Usage**

```
load_templates_xlsx(template_file, template_filename = NULL)
```

**Arguments**

```
template_file  character, file path(s) to template(s)
template_filename
                character, file name(s)
```

**Value**

data.table with templates data

---

manifest_path	<i>Method manifest_path</i>
---------------	-----------------------------

---

**Description**

Method for object gdr\_test\_data - access to slot manifest\_path

**Usage**

```
manifest_path(x)

## S4 method for signature 'gdr_test_data'
manifest_path(x)
```

**Arguments**

```
x                object class gdr_test_data
```

**Value**

value of slot manifest\_path

**Examples**

```
td <- get_test_data()
manifest_file_path <- manifest_path(td)
```

---

mgrepl	<i>grep wrapper to support multiple patterns</i>
--------	--

---

**Description**

grep wrapper to support multiple patterns

**Usage**

```
mgrepl(patterns, x, do_unlist = TRUE, ...)
```

**Arguments**

patterns	charvec with patterns to be checked
x	charvec with data
do_unlist	logical_flag unlist the final results?
...	additional argument

**Value**

list of charvec with grep output

---

parse_D300_xml	<i>Parse D300</i>
----------------	-------------------

---

**Description**

This function parses a D300 \*.tdd file (XML format) into a data.table

**Usage**

```
parse_D300_xml(D300_file)
```

**Arguments**

D300_file	string, file path to D300 .tdd file
-----------	-------------------------------------

**Value**

data.table representing input D300\_file.

**Examples**

```
td3 <- get_test_D300_data()
fs <- td3[["f_96w"]]
dose_df <- parse_D300_xml(fs[["d300"]])
```

---

read\_EnVision\_delim    *Read EnVision delimited text files*

---

**Description**

This function reads file from the EnVision Workstation

**Usage**

```
read_EnVision_delim(file, nrows = 10000, seps = c(", ", "\t"))
```

**Arguments**

file	string to path of input file from EnVision scanner
nrows	maximum number of file rows to be processed
seps	potential field separators of the input file

**Value**

a list containing the data table, n\_col, n\_row, and if is edited

---

read\_EnVision\_xlsx    *Read in single xlsx data from EnVision*

---

**Description**

Read in single xlsx data from EnVision

**Usage**

```
read_EnVision_xlsx(results_file, results_sheet)
```

**Arguments**

results_file	character, file path(s) to results file(s)
results_sheet	results sheet names

**Value**

data.table with results data

---

read\_excel\_to\_dt      *Read excel file and transform it into data.table object*

---

**Description**

Read excel file and transform it into data.table object

**Usage**

```
read_excel_to_dt(path, ...)
```

**Arguments**

path                    path to excel file  
...                    other arguments that should be passed into readxl::read\_excel

**Value**

data.table object with read excel file

**Examples**

```
datasets <- readxl::readxl_example("datasets.xlsx")  
read_excel_to_dt(datasets)
```

---

read\_in\_EnVision\_file      *Read EnVision file*

---

**Description**

This function reads file from the EnVision Workstation

**Usage**

```
read_in_EnVision_file(file, nrows, seps)
```

**Arguments**

file                    input file from EnVision  
nrows                   maximum number of file rows to be processed  
seps                    potential field separators of the input file

**Value**

list with one element per EnVisoin input file

read\_in\_manifest\_file *read manifest files*

---

**Description**

read manifest files

**Usage**

```
read_in_manifest_file(manifest_file, available_formats)
```

**Arguments**

manifest\_file character, file path(s) to manifest(s)  
available\_formats charvec with available file formats

**Value**

a data.table with manifest data

---

read\_in\_results\_Tecan *read in Tecan data*

---

**Description**

read in Tecan data

**Usage**

```
read_in_results_Tecan(results_file, results_sheets, headers)
```

**Arguments**

results\_file string, file path to a result file  
results\_sheets template sheet names  
headers list of headers identified in the manifest

**Value**

data.table derived from Tecan data

---

read\_in\_result\_files *Read in results files*

---

**Description**

Read in results files

**Usage**

```
read_in_result_files(results_file, results_filename, headers)
```

**Arguments**

results\_file    data.table, with datapaths and names of results file(s) or character with file path of results file(s)

results\_filename    charvect with file names

headers        list of headers identified in the result files

**Value**

data.table with results data

---

read\_in\_template\_sheet\_xlsx  
*Read in data from xlsx template sheet*

---

**Description**

Read in data from xlsx template sheet

**Usage**

```
read_in_template_sheet_xlsx(template_file, template_sheets, idx, plate_info)
```

**Arguments**

template\_file    character, file path(s) to template(s)

template\_sheets    template sheet names

idx            template file index

plate\_info      list with plate info

**Value**

data.table with template data

---

read\_in\_template\_xlsx *Read in xlsx template files*

---

**Description**

Read in xlsx template files

**Usage**

```
read_in_template_xlsx(template_file, template_filename, template_sheets)
```

**Arguments**

template\_file character, file path(s) to template(s)  
template\_filename  
character, file name(s)  
template\_sheets  
template sheet names

**Value**

data.table with templates data

---

read\_in\_tsv\_template\_files  
*read in tsv template files*

---

**Description**

read in tsv template files

**Usage**

```
read_in_tsv_template_files(template_file, template_filename, templates)
```

**Arguments**

template\_file character, file path(s) to template(s)  
template\_filename  
character, file name(s)  
templates list with templates data

**Value**

data.table with templates data

---

read_ref_data	<i>read_ref_data</i>
---------------	----------------------

---

**Description**

Read reference data

**Usage**

```
read_ref_data(inDir, prefix = "ref")
```

**Arguments**

inDir	a directory path of reference data
prefix	a prefix of reference file names ('ref' by default)

**Value**

a list of reference data

---

result_path	<i>Method result_path</i>
-------------	---------------------------

---

**Description**

Method for object gdr\_test\_data - access to slot result\_path

**Usage**

```
result_path(x)

## S4 method for signature 'gdr_test_data'
result_path(x)
```

**Arguments**

x	object class gdr_test_data
---	----------------------------

**Value**

value of slot result\_path

**Examples**

```
td <- get_test_data()
result_file_path <- result_path(td)
```

save\_drug\_info\_per\_well

*for each drug create a Gnumber and Concentration information for each well*

---

**Description**

for each drug create a Gnumber and Concentration information for each well

**Usage**

```
save_drug_info_per_well(trt_info, trt_gnumber_conc, wb, idfs)
```

**Arguments**

trt_info	list with treatment info
trt_gnumber_conc	list with treatment data
wb	pointer to xlsx workbook
idfs	charvec with identifiers

**Value**

NULL invisibly.

---

setEnvForPSet

*Adjust environment variables to meet gDR standards*

---

**Description**

Adjust environment variables to meet gDR standards

**Usage**

```
setEnvForPSet()
```

**Value**

NULL

**Examples**

```
setEnvForPSet()  
gDRutils::reset_env_identifiers()
```

---

```
standardize_record_values
      standardize_record_values
```

---

**Description**

map values to a dictionary

**Usage**

```
standardize_record_values(x, dictionary = DICTIONARY)
```

**Arguments**

x	a named array
dictionary	a named array

**Value**

a named array with updated names

**Examples**

```
standardize_record_values(c("Vehicle", "vehcle"))
```

---

```
template_path      Method template_path
```

---

**Description**

Method for object gdr\_test\_data - access to slot template\_path

**Usage**

```
template_path(x)

## S4 method for signature 'gdr_test_data'
template_path(x)
```

**Arguments**

x	object class gdr_test_data
---	----------------------------

**Value**

value of slot template\_path

**Examples**

```
td <- get_test_data()
template_file_path <- template_path(td)
```

---

`validate_template_xlsx`*Validate template xlsx data*

---

**Description**

Validate template xlsx data

**Usage**

```
validate_template_xlsx(template_file, template_filename, template_sheets, idx)
```

**Arguments**

<code>template_file</code>	character, file path(s) to template(s)
<code>template_filename</code>	character, file name(s)
<code>template_sheets</code>	template sheet names
<code>idx</code>	template file index

**Value**

NULL invisibly.

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