

# Package: gDR (via r-universe)

June 14, 2026

**Type** Package

**Title** Umbrella package for R packages in the gDR suite

**Version** 1.10.0

**Date** 2025-10-30

**Description** Package is a part of the gDR suite. It reexports functions from other packages in the gDR suite that contain critical processing functions and utilities. The vignette walks through the full processing pipeline for drug response analyses that the gDR suite offers.

**License** Artistic-2.0

**Depends** R (>= 4.2), gDRcore (>= 1.7.1), gDRimport (>= 1.7.1), gDRutils (>= 1.7.1)

**Suggests** BiocStyle, BumpyMatrix, futile.logger, gDRstyle (>= 1.7.1), gDRtestData (>= 1.7.1), kableExtra, knitr, markdown, purrr, rmarkdown, SummarizedExperiment, testthat, yaml

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

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

**biocViews** Software, DataImport, ShinyApps

**VignetteBuilder** knitr

**ByteCompile** TRUE

**LazyLoad** yes

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.1

**SwitchrLibrary** gDR

**DeploySubPath** gDR

**Encoding** UTF-8

**Config/pak/sysreqs** cmake libgmp-dev make libicu-dev libuv1-dev libxml2-dev libssl-dev libnode-dev libx11-dev zlib1g-dev

**Repository** <https://bioc-release.r-universe.dev>

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**RemoteUrl** <https://github.com/bioc/gDR>

**RemoteRef** RELEASE\_3\_23

**RemoteSha** bb3828080d224cd21f1db1a7f5a2b8749b592864

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import_data	<i>Import raw data</i>
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## Description

Import raw data

## Usage

```
import_data(
  manifest_file,
  template_file,
  results_file,
  instrument = "EnVision"
)
```

## Arguments

manifest_file	character, file path(s) to manifest(s)
template_file	character, with datapaths and names of results file(s) or character with file path of templates file(s)
results_file	character, with datapaths and names of results file(s) or character with file path of results file(s)
instrument	string with type of instrument used

## Value

a data.table

## Examples

```
td <- get_test_data()
i_df <- import_data(manifest_path(td), template_path(td), result_path(td))
```

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small_combo_data	<i>Small data.table with raw combo data used for processing via gDR</i>
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## Description

A dataset containing the ReadoutValues for combo experiments made-up of 3 drugs, 2 co-drugs, and 2 cell lines

## Usage

```
data(small_combo_data)
```

## Format

A data frame with 3600 rows and 16 variables:

**Barcode** barcode  
**clid** cell line id  
**CellLineName** cell line name  
**Tissue** cell line tissue  
**ReferenceDivisionTime** cell line division time  
**Gnumber** drug id  
**DrugName** drug name  
**drug\_moa** drug mode of action  
**Concentration** drug concentration  
**Gnumber\_2** co-drug id  
**DrugName\_2** co-drug name  
**drug\_moa\_2** co-drug mode of action  
**Concentration\_2** co-drug concentration  
**ReadoutValue** readout value  
**BackgroundValue** background value  
**Duration** duration

## Value

data.table

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`small_data`*Small data.table with raw data used for processing via gDR*

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**Description**

A dataset containing the ReadoutValues for single-agent experiments made-up of 10 drugs and 10 cell lines

**Usage**

```
data(small_data)
```

**Format**

A data frame with 3300 rows and 12 variables:

**Barcode** barcode

**clid** cell line id

**CellLineName** cell line name

**Tissue** cell line tissue

**ReferenceDivisionTime** cell line division time

**Gnumber** drug id

**DrugName** drug name

**drug\_moa** drug mode of action

**Concentration** drug concentration

**ReadoutValue** readout value

**BackgroundValue** background value

**Duration** duration

**Value**

data.table

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