

# Package ‘pogos’

November 28, 2025

**Title** PharmacOGenomics Ontology Support

**Description** Provide simple utilities for querying bhklab PharmacODB, modeling API outputs, and integrating to cell and compound ontologies.

**Version** 1.31.0

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**Suggests** knitr, DT, ontologyPlot, testthat, rmarkdown, BiocStyle

**Imports** methods, S4Vectors, utils, shiny, ontoProc, ggplot2, graphics

**Depends** R (>= 3.5.0), rjson (>= 0.2.15), httr (>= 1.3.1)

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**License** Artistic-2.0

**LazyLoad** yes

**LazyData** yes

**biocViews** Pharmacogenomics, PooledScreens, ImmunoOncology

**RoxygenNote** 7.3.2

**VignetteBuilder** knitr

**Encoding** UTF-8

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|              |                                                        |
|--------------|--------------------------------------------------------|
| basicDecoder | <i>convert binary output of GET()\$content to list</i> |
|--------------|--------------------------------------------------------|

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**Description**

convert binary output of GET()\$content to list

**Usage**

basicDecoder(x)

**Arguments**

x                      string suitable for input to GET as GET(x)

**Value**

output of fromJSON, typically a list

**Examples**

```
cl = try(basicDecoder('https://pharmacodb.pmgenomics.ca/api/v1/cell_lines'))
if (!inherits(cl, "try-error")) unlist(cl) # or pmgenomics is down
```

---

|                 |                                                                 |
|-----------------|-----------------------------------------------------------------|
| compoundsByCell | <i>initial version of compound browser over pharmacDb cells</i> |
|-----------------|-----------------------------------------------------------------|

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**Description**

initial version of compound browser over pharmacDb cells

**Usage**

compoundsByCell()

**Value**

only used for side effect of running shiny app

**Note**

Simple shiny app demonstrating coverage of PharmacoDb compounds by CHEBI. If a cell line selected is not present in selected dataset, the app will wait for a compatible selection to be made.

**Examples**

```
if (!requireNamespace("shiny")) stop("install shiny to use compoundsByCell")
if (interactive()) print(compoundsByCell())
```

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|              |                                                                         |
|--------------|-------------------------------------------------------------------------|
| compounds_v1 | <i>compounds_v1: serialization of compounds info from PharmacoDb v1</i> |
|--------------|-------------------------------------------------------------------------|

---

**Description**

compounds\_v1: serialization of compounds info from PharmacoDb v1

**Usage**

```
compounds_v1
tissues_v1
cell_lines_v1
datasets_v1
CCLE_drts
```

**Format**

```
S4Vectors DataFrame instance
S4Vectors DataFrame instance
S4Vectors DataFrame instance
S4Vectors DataFrame instance
DRTraceSet instance
```

**Source**

```
PharmacoDb Sept 2017
PharmacoDb Sept 2017
PharmacoDb Sept 2017
PharmacoDb Sept 2017
PharmacoDb April 2018
```

**Examples**

```
data(compounds_v1)
head(compounds_v1)
data(tissues_v1)
head(tissues_v1)
data(cell_lines_v1)
head(cell_lines_v1)
data(datasets_v1)
head(datasets_v1)
data(CCLE_drts)
CCLE_drts
```

---

|                 |                                                                                                                     |
|-----------------|---------------------------------------------------------------------------------------------------------------------|
| DRProfile-class | <i>DRProfSet is a class for managing dose-response information about cell lines from a pharmacogenomics dataset</i> |
|-----------------|---------------------------------------------------------------------------------------------------------------------|

---

**Description**

DRProfSet is a class for managing dose-response information about cell lines from a pharmacogenomics dataset

getDrugs extracts drug list

DRProfSet manages all data from a given cell line from a pharmacogenomics source

**Usage**

```
getDrugs(x)

DRProfSet(cell_line = "MCF7", dataset = "CCLE")

## S4 method for signature 'DRProfSet,missing'
plot(x, y, ...)
```

**Arguments**

|           |                                                       |
|-----------|-------------------------------------------------------|
| x         | instance of DRProfSet                                 |
| cell_line | character(1) cell line name, entries in cell_lines_v1 |
| dataset   | character(1) resource name, entries in datasets_v1    |
| y         | for plot: not used                                    |
| ...       | not used                                              |

**Value**

getDrugs: character vector  
instance of DRProfSet

**Examples**

```

if (interactive()) trs = DRTraceSet() else trs = iriCCLE()
ps = traces(trs)[[1]]
ps
getDrugs(ps)
if (interactive()) DRProfSet()

```

---

|                  |                                                                                                  |
|------------------|--------------------------------------------------------------------------------------------------|
| DRTraceSet-class | <i>DRTraceSet class manages dose-response information for a single cell line, multiple drugs</i> |
|------------------|--------------------------------------------------------------------------------------------------|

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**Description**

DRTraceSet class manages dose-response information for a single cell line, multiple drugs

DRTraceSet constructor for multiple cell lines, single drug, single dataset

**Usage**

```

## S4 method for signature 'DRTraceSet,missing'
plot(x, y, ...)

DRTraceSet(
  cell_lines = c("SK-ES-1", "TC-71", "MHH-ES-1", "HCC-56", "SK-HEP-1"),
  drug = "Irinotecan",
  dataset = "CCLE"
)

```

**Arguments**

|            |                                                                                             |
|------------|---------------------------------------------------------------------------------------------|
| x          | for plot: instance of DRTraceSet                                                            |
| y          | for plot: not used                                                                          |
| ...        | not used                                                                                    |
| cell_lines | character vector of cell line names, must be found in 'cell_lines_v1' data of pogos package |
| drug       | character(1) drug name in 'compounds_v1'                                                    |
| dataset    | character(1) dataset known to pharmacodb.pmgenomics.ca                                      |

**Value**

instance of DRTraceSet

**Note**

Will query pharmacodb for relevant dose-response information

**Examples**

```
val = try(DRTraceSet())
if (!inherits(val, "try-error")) val
# otherwise pharmacodb.pmgenomics.ca is down
```

---

|         |                                                                                           |
|---------|-------------------------------------------------------------------------------------------|
| iriCCLE | <i>obtain an example trace set stored locally, for irinotecan and selected cell lines</i> |
|---------|-------------------------------------------------------------------------------------------|

---

**Description**

obtain an example trace set stored locally, for irinotecan and selected cell lines

**Usage**

```
iriCCLE()
```

**Value**

an instance of DRTraceSet

**Examples**

```
iri = iriCCLE()
iri
plot(iri)
```

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|              |                                                                                              |
|--------------|----------------------------------------------------------------------------------------------|
| rxdbQuery_v1 | <i>very simple query formulation, build queries using endpoints of bhklab PharmacODB API</i> |
|--------------|----------------------------------------------------------------------------------------------|

---

**Description**

very simple query formulation, build queries using endpoints of bhklab PharmacODB API

**Usage**

```
rxdbQuery_v1(
  ...,
  url = "https://pharmacodb.pmgenomics.ca/api/v1/",
  decoder = basicDecoder
)
```

**Arguments**

|         |                                                                                                                   |
|---------|-------------------------------------------------------------------------------------------------------------------|
| ...     | typically a string representing an API endpoint, will be processed by unlist() and then to paste0 preceded by url |
| url     | of a PharmacODB server API target                                                                                 |
| decoder | a function of one argument that will be applied to API response (typically JSON)                                  |

**Value**

typically a list, dependent on decoder parameter

**Examples**

```
qout = try(rxdbQuery_v1('cell_lines')) # yields 30; append '?all=true' to retrieve all
if (!inherits(qout, "try-error")) unlist(lapply(qout, function(x) x[[2]]))
# or pmgenomics.ca is down
```

---

|                 |                                                                     |
|-----------------|---------------------------------------------------------------------|
| topEndpoints_v1 | <i>enumerate top level endpoint terms for bhklab PharmacODB API</i> |
|-----------------|---------------------------------------------------------------------|

---

**Description**

enumerate top level endpoint terms for bhklab PharmacODB API

**Usage**

```
topEndpoints_v1()
```

**Value**

a character vector of available endpoints

**Examples**

```
topEndpoints_v1()
```

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|        |                        |
|--------|------------------------|
| traces | <i>trace extractor</i> |
|--------|------------------------|

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**Description**

trace extractor

**Usage**

traces(x)

**Arguments**

x                      instance of DRTraceSet

**Value**

a list of DRProfile instances

**Examples**

```
iri = iriCCLE()
str(traces(iri)[[1]])
```

---

|                                      |                                                                                                       |
|--------------------------------------|-------------------------------------------------------------------------------------------------------|
| [,DRProfSet,character,ANY,ANY-method | <i>subscribing on DRProfSet extracts a profile for a single drug whose name constitutes the index</i> |
|--------------------------------------|-------------------------------------------------------------------------------------------------------|

---

**Description**

subscribing on DRProfSet extracts a profile for a single drug whose name constitutes the index

**Usage**

```
## S4 method for signature 'DRProfSet,character,ANY,ANY'
x[i, j, ..., drop = TRUE]
```

**Arguments**

|      |                        |
|------|------------------------|
| x    | instance of DRProfSet  |
| i    | character(1) drug name |
| j    | not used               |
| ...  | not used               |
| drop | logical(1) not used    |



*[,DRProfSet,character,ANY,ANY-method*

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**Value**

a DRProfSet instance restricted to experiments involving the selected drug

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