

# Package ‘pogos’

May 16, 2025

**Title** PharmacOGenomics Ontology Support

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

**Version** 1.29.0

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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

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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
```

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compoundsByCell	<i>initial version of compound browser over pharmacoDb cells</i>
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**Description**

initial version of compound browser over pharmacoDb 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())
```

---

`compounds_v1`*compounds\_v1: serialization of compounds info from PharmacoDb v1*

---

**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
```

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

---

### 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>
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---

**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
```

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

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

---

### Description

subscripting 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

### Value

a DRProfSet instance restricted to experiments involving the selected drug



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