

# Package ‘PhenotypeLibrary’

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**Type** Package

**Title** The OHDSI Phenotype Library

**Version** 3.30.1

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**Description** A repository to store the content of the OHDSI Phenotype library.

**Depends** R (>= 4.1.0)

**Imports** checkmate,  
readr,  
stringr,  
dplyr,  
rlang

**Suggests** reactable,  
testthat,  
knitr

**License** Apache License

**RoxygenNote** 7.2.3

**Roxygen** list(markdown = TRUE)

**Encoding** UTF-8

**Language** en-US

**VignetteBuilder** knitr

**URL** <https://ohdsi.github.io/PhenotypeLibrary/>, <https://github.com/OHDSI/PhenotypeLibrary>

**BugReports** <https://github.com/OHDSI/PhenotypeLibrary/issues>

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getPhenotypeLog	<i>Get phenotype log</i>
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**Description**

Get phenotype log

**Usage**

```
getPhenotypeLog(cohortIds = NULL, showHidden = FALSE)
```

**Arguments**

cohortIds	IDs of cohorts to extraction from the library.
showHidden	Some cohorts in the library are designed to be hidden. They are not retrieved by default. To retrieve such cohorts, please set showHidden as TRUE. Examples of hidden cohorts are withdrawn, deprecated, referrent cohorts.

**Value**

Returns a table with one row per cohort definitions with log information such as its release cycle. Example, this function gives us insight on when a cohort definition was added/updated/deprecated by the OHDSI PhenotypeLibrary.

A tibble.

**Examples**

```
getPhenotypeLog(cohortIds = c(1, 2))
```

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getPlCohortDefinitionSet	<i>Get a cohort definition set</i>
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**Description**

Get a cohort definition set

**Usage**

```
getPlCohortDefinitionSet(cohortIds)
```

**Arguments**

cohortIds	IDs of cohorts to extraction from the library.
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**Value**

A tibble with the cohort ID, name, sql, and JSON for the provided cohort IDs. Can be used by the CohortGenerator package.

**Examples**

```
cohorts <- getPhenotypeLog()
subsetIds <- cohorts$cohortId[1:3]
getPlCohortDefinitionSet(subsetIds)
```

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```
getPlConceptDefinitionSet
```

*Get conceptSets in cohorts*

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**Description**

Get conceptSets in cohorts

**Usage**

```
getPlConceptDefinitionSet(cohortIds = getPhenotypeLog()$cohortId)
```

**Arguments**

cohortIds            IDs of cohorts to extraction from the library.

**Value**

Returns a table with one row per concept set for given cohort definitions.  
A tibble.

**Examples**

```
getPhenotypeLog(cohortIds = c(1, 2))
```

---

```
listPhenotypes
```

*Deprecated. List all phenotypes in the library.*

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**Description**

Deprecated. List all phenotypes in the library.

**Usage**

```
listPhenotypes()
```

**Value**

A tibble with the cohort ID and name. Deprecated. Please use getPhenotypeLog

**Examples**

```
listPhenotypes()
```

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