

# Package ‘PhenotypeLibrary’

July 9, 2022

**Type** Package

**Title** The OHDSI Phenotype library

**Version** 3.1.2

**Date** 2022-07-09

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

**Imports** checkmate,

readr,

dplyr,

rlang

**Suggests** DatabaseConnector,

testthat,

rmarkdown,

knitr

**License** Apache License

**RoxygenNote** 7.2.0

**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 = listPhenotypes()$cohortId)
```

**Arguments**

cohortIds      IDs of cohorts to extraction from the library.

**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**

```
getPhenotypeReport(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.

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

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`listPhenotypes`*List all phenotypes in the library*

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**Description**

List all phenotypes in the library

**Usage**

```
listPhenotypes()
```

**Value**

A tibble with the cohort ID and name.

**Examples**

```
listPhenotypes()
```

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