

# Package ‘PhenotypeLibrary’

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**Type** Package

**Title** The OHDSI Phenotype Library

**Version** 3.22.2

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

**Depends** R (>= 4.1.0)

**Imports** checkmate,  
readr,  
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)
```

**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**

```
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.

**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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