

# Package: PACMOSData (via r-universe)

June 20, 2026

**Title** ExperimentHub Data for PACMOS

**Version** 0.99.0

**Description** Large reference datasets used by the PACMOS package for multi-omics and MOFA analysis of lung neuroendocrine neoplasms and MESOMICS data.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** false

**Depends** R (>= 4.3.0)

**Imports** ExperimentHub, AnnotationHub

**Suggests** ExperimentHubData, knitr, rmarkdown,

**VignetteBuilder** knitr

**biocViews** ExperimentData, Homo\_sapiens\_Data, CancerData, SequencingData, ExperimentHub

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.2

**Config/pak/sysreqs** libicu-dev libpng-dev libssl-dev zlib1g-dev

**Repository** <https://biocstaging.r-universe.dev>

**Date/Publication** 2026-05-22 17:39:51 UTC

**RemoteUrl** <https://github.com/BiocStaging/PACMOSData>

**RemoteRef** HEAD

**RemoteSha** 03c83e8ef9693f0386478de54b5c84224c4b2c91

## Contents

load_pacmos_data . . . . .	2
<b>Index</b>	<b>3</b>

---

load\_pacmos\_data      *Load PACMOSData resources by dataset*

---

**Description**

Load PACMOSData resources by dataset

**Usage**

```
load_pacmos_data(dataset = c("MESOMICS", "lungNENomics", "test"))
```

**Arguments**

dataset            One of "MESOMICS", "lungNENomics", or "test".

**Value**

A named list of PACMOSData resources.

**Examples**

```
library(PACMOSData)

mesomics <- load_pacmos_data("MESOMICS")
lungnen <- load_pacmos_data("lungNENomics")
test <- load_pacmos_data("test")
```

# Index

load\_pacmos\_data, [2](#)