

# Package ‘CLAMPData’

June 25, 2026

**Type** Package

**Title** Experiment data for CLAMP package

**Version** 0.99.5

**Description** Curated CLAMP resources (latent variables, loadings, priors, and example matrices) for use with the CLAMP package, distributed via ExperimentHub.

**License** MIT + file LICENSE

**Encoding** UTF-8

**LazyData** false

**Depends** R (>= 4.6.0)

**Imports** ExperimentHub, utils

**Suggests** ExperimentHubData, knitr, rmarkdown, BiocStyle, rhdf5, testthat (>= 3.0.0)

**VignetteBuilder** knitr

**biocViews** ExperimentHub, ExperimentData, RNASeqData, ExpressionData

**BugReports** <https://github.com/pivlab/CLAMPData/issues>

**URL** <https://github.com/pivlab/CLAMPData>

**Config/roxygen2/version** 8.0.0

**git\_url** <https://git.bioconductor.org/packages/CLAMPData>

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clamp_h5_schema	<i>Expected HDF5 schema for CLAMP expression files</i>
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### Description

Returns a data frame of the paths, types, and purpose of each dataset required in a CLAMP HDF5 expression file.

### Usage

```
clamp_h5_schema()
```

### Value

A data frame with columns path, type, and description.

### Examples

```
clamp_h5_schema()
```

---

GSE164416_DP_htseq_counts_txt_gz	<i>GSE164416_DP_htseq_counts_txt_gz</i>
----------------------------------	---

---

### Description

Retrieves the raw count matrix (path to gzipped file) for the GSE164416 dataset from ExperimentHub.

### Usage

```
GSE164416_DP_htseq_counts_txt_gz()
```

### Value

A character string representing the local file path to the downloaded resource.

**Examples**

```
if (interactive()) {
  counts_path <- GSE164416_DP_htseq_counts_txt_gz()
  print(counts_path)
}
```

---

```
human_gene_v2_5_alz_h5
  human_gene_v2_5_alz_h5
```

---

**Description**

Retrieves the H5 file (path) containing gene sets and pathway priors from ExperimentHub.

**Usage**

```
human_gene_v2_5_alz_h5()
```

**Value**

A character string representing the local file path to the downloaded resource.

**Examples**

```
if (interactive()) {
  h5_path <- human_gene_v2_5_alz_h5()
  print(h5_path)
}
```

---

```
islets_metadata_csv  islets_metadata_csv
```

---

**Description**

Retrieves the metadata CSV file (path) for the islets example from ExperimentHub.

**Usage**

```
islets_metadata_csv()
```

**Value**

A character string representing the local file path to the downloaded resource.

**Examples**

```
if (interactive()) {
  metadata_path <- islets_metadata_csv()
  print(metadata_path)
}
```

---

list\_clamp\_data      *List available CLAMPData datasets*

---

### Description

Returns a data frame of all datasets in the package, one row per resource. The accessor column names the function that returns the local file path for each resource.

### Usage

```
list_clamp_data()
```

### Value

A data.frame with columns name, accessor, description, type, species, eh\_id, and version.

### Examples

```
datasets <- list_clamp_data()
datasets[, c("name", "type", "eh_id")]
```

---

read\_clamp\_alz\_expression  
*Load the Alzheimer expression matrix*

---

### Description

Downloads the Alzheimer HDF5 file via ExperimentHub, validates it against [clamp\\_h5\\_schema](#), and returns the expression matrix oriented as genes x samples with gene symbols and sample identifiers as row and column names

### Usage

```
read_clamp_alz_expression()
```

### Value

A numeric matrix with gene symbols as row names and sample identifiers as column names.

### Examples

```
if (interactive()) {
  expr <- read_clamp_alz_expression()
  dim(expr)
}
```

---

read\_islet\_counts      *Load islet count table*

---

**Description**

Downloads the GSE164416 HTSeq count file via ExperimentHub and reads it as a data frame

**Usage**

```
read_islet_counts()
```

**Value**

A data frame with an `ensembl_gene-ID` column and one count column per sample.

**Examples**

```
if (interactive()) {  
  counts <- read_islet_counts()  
  dim(counts)  
}
```

---

read\_islet\_metadata      *Load islet sample metadata*

---

**Description**

Downloads the islet sample metadata CSV via ExperimentHub and reads it as a data frame

**Usage**

```
read_islet_metadata()
```

**Value**

A data frame with one row per sample.

**Examples**

```
if (interactive()) {  
  meta <- read_islet_metadata()  
  head(meta)  
}
```

---

validate_clamp_h5	<i>Validate a CLAMP HDF5 file</i>
-------------------	-----------------------------------

---

**Description**

Checks that an HDF5 file contains the datasets CLAMP expects (see [clamp\\_h5\\_schema](#)).

**Usage**

```
validate_clamp_h5(path)
```

**Arguments**

path	Path to an HDF5 file.
------	-----------------------

**Value**

TRUE invisibly if the file is valid; otherwise stops with a message listing the missing datasets.

**Examples**

```
if (interactive()) {  
  validate_clamp_h5(human_gene_v2_5_alz_h5())  
}
```

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