

# Package ‘ewceData’

May 21, 2026

**Title** The ewceData package provides reference data required for ewce

**Version** 1.21.0

**Description** This package provides reference data required for ewce. Expression Weighted Celltype Enrichment (EWCE) is used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies. The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

**URL** <https://github.com/neurogenomics/ewceData>

**License** Artistic-2.0

**Encoding** UTF-8

**Depends** R (>= 4.1), ExperimentHub

**Suggests** knitr, BiocStyle, ggplot2, cowplot, rmarkdown, markdown, rbibutils, testthat (>= 3.0.0)

**biocViews** ExperimentData, ExperimentHub, ExpressionData, Genome, Proteome, MicroarrayData, SequencingData, SingleCellData, RNASeqData

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.3.3

**VignetteBuilder** knitr

**Config/testthat/edition** 3

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all\_hgnc

*all\_hgnc*

---

### Description

all\_hgnc returns the all\_hgnc dataset

### Usage

```
all_hgnc(localHub = FALSE)
```

### Arguments

localHub      If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

### Value

all\_hgnc dataset

### Examples

```
all_hgnc()
```

---

all\_hgnc\_wtEnsembl      *all\_hgnc\_wtEnsembl*

---

**Description**

all\_hgnc\_wtEnsembl returns the all\_hgnc\_wtEnsembl dataset

**Usage**

```
all_hgnc_wtEnsembl(localHub = FALSE)
```

**Arguments**

localHub      If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

all\_hgnc\_wtEnsembl dataset

**Examples**

```
all_hgnc_wtEnsembl()
```

---

all\_mgi      *all\_mgi*

---

**Description**

all\_mgi returns the all\_mgi dataset

**Usage**

```
all_mgi(localHub = FALSE)
```

**Arguments**

localHub      If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

all\_mgi dataset

**Examples**

```
all_mgi()
```

---

`all_mgi_wtEnsembl`      *all\_mgi\_wtEnsembl*

---

**Description**

`all_mgi_wtEnsembl` returns the `all_mgi_wtEnsembl` dataset

**Usage**

```
all_mgi_wtEnsembl(localHub = FALSE)
```

**Arguments**

`localHub`      If working offline, add argument `localHub=TRUE` to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

`all_mgi_wtEnsembl` dataset

**Examples**

```
all_mgi_wtEnsembl()
```

---

`alzh_gwas_top100`      *alzh\_gwas\_top100*

---

**Description**

`alzh_gwas_top100` returns the `alzh_gwas_top100` dataset

**Usage**

```
alzh_gwas_top100(localHub = FALSE)
```

**Arguments**

`localHub`      If working offline, add argument `localHub=TRUE` to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

`alzh_gwas_top100` dataset

**Examples**

```
alzh_gwas_top100
```

---

cortex_mrna	<i>cortex_mrna</i>
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---

**Description**

cortex\_mrna returns the cortex\_mrna dataset

**Usage**

```
cortex_mrna(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

cortex\_mrna dataset

**Examples**

```
cortex_mrna()
```

---

ctd	<i>ctd</i>
-----	------------

---

**Description**

ctd returns the ctd dataset

**Usage**

```
ctd(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

ctd dataset

**Examples**

```
ctd()
```

---

```
ensembl_transcript_lengths_GCcontent
  ensembl_transcript_lengths_GCcontent
```

---

**Description**

ensembl\_transcript\_lengths\_GCcontent returns the ensembl\_transcript\_lengths\_GCcontent dataset

**Usage**

```
ensembl_transcript_lengths_GCcontent(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
----------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

**Value**

ensembl\_transcript\_lengths\_GCcontent dataset

**Examples**

```
ensembl_transcript_lengths_GCcontent()
```

---

ewceData	<i>The ewceData package provides reference data required for ewce</i>
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**Description**

This package provides reference data required for ewce. Expression Weighted Celltype Enrichment (EWCE) is used to determine which cell types are enriched within gene lists. The package provides tools for testing enrichments within simple gene lists (such as human disease associated genes) and those resulting from differential expression studies. The package does not depend upon any particular Single Cell Transcriptome dataset and user defined datasets can be loaded in and used in the analyses.

**Arguments**

metadata	logical value indicating whether metadata only should be returned or if the resource should be loaded. Default behavior(metadata=FALSE) loads the data.
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**Value**

These accessor functions return differing dataset types

**Source**

These datasets have been sourced from various repositories, see the ExperimentHub database for details

**Examples**

```
alzh_gwas_top100()
```

---

example_genelist	<i>example_genelist</i>
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---

**Description**

example\_genelist returns the example\_genelist dataset

**Usage**

```
example_genelist(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

example\_genelist dataset

**Examples**

```
example_genelist()
```

---

hpsd_genes	<i>hpsd_genes</i>
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---

**Description**

hpsd\_genes returns the hpsd\_genes dataset

**Usage**

```
hpsd_genes(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

hpsd\_genes dataset

**Examples**

```
hpsd_genes()
```

---

hypothalamus_mrna	<i>hypothalamus_mrna</i>
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---

**Description**

hypothalamus\_mrna returns the hypothalamus\_mrna dataset

**Usage**

```
hypothalamus_mrna(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

hypothalamus\_mrna dataset

**Examples**

```
hypothalamus_mrna()
```

---

id_genes	<i>id_genes</i>
----------	-----------------

---

**Description**

id\_genes returns the id\_genes dataset

**Usage**

```
id_genes(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

id\_genes dataset

**Examples**

```
id_genes()
```

---

mgi_synonym_data	<i>mgi_synonym_data</i>
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---

**Description**

mgi\_synonym\_data returns the mgi\_synonym\_data dataset

**Usage**

```
mgi_synonym_data(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

mgi\_synonym\_data dataset

**Examples**

```
mgi_synonym_data()
```

---

mouse_to_human_homologs	<i>mouse_to_human_homologs</i>
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---

**Description**

mouse\_to\_human\_homologs returns the mouse\_to\_human\_homologs dataset

**Usage**

```
mouse_to_human_homologs(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
----------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

**Value**

mouse\_to\_human\_homologs dataset

**Examples**

```
mouse_to_human_homologs()
```

---

rbfox_genes	<i>rbfox_genes</i>
-------------	--------------------

---

**Description**

rbfox\_genes returns the rbfox\_genes dataset

**Usage**

```
rbfox_genes(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
----------	---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------

**Value**

rbfox\_genes dataset

**Examples**

```
rbfox_genes()
```

---

schiz_genes	<i>schiz_genes</i>
-------------	--------------------

---

**Description**

schiz\_genes returns the schiz\_genes dataset

**Usage**

```
schiz_genes(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

schiz\_genes dataset

**Examples**

```
schiz_genes()
```

---

tt\_alzh

*tt\_alzh*

---

**Description**

tt\_alzh returns the tt\_alzh dataset

**Usage**

```
tt_alzh(localHub = FALSE)
```

**Arguments**

localHub      If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

tt\_alzh dataset

**Examples**

```
tt_alzh()
```

---

tt\_alzh\_BA36

*tt\_alzh\_BA36*

---

**Description**

tt\_alzh\_BA36 returns the tt\_alzh\_BA36 dataset

**Usage**

```
tt_alzh_BA36(localHub = FALSE)
```

**Arguments**

localHub      If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.

**Value**

tt\_alzh\_BA36 dataset

**Examples**

```
tt_alzh_BA36()
```

---

tt\_alzh\_BA44

*tt\_alzh\_BA44*

---

**Description**

tt\_alzh\_BA44 returns the tt\_alzh\_BA44 dataset

**Usage**

```
tt_alzh_BA44(localHub = FALSE)
```

**Arguments**

localHub	If working offline, add argument localHub=TRUE to work with a local, non-updated hub; It will only have resources available that have previously been downloaded. If offline, Please also see BiocManager vignette section on offline use to ensure proper functionality.
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**Value**

tt\_alzh\_BA44 dataset

**Examples**

```
tt_alzh_BA44()
```

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