

# Package ‘ewceData’

March 21, 2023

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

**Version** 1.6.0

**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, testthat (>= 3.0.0)

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

**Roxygen** list(markdown = TRUE)

**RoxygenNote** 7.1.1

**VignetteBuilder** knitr

**Config/testthat/edition** 3

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

**git\_branch** RELEASE\_3\_16

**git\_last\_commit** d736e8b

**git\_last\_commit\_date** 2022-11-01

**Date/Publication** 2023-03-21

**NeedsCompilation** no

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## R topics documented:

all_hgnc . . . . .	2
all_hgnc_wtEnsembl . . . . .	3
all_mgi . . . . .	3
all_mgi_wtEnsembl . . . . .	4
alz_h_gwas_top100 . . . . .	4
cortex_mrna . . . . .	5
ctd . . . . .	5
ensembl_transcript_lengths_GCcontent . . . . .	6
ewceData . . . . .	6
example_genelist . . . . .	7
hpsd_genes . . . . .	7
hypothalamus_mrna . . . . .	8
id_genes . . . . .	8
mgi_synonym_data . . . . .	9
mouse_to_human_homologs . . . . .	9
rbfox_genes . . . . .	10
schiz_genes . . . . .	10
tt_alzh . . . . .	11
tt_alzh_BA36 . . . . .	11
tt_alzh_BA44 . . . . .	12
<b>Index</b>	<b>13</b>

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all_hgnc	<i>all_hgnc</i>
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### Description

all\_hgnc returns the all\_hgnc dataset

### Usage

```
all_hgnc()
```

### 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()`

**Value**

`all_hgnc_wtEnsembl` dataset

**Examples**

`all_hgnc_wtEnsembl()`

---

`all_mgi`      *all\_mgi*

---

**Description**

`all_mgi` returns the `all_mgi` dataset

**Usage**

`all_mgi()`

**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()
```

**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()
```

**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()

**Value**

cortex\_mrna dataset

**Examples**

cortex\_mrna()

---

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

**Description**

ctd returns the ctd dataset

**Usage**

ctd()

**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()
```

**Value**

ensembl\_transcript\_lengths\_GCcontent dataset

**Examples**

```
ensembl_transcript_lengths_GCcontent()
```

---

```
ewceData          The ewceData package provides reference data required for ewce
```

---

**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.

**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()
```

---

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

**Description**

`example_genelist` returns the `example_genelist` dataset

**Usage**

```
example_genelist()
```

**Value**

`example_genelist` dataset

**Examples**

```
example_genelist()
```

---

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

**Description**

`hpsd_genes` returns the `hpsd_genes` dataset

**Usage**

```
hpsd_genes()
```

**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()
```

**Value**

hypothalamus\_mrna dataset

**Examples**

```
hypothalamus_mrna()
```

---

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

---

**Description**

id\_genes returns the id\_genes dataset

**Usage**

```
id_genes()
```

**Value**

id\_genes dataset

**Examples**

```
id_genes()
```



---

`mgc_synonym_data`      *mgc\_synonym\_data*

---

**Description**

`mgc_synonym_data` returns the `mgc_synonym_data` dataset

**Usage**

`mgc_synonym_data()`

**Value**

`mgc_synonym_data` dataset

**Examples**

`mgc_synonym_data()`

---

`mouse_to_human_homologs`  
*mouse\_to\_human\_homologs*

---

**Description**

`mouse_to_human_homologs` returns the `mouse_to_human_homologs` dataset

**Usage**

`mouse_to_human_homologs()`

**Value**

`mouse_to_human_homologs` dataset

**Examples**

`mouse_to_human_homologs()`

---

rbfox\_genes

*rbfox\_genes*

---

**Description**

rbfox\_genes returns the rbfox\_genes dataset

**Usage**

```
rbfox_genes()
```

**Value**

rbfox\_genes dataset

**Examples**

```
rbfox_genes()
```

---

schiz\_genes

*schiz\_genes*

---

**Description**

schiz\_genes returns the schiz\_genes dataset

**Usage**

```
schiz_genes()
```

**Value**

schiz\_genes dataset

**Examples**

```
schiz_genes()
```

---

tt_alzh	<i>tt_alzh</i>
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---

**Description**

tt\_alzh returns the tt\_alzh dataset

**Usage**

```
tt_alzh()
```

**Value**

tt\_alzh dataset

**Examples**

```
tt_alzh()
```

---

tt_alzh_BA36	<i>tt_alzh_BA36</i>
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---

**Description**

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

**Usage**

```
tt_alzh_BA36()
```

**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()
```

**Value**

`tt_alzh_BA44` dataset

**Examples**

```
tt_alzh_BA44()
```

# Index

## \* datasets

- ewceData, [6](#)
  
- all\_hgnc, [2](#)
- all\_hgnc\_wtEnsembl, [3](#)
- all\_mgi, [3](#)
- all\_mgi\_wtEnsembl, [4](#)
- alz\_h\_gwas\_top100, [4](#)
  
- cortex\_mrna, [5](#)
- ctd, [5](#)
  
- ensembl\_transcript\_lengths\_GCcontent,  
[6](#)
- ewceData, [6](#)
- ewceData-package (ewceData), [6](#)
- example\_genelist, [7](#)
  
- hpsd\_genes, [7](#)
- hypothalamus\_mrna, [8](#)
  
- id\_genes, [8](#)
  
- mgi\_synonym\_data, [9](#)
- mouse\_to\_human\_homologs, [9](#)
  
- rbfox\_genes, [10](#)
  
- schiz\_genes, [10](#)
  
- tt\_alzh, [11](#)
- tt\_alzh\_BA36, [11](#)
- tt\_alzh\_BA44, [12](#)