

# Package ‘EGSEAdata’

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**Title** Gene set collections for the EGSEA package

**Version** 1.0.1

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**Description** This package includes gene set collections that are used for the Ensemble of Gene Set Enrichment Analyses (EGSEA) method for gene set testing. It includes Human and Mouse versions of the MSidDB (Subramanian, et al. (2005) PNAS, 102(43):15545-15550) and GeneSetDB (Araki, et al. (2012) FEBS Open Bio, 2:76-82) collections.

**biocViews** ExperimentData

**Depends** R (>= 3.3)

**License** file LICENSE

**LazyLoad** yes

**NeedsCompilation** no

**Suggests** EGSEA

**RoxygenNote** 5.0.1

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EGSEAdata-package	<i>Gene Set Collections for the EGSEA package</i>
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### Description

This package includes gene set collections that are used for the Ensemble of Gene Set Enrichment Analyses (EGSEA) method for gene set testing. It includes Human and Mouse versions of the MSidDB (Subramanian, et al. (2005) PNAS, 102(43):15545-15550) and GeneSetDB (Araki, et al. (2012) FEBS Open Bio, 2:76-82) collections.

### Author(s)

Monther Alhamdoosh, Yifang Hu and Gordon K. Smyth

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genesetdb.mouse	<i>GeneSetDB Mouse Collections</i>
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### Description

Mouse gene set collections from the GeneSetDB

### Format

list

### Source

Araki Hiromitsu,Knapp Christoph,Tsai Peter and Print Cristin(2012), GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis, FEBS Open Bio, 2, doi: 10.1016/j.fob.2012.04.003

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genesetdb.rat

*GeneSetDB Rat Collections*

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**Description**

Rat gene set collections from the GeneSetDB

**Format**

list

**Source**

Araki Hiromitsu, Knapp Christoph, Tsai Peter and Print Cristin (2012), GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis, FEBS Open Bio, 2, doi: 10.1016/j.fob.2012.04.003

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gsc.a115

*MSigDB Gene Set Collections*

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**Description**

Human gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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gsetdb.all

*GeneSetDB Human Collections*

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**Description**

Human gene set collections from the GeneSetDB

**Format**

list

**Source**

Araki Hiromitsu, Knapp Christoph, Tsai Peter and Print Cristin (2012), GeneSetDB: A comprehensive meta-database, statistical and visualisation framework for gene set analysis, FEBS Open Bio, 2, doi: 10.1016/j.fob.2012.04.003

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il13.data

*Human IL-13 dataset*

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**Description**

The voom object calculated from the TMM normalized count matrix of RNA-seq performed on samples of human normal PBMCs, IL-13 stimulated PBMCs and IL-13R antagonist PBMCs. It also contains the contrast matrix of this experiment.

**Format**

A List object with two components: voom and contra.

**Source**

The count matrix of this experiment is available from the GEO database [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) as series GSE79027.

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`il13.data.cnt`*Human IL-13 dataset - Raw Counts*

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**Description**

It contains the raw count matrix of RNA-seq performed on samples of human normal PBMCs, IL-13 stimulated PBMCs and IL-13R antagonist PBBMCs. It also contains the contrast and design matrices of this experiment. The gene symbols mapping is also included.

**Format**

A List object with five components: counts, group, design, contra and genes.

**Source**

The FASTQ files of this experiment are available from the GEO database [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) as series GSE79027.

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`kegg.pathways`*KEGG Pathways Collections*

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**Description**

Human, Mouse and Rat gene set collections from the KEGG database

**Format**

list

**Source**

Luo, W., Friedman, M., Shedden K., Hankenson, K. and Woolf, P GAGE: Generally Applicable Gene Set Enrichment for Pathways Analysis. BMC Bioinformatics 2009, 10:161

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mam.data

*Mouse mammary cell dataset*

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### Description

The voom object calculated from TMM normalized count matrix of RNA-seq performed on samples of the epithelial cells of the mouse mammary glands from three populations: basal, luminal progenitor and mature luminal. It also contains the contrast matrix of this experiment.

### Format

A List object with two components: voom and contra.

### Source

The count matrix of this experiment is available from the GEO database [www.ncbi.nlm.nih.gov/geo/](http://www.ncbi.nlm.nih.gov/geo/) as series GSE63310.

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Mm.c2

*Mouse C2 MSigDB Gene Set Collections*

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### Description

Mouse orthologs gene set collections from the MSigDB database Version 5

### Format

list

### Source

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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Mm. c3

*Mouse C3 MSigDB Gene Set Collections*

---

**Description**

Mouse orthologs gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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Mm. c4

*Mouse C4 MSigDB Gene Set Collections*

---

**Description**

Mouse orthologs gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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Mm.c5

*Mouse C5 MSigDB Gene Set Collections*

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**Description**

Mouse orthologs gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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Mm.c6

*Mouse C6 MSigDB Gene Set Collections*

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**Description**

Mouse orthologs gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550



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Mm.c7

*Mouse C7 MSigDB Gene Set Collections*

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**Description**

Mouse orthologs gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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Mm.H

*Mouse H MSigDB Gene Set Collections*

---

**Description**

Mouse orthologs gene set collections from the MSigDB database Version 5

**Format**

list

**Source**

<http://bioinf.wehi.edu.au/software/MSigDB/>. Extracted from Aravind Subramanian, Pablo Tamayo, Vamsi K. Mootha, Sayan Mukherjee, Benjamin L. Ebert, Michael A. Gillette, Amanda Paulovich, Scott L. Pomeroy, Todd R. Golub, Eric S. Lander, and Jill P. Mesirov Gene set enrichment analysis: A knowledge-based approach for interpreting genome-wide expression profiles PNAS 2005 102 (43) 15545-15550

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