

# Package ‘enrichR’

April 2, 2017

**Title** Provides an R Interface to 'Enrichr'

**Version** 1.0

**Description** Provides an R interface to all 'Enrichr' databases, a web-based tool for analysing gene sets and returns any enrichment of common annotated biological functions. <<http://amp.pharm.mssm.edu/Enrichr/>>.

**Depends** R (>= 3.0.0)

**License** GPL (>= 2)

**Encoding** UTF-8

**LazyData** true

**Imports** httr, rjson

**RoxygenNote** 6.0.1

**Suggests** knitr, rmarkdown

**VignetteBuilder** knitr

**NeedsCompilation** no

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**Repository** CRAN

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enrichr                      *Gene enrichment using Enrichr*

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**Description**

Gene enrichment using Enrichr

**Usage**

```
enrichr(genes, databases = NULL)
```

**Arguments**

genes                      Character vector of gene names or dataframe of gene names in first column and a score between 0 and 1 in the other.

databases                  Character vector of databases to search. See <http://amp.pharm.mssm.edu/Enrichr/> for available databases.

**Details**

Gene enrichment using Enrichr

**Value**

Returns a data frame of enrichment terms, p-values, ...

**Author(s)**

Wajid Jawaid

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listEnrichrDbs              *Look up available databases on Enrichr*

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**Description**

Look up available databases on Enrichr

**Usage**

```
listEnrichrDbs()
```

**Details**

Look up available databases on Enrichr

**Value**

dataframe of available Enrichr databases

**Author(s)**

Wajid Jawaid

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printEnrich                      *Print Enrichr output to text file.*

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**Description**

Print Enrichr output.

**Usage**

```
printEnrich(data, file, sep = "\t", columns = c(2, 3, 6))
```

**Arguments**

data	Output from Enrichr function.
file	Name of output file.
sep	Default TAB. How to separate fields.
columns	Columns from each entry of data. 1-"Index", 2-"Name", 3-"Adjusted_P-value", 4-"Z-score" 5-"Combined_Score", 6-"Genes", 7-"Overlap_P-value"

**Details**

Print Enrichr output to text file.

**Value**

Produces file.

**Author(s)**

Wajid Jawaid

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