

# Package ‘rDGIdb’

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**Type** Package

**Title** R Wrapper for DGIdb

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**Description** The rDGIdb package provides a wrapper for the Drug Gene Interaction Database (DGIdb). For simplicity, the wrapper query function and output resembles the user interface and results format provided on the DGIdb website (<http://www.dgidb.org/>).

**License** MIT + file LICENSE

**LazyData** TRUE

**Imports** jsonlite,httr,methods,graphics

**Collate** rDGIdbResult.R queryDGIdb.R plotInteractionsBySource.R  
resourceVersions.R

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plotInteractionsBySource

*Interactions by source*

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### **Description**

Creates a plot to visualize the number of interactions per source.

### **Usage**

```
plotInteractionsBySource(queryResult, ...)
```

### **Arguments**

`queryResult`     A [rDGIdbResult](#) object obtained from [queryDGIdb](#).  
`...`             Other arguments passed to `barplot`.

### **Value**

A plot is created on the current graphics device.

### **Author(s)**

Thomas Thurnherr <[thomas.thurnherr@gmail.com](mailto:thomas.thurnherr@gmail.com)>

### **References**

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

### **See Also**

[rDGIdbResult](#), [queryDGIdb](#), [rDGIdbFilters](#)

### **Examples**

```
queryResult <- queryDGIdb('KRAS')  
plotInteractionsBySource(queryResult)
```

---

`queryDGIdb`*Query DGIdb using R*

---

**Description**

Provides an interface to query DGIdb from within R using the DGIdb API. The function is implemented to reflect the as good as possible the web-interface.

**Usage**

```
queryDGIdb(genes,  
           sourceDatabases = NULL,  
           geneCategories = NULL,  
           interactionTypes = NULL)
```

**Arguments**

`genes` A character vector of genes for which drug interactions are queried.

`sourceDatabases` A character vector of source databases to be queried. To query all available databases, skip argument or use `NULL`. To see available options, type `sourceDatabases()`.

`geneCategories` A character vector of gene categories to be queried. To query for all gene categories, skip argument or use `NULL`. To see available options, type `geneCategories()`.

`interactionTypes` A character vector of interaction types to be queried. To query for all interaction types, skip argument or use `NULL`. To see available options, type `interactionTypes()`.

**Details**

Only the first argument (`genes`) is required, all other arguments are optional. When optional arguments are not provided, the query considers all available possibilities for optional arguments: `sourceDatabases`, `geneCategories`, and `interactionTypes`.

**Value**

A S4 object of type `rDGIdbResult`.

**Author(s)**

Thomas Thurnherr <thomas.thurnherr@gmail.com>

**References**

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

**See Also**

[rDGIdbResult](#), [rDGIdbFilters](#), [plotInteractionsBySource](#)

## Examples

```
genes <- c("XYZA", "TNF", "IL6", "IL8")
result <- queryDGIdb(genes = genes)

result <- queryDGIdb(genes = genes,
                     sourceDatabases = c("MyCancerGenome", "TEND", "TTD"),
                     geneCategories = "CELL SURFACE",
                     interactionTypes = c("activator", "inhibitor"))
```

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rDGIdbFilters

*Filter options for rDGIdb queries.*

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## Description

The gene categories, interaction types, and source databases available to filter queries with [queryDGIdb](#).

## Usage

```
geneCategories()

interactionTypes()

sourceDatabases()
```

## Value

`geneCategories` returns a character vector of available gene categories which can be used to filter DGIdb queries with [queryDGIdb](#).

`interactionTypes` returns a character vector of available interaction types which can be used to filter DGIdb queries with [queryDGIdb](#).

`sourceDatabases` returns a character vector of available source databases which can be used to filter DGIdb queries with [queryDGIdb](#).

## Author(s)

Thomas Thurnherr <thomas.thurnherr@gmail.com>

## References

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

## See Also

[queryDGIdb](#), [rDGIdbResult](#), [plotInteractionsBySource](#)

## Examples

```
geneCategories()
interactionTypes()
sourceDatabases()
res <- queryDGIdb(genes = "AP1",
                 interactionTypes = NULL,
                 geneCategories = NULL,
                 sourceDatabases = NULL)
```

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rDGIdbResult

*Result object of a rDGIdb query*

---

## Description

S4 helper functions to access DGIdb results, formatted in a similar way as result tables on the DGIdb web interface.

## Usage

```
## S4 method for signature 'rDGIdbResult'
resultSummary(object)

## S4 method for signature 'rDGIdbResult'
detailedResults(object)

## S4 method for signature 'rDGIdbResult'
byGene(object)

## S4 method for signature 'rDGIdbResult'
searchTermSummary(object)
```

## Arguments

**object**            A rDGIdbResult object returned by [queryDGIdb](#).

## Value

`resultSummary` returns a `data.frame` that summarizes drug-gene interactions by the source(s) that reported them.

`detailedResult` returns a `data.frame` with search terms matching exactly one gene that has one or more drug interactions.

`byGene` returns a `data.frame` with drug interaction count and druggable categories associated with each gene.

`searchTermSummary` returns a `data.frame` that summarizes the attempt to map gene names supplied by the user to gene records in DGIdb.

## Author(s)

Thomas Thurnherr <thomas.thurnherr@gmail.com>

## References

Wagner AH, Coffman AC, Ainscough BJ, Spies NC, Skidmore ZL, Campbell KM, Krysiak K, Pan D, McMichael JF, Eldred JM, Walker JR, Wilson RK, Mardis ER, Griffith M, Griffith OL. DGIdb 2.0: mining clinically relevant drug-gene interactions. *Nucleic Acids Research*. 2016 Jan 4;44(D1):D1036-44. doi:10.1093/nar/gkv1165.

## See Also

[queryDGIdb](#), [rDGIdbFilters](#), [plotInteractionsBySource](#)

## Examples

```
genes <- c("XYZA", "TNF", "IL6", "IL8")
result <- queryDGIdb(genes = genes)
resultSummary(result)
detailedResults(result)
byGene(result)
searchTermSummary(result)
```

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resourceVersions

*Version numbers of DGIdb resources*

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## Description

Prints the version numbers of all DGIdb resources.

## Usage

```
resourceVersions()
```

## Value

Returns a data.frame with two columns, the name and the version numbers of the resources.

## Author(s)

Thomas Thurnherr <thomas.thurnherr@gmail.com>

## See Also

<http://dgidb.genome.wustl.edu/sources>

## Examples

```
resourceVersions()
```

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