

# Package: mygene (via r-universe)

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**Type** Package

**Title** Access MyGene.Info\_ services

**Version** 1.41.0

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**Description** MyGene.Info\_ provides simple-to-use REST web services to query/retrieve gene annotation data. It's designed with simplicity and performance emphasized. \*mygene\*, is an easy-to-use R wrapper to access MyGene.Info\_ services.

**License** Artistic-2.0

**Depends** R (>= 3.2.1), GenomicFeatures, txdbmaker

**Imports** methods, utils, stats, httr (>= 0.3), jsonlite (>= 0.9.7), Hmisc, sqldf, plyr, S4Vectors

**Suggests** BiocStyle

**biocViews** Annotation

**Repository** <https://bioc.r-universe.dev>

**RemoteUrl** <https://github.com/bioc/mygene>

**RemoteRef** HEAD

**RemoteSha** 486275d60524b799b1eb8538b13949480333ba67

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getGene	<i>Return the gene object for the given geneid.</i>
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### Description

This is a wrapper for GET query of "/gene/<geneid>" service.

### Usage

```
getGene(geneid, fields = c("symbol", "name", "taxid", "entrezgene"),
        ..., return.as=c("records", "text"), mygene)
```

### Arguments

geneid	Entrez/ensembl gene id
fields	Fields to return, a list of a comma-sep string. If fields=="all", all available fields are returned.
...	Includes species as well as several other fields. View available fields by calling ?metadata. Also, see <a href="http://docs.mygene.info/en/latest/doc/annotation_service.html">http://docs.mygene.info/en/latest/doc/annotation_service.html</a> for complete argument details and syntax.
return.as	"records" (list), "text" (JSON).
mygene	A MyGene object that describes how to connect to data resources. See <a href="#">MyGene-class</a> . If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

### Value

returns a gene object containing the queried annotations

### References

Ref: [http://docs.mygene.info/en/latest/doc/annotation\\_service.html](http://docs.mygene.info/en/latest/doc/annotation_service.html)

### See Also

[getGenes query queryMany](#)

### Examples

```
## return the gene object for the given gene id
getGene(1017)

## customize fields
getGene(1017, fields=c("name", "symbol", "refseq"), return.as="text")

## all fields
getGene(1017, fields="all")
```

---

getGenes	<i>Return the list of gene objects for the given list of geneids.</i>
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### Description

This is a wrapper for POST query of "/gene" service.

### Usage

```
getGenes(geneids, fields = c("symbol", "name", "taxid", "entrezgene"), ...,
        return.as=c("DataFrame", "records", "text"), mygene)
```

### Arguments

geneids	A vector, list, or comm-sep string entrez/ensembl gene ids
fields	A vector of fields to return. If fields=="all", all available fields are returned.
...	Includes species as well as several other fields. View available fields by calling ?metadata. Also, see <a href="http://docs.mygene.info/en/latest/doc/annotation_service.html">http://docs.mygene.info/en/latest/doc/annotation_service.html</a> for complete argument details and syntax.
return.as	"DataFrame" (default), "records" (list), "text" (JSON).
mygene	A MyGene object that describes how to connect to data resources. See <a href="#">MyGene-class</a> . If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

### Value

returns a gene object (DataFrame, list, or JSON text) containing the queried annotations

### References

Ref: [http://docs.mygene.info/en/latest/doc/annotation\\_service.html](http://docs.mygene.info/en/latest/doc/annotation_service.html)

### See Also

[getGene query queryMany](#)

### Examples

```
## Return the list of gene object for the given list of gene ids.
getGenes(c(1017,1018))

## mix types of gene ids
getGenes(c(1017,1018,"ENSG00000148795"))
```

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makeTxDbFromMyGene     *makeTxDbFromMyGene*

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## Description

makeTxDbFromMyGene allows the user to make a TxDb object in the Genomic Features package from a mygene "exons" query using a default MyGene object.

## Usage

```
makeTxDbFromMyGene(gene.list, scopes, species, returnall=FALSE)
```

## Arguments

gene.list	A list, vector, or comma-separated string of query terms.
scopes	Type of types of identifiers, either a list, vector, or a comma-separated fields to specify type of input qterms, e.g. c("reporter", "ensembl.gene", "symbol") refer to "http://docs.mygene.info/en/latest/doc/data.html#available-fields" for full list of fields.
species	Names or taxonomy ids
returnall	Logical, if TRUE, return list of genes without exons annotations. False by Default.

## Details

makeTxDbFromMyGene invokes either the query or queryMany method and passes the response to construct a TxDb object. See ?TxDb for utilizing transcript annotations.

## Value

returns TxDb object

## See Also

[makeTxDb](#)

## Examples

```
xli <- c('DDX26B', 'CCDC83', 'MAST3', 'RPL11')
txdb <- makeTxDbFromMyGene(xli, scopes="symbol", species="human")
```

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metadata	<i>metadata</i>
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**Description**

Get metadata for MyGene.info services.

**Usage**

```
metadata(x, ...)
```

**Arguments**

x	MyGene object
...	MyGene object slot parameters

**Value**

returns the metadata including available fields, genome assemblies, sources, statistics, taxonomy, and timestamp

**References**

<http://mygene.info/v2/metadata>

**Examples**

```
## Get metadata
mygene<-MyGene()
metadata(mygene)

## get available fields to return
metadata(mygene)$available_fields
```

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MyGene	<i>MyGene</i>
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**Description**

Construct a MyGene object.

**Usage**

```
MyGene(...)
```

**Arguments**

... See help page for MyGene-class

**Value**

MyGene object

**Examples**

```
MyGene()
```

---

mygene

*Access MyGene.info annotation services*

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**Description**

MyGene.Info\_ provides simple-to-use REST web services to query/retrieve gene annotation data. It's designed with simplicity and performance emphasized. \*mygene\* is an easy-to-use R wrapper to access MyGene.info services.

**Details**

Package: mygene  
Type: Package  
Version: 0.99.0  
Date: 2014-04-18  
License: BSD  
Depends: httr jsonlite Hmisc

**Author(s)**

Adam Mark, Chunlei Wu

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**References**

Wu C, MacLeod I, Su AI (2013) BioGPS and MyGene.info: organizing online, gene-centric information. Nucl. Acids Res. 41(D1): D561-D565. [http://mygene.info/doc/annotation\\_service.html](http://mygene.info/doc/annotation_service.html)  
[http://mygene.info/doc/query\\_service.html](http://mygene.info/doc/query_service.html)

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MyGene-class	Class "MyGene"
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### Description

R Client to access MyGene.Info annotation services

### Objects from the Class

Objects can be created by calls of the form `MyGene(base.url="http://mygene.info/v2", delay=1, step=1000, version=version, verbose=TRUE, debug=FALSE)`.

### Slots

`base.url`: "http://mygene.info/v2". Object of class "character"  
`delay`: Sleep time between batch retrieval. Object of class "numeric"  
`step`: Batch limit. Object of class "numeric"  
`version`: httr package version. Object of class "character"  
`verbose`: Object of class "logical"  
`debug`: Object of class "logical"

### Methods

`getGene(geneid, fields = c("symbol", "name", "taxid", "entrezgene"), ... , return.as=c("records", "text")`  
 Return the gene object for the given geneid  
`getGenes(geneids, fields = c("symbol", "name", "taxid", "entrezgene"), ... , return.as=c("DataFrame", "records")`  
 Return the list of gene object for the given list of geneids.  
`query(q, fields=c("name", "symbol", "taxid", "entrezgene"), ... , return.as=c("DataFrame", "records", "text")`  
 Return the query result.  
`queryMany(qterms, scopes=NULL, fields=c("name", "symbol", "taxid", "entrezgene"), ... , return.as=c("DataFrame", "records", "text")`  
 Return the batch query result.  
`metadata(x, ...)`: Get metadata for MyGene.info services.  
`makeTxDbFromMyGene(gene.list, scopes, species, returnall=FALSE)`: Make a TxDb object from transcript annotations

### Author(s)

Adam Mark, Chunlei Wu, Ryan Thompson

### References

Wu C, MacLeod I, Su AI (2013) BioGPS and MyGene.info: organizing online, gene-centric information. *Nucl. Acids Res.* 41(D1): D561-D565.

### Examples

```
showClass("MyGene")
```

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query	<i>Return the query result.</i>
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### Description

This is a wrapper for GET query of `"/query?q=<query>"` service.

### Usage

```
query(q, ..., return.as=c("DataFrame", "records", "text"), mygene)
```

### Arguments

q	query term(s), see query syntax at <a href="http://mygene.info/doc/query_service.html#query-syntax">http://mygene.info/doc/query_service.html#query-syntax</a>
...	Commonly queried fields include species, fields, size as well as several other fields. View available fields by calling <code>?metadata</code> . Also, see <a href="http://docs.mygene.info/en/latest/doc/q">http://docs.mygene.info/en/latest/doc/q</a> for complete argument details and syntax.
return.as	"DataFrame" (default), "records" (list), or "text" (JSON).
mygene	A MyGene object that describes how to connect to data resources. See <a href="#">MyGene-class</a> . If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

### Value

returns a gene object (DataFrame, list, or JSON text) containing the queried annotations

### References

Ref: [http://docs.mygene.info/en/latest/doc/query\\_service.html](http://docs.mygene.info/en/latest/doc/query_service.html)

### See Also

[queryMany](#) [getGene](#) [getGenes](#)

### Examples

```
## return the query result
query("cdk2", size=5)

query("reporter:1000_at")

query("symbol:cdk2", return.as="text")

query(q="cyclin-dependent kinase", fields="uniprot")
```



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queryMany	<i>Return the batch query result.</i>
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### Description

This is a wrapper for POST query of `"/query"` service.

### Usage

```
queryMany(qterms, scopes=NULL, ..., return.as=c("DataFrame", "records", "text"), mygene)
```

### Arguments

qterms	A vector or list, or string of comma-separated query terms
scopes	Type of types of identifiers, either a list or a comma-separated fields to specify type of input qterms, e.g. <code>c("reporter", "ensembl.gene", "symbol")</code> refer to <code>"http://mygene.info/doc/query_service.html#available_fields"</code> for full list of fields.
...	Commonly queried fields include <code>species</code> , <code>fields</code> , <code>size</code> as well as several other fields. <code>return.all</code> returns a list of all related data including duplicated and missing qterms. <code>False</code> by default. View available fields by calling <code>?metadata</code> . Also, see <code>http://docs.mygene.info/en/latest/doc/query_service.html</code> for complete argument details and syntax.
return.as	"DataFrame" (default), "records" (list), "text" (JSON).
mygene	A MyGene object that describes how to connect to data resources. See <a href="#">MyGene-class</a> . If missing, default object will be used that accesses the main MyGene.info portal. Default is recommended.

### Value

returns a gene object (DataFrame, list, or JSON text) containing the queried annotations

### References

Ref: [http://docs.mygene.info/en/latest/doc/query\\_service.html](http://docs.mygene.info/en/latest/doc/query_service.html)

### See Also

[query](#) [getGene](#) [getGenes](#)

### Examples

```
## return the batch query result
queryMany(c('1053_at', '117_at', '121_at'), scopes="reporter", fields="ensembl.gene",
          species="human", return.as="records")

queryMany(c('1053_at', '117_at', '121_at'), scopes="reporter", species=9606)
```

```
queryMany(c('DDX26B', 'CCDC83', 'MAST3', 'FLOT1'), scopes="symbol", fields="entrezgene", species="human")
```

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