

# MyGene.info R Client

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May 27, 2014

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## 1 Overview

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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.

## 2 Gene Annotation Service

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## 2.1 `mg.getgene`

- Use `mg.getgene`, the wrapper for GET query of `"/gene/<geneid>"` service, to return the gene object for the given geneid.

```
> mg.getgene("1017", fields=c("name", "symbol", "taxid", "entrezgene"))

chr [1:4] "name" "symbol" "taxid" "entrezgene"
$`__need_your_help`
[1] "We are working on a grant based on MyGene.info, please send us an email at cwu@scripps.edu"

$`_id`
[1] "1017"

$entrezgene
[1] 1017

$name
[1] "cyclin-dependent kinase 2"

$symbol
[1] "CDK2"

$taxid
[1] 9606
```

## 2.2 `mg.getgenes`

- Use `mg.getgenes`, the wrapper for POST query of `"/gene"` service, to return the list of gene objects for the given character vector of geneids.

```
> mg.getgenes(c("1017", "1018", "ENSG00000148795"), species="human")

chr "human"
chr "symbol,name,taxid,entrezgene"
[[1]]
[[1]]$name
[1] "cyclin-dependent kinase 2"

[[1]]$symbol
[1] "CDK2"

[[1]]$taxid
[1] 9606

[[1]]$entrezgene
[1] 1017
```

```
[[1]]$query
```

```
[1] "1017"
```

```
[[1]]$`_id`
```

```
[1] "1017"
```

```
[[2]]
```

```
[[2]]$name
```

```
[1] "cyclin-dependent kinase 3"
```

```
[[2]]$symbol
```

```
[1] "CDK3"
```

```
[[2]]$taxid
```

```
[1] 9606
```

```
[[2]]$entrezgene
```

```
[1] 1018
```

```
[[2]]$query
```

```
[1] "1018"
```

```
[[2]]$`_id`
```

```
[1] "1018"
```

```
[[3]]
```

```
[[3]]$name
```

```
[1] "cytochrome P450, family 17, subfamily A, polypeptide 1"
```

```
[[3]]$symbol
```

```
[1] "CYP17A1"
```

```
[[3]]$taxid
```

```
[1] 9606
```

```
[[3]]$entrezgene
```

```
[1] 1586
```

```
[[3]]$query
```

```
[1] "ENSG00000148795"
```

```
[[3]]$`_id`
```

```
[1] "1586"
```

### 3 Gene Query Service

---

#### 3.1 mg.query

- Use `mg.query`, a wrapper for GET query of `"/query?q=<query>"` service, to return the query result.

```
> mg.query("cdk2", size=5)
```

```
$`__need_your_help`
```

```
[1] "We are working on a grant based on MyGene.info, please send us an email at cwu@scripps.edu"
```

```
$hits
```

	entrezgene	name	_score	symbol	_id	taxid
1	1017	cyclin-dependent kinase 2	380.14430	CDK2	1017	9606
2	12566	cyclin-dependent kinase 2	339.55472	Cdk2	12566	10090
3	362817	cyclin dependent kinase 2	269.77985	Cdk2	362817	10116
4	52004	CDK2-associated protein 2	20.42308	Cdk2ap2	52004	10090
5	143384	CDK2-associated, cullin domain 1	19.47708	CACUL1	143384	9606

```
$max_score
```

```
[1] 380.1443
```

```
$took
```

```
[1] 7
```

```
$total
```

```
[1] 26
```

```
> mg.query("symbol:cdk2", species="human")
```

```
$`__need_your_help`
```

```
[1] "We are working on a grant based on MyGene.info, please send us an email at cwu@scripps.edu"
```

```
$hits
```

	entrezgene	name	_score	symbol	_id	taxid
1	1017	cyclin-dependent kinase 2	88.02286	CDK2	1017	9606

```
$max_score
```

```
[1] 88.02286
```

```
$took
```

```
[1] 4
```

```
$total
[1] 1
```

### 3.2 mg.querymany

- Use mg.query, a wrapper for POST query of "/query" service, to return the batch query result.

```
> mg.querymany(c("1017", "695"), scopes="entrezgene", species="human")
```

Finished

Pass returnall=TRUE to return lists of duplicate or missing query terms.

DataFrame with 2 rows and 6 columns

	name	symbol	taxid	entrezgene
	<CharacterList>	<CharacterList>	<NumericList>	<NumericList>
1	cyclin-dependent kinase 2	CDK2	9606	1017
2	Bruton agammaglobulinemia tyrosine kinase	BTK	9606	695
	query	X_id		
	<CharacterList>	<CharacterList>		
1	1017	1017		
2	695	695		

```
> mg.querymany(c("1017","695"), scopes="entrezgene", species="9606", returnall=TRUE)
```

Finished

\$out

DataFrame with 2 rows and 6 columns

	name	symbol	taxid	entrezgene
	<CharacterList>	<CharacterList>	<NumericList>	<NumericList>
1	cyclin-dependent kinase 2	CDK2	9606	1017
2	Bruton agammaglobulinemia tyrosine kinase	BTK	9606	695
	query	X_id		
	<CharacterList>	<CharacterList>		
1	1017	1017		
2	695	695		

\$dup

list()

\$missing

list()

## 4 Tutorial, ID mapping

---

ID mapping is a very common, often not fun, task for every bioinformatician. Supposedly you have a list of gene symbols or reporter ids from an upstream analysis, and then your next analysis requires to use gene ids (e.g. Entrez gene ids or Ensembl gene ids). So you want to convert that list of gene symbols or reporter ids to corresponding gene ids.

Here we want to show you how to do ID mapping quickly and easily.

### 4.1 Mapping gene symbols to Entrez gene ids

Suppose `xli` is a list of gene symbols you want to convert to entrez gene ids:

```
> xli<-c('DDX26B',
+ 'CCDC83',
+ 'MAST3',
+ 'FLOT1',
+ 'RPL11',
+ 'ZDHHC20',
+ 'LUC7L3',
+ 'SNORD49A',
+ 'CTSH',
+ 'ACOT8')
```

you can then call `mg.querymany` method, telling it your input is symbol, and you want entrezgene (Entrez gene ids) back.

```
> mg.querymany(xli, scopes="symbol", fields="entrezgene", species="human")
```

Finished

Pass `returnall=TRUE` to return lists of duplicate or missing query terms.

DataFrame with 10 rows and 3 columns

	query	entrezgene	X_id
	<CharacterList>	<NumericList>	<CharacterList>
1	DDX26B	203522	203522
2	CCDC83	220047	220047
3	MAST3	23031	23031
4	FLOT1	10211	10211
5	RPL11	6135	6135
6	ZDHHC20	253832	253832
7	LUC7L3	51747	51747
8	SNORD49A	26800	26800
9	CTSH	1512	1512
10	ACOT8	10005	10005

## 4.2 Mapping gene symbols to Ensembl gene ids

Now if you want Ensembl gene ids back:

```
> out<-mg.querymany(xli, scopes="symbol", fields="ensembl.gene", species="human")
```

Finished

Pass returnall=TRUE to return lists of duplicate or missing query terms.

```
> out
```

DataFrame with 10 rows and 3 columns

	ensembl.gene <CharacterList>	X_id <CharacterList>	query <CharacterList>
1	ENSG00000165359,ENSG00000268630	203522	DDX26B
2	ENSG00000150676	220047	CCDC83
3	ENSG00000099308	23031	MAST3
4	ENSG00000137312,ENSG00000206379,ENSG00000206480,...	10211	FLOT1
5	ENSG00000142676	6135	RPL11
6	ENSG00000180776	253832	ZDHC20
7	ENSG00000108848	51747	LUC7L3
8	ENSG00000206956,ENSG00000175061	26800	SNORD49A
9	ENSG00000103811	1512	CTSH
10	ENSG00000101473	10005	ACOT8

```
> out$ensembl.gene[[4]]
```

```
[1] "ENSG00000137312" "ENSG00000206379" "ENSG00000206480" "ENSG00000223654"
[5] "ENSG00000224740" "ENSG00000230143" "ENSG00000232280" "ENSG00000236271"
```

## 4.3 When an input has no matching gene

In case that an input id has no matching gene, you will be notified from the output. The returned list for this query term contains notfound value as True.

```
> xli<-c('DDX26B',
+ 'CCDC83',
+ 'MAST3',
+ 'FLOT1',
+ 'RPL11',
+ 'Gm10494')
> mg.querymany(xli, scopes="symbol", fields="entrezgene", species="human")
```

Finished

Pass returnall=TRUE to return lists of duplicate or missing query terms.

DataFrame with 6 rows and 3 columns

query <CharacterList>	entrezgene <NumericList>	X_id <CharacterList>
--------------------------	-----------------------------	-------------------------

1	DDX26B	203522	203522
2	CCDC83	220047	220047
3	MAST3	23031	23031
4	FLOT1	10211	10211
5	RPL11	6135	6135
6	Gm10494		

## 4.4 When input ids are not just symbols

```
> xli<-c('DDX26B',
+ 'CCDC83',
+ 'MAST3',
+ 'FLOT1',
+ 'RPL11',
+ 'Gm10494',
+ '1007_s_at',
+ 'AK125780')
>
```

Above id list contains symbols, reporters and accession numbers, and supposedly we want to get back both Entrez gene ids and uniprot ids. Parameters scopes, fields, species are all flexible enough to support multiple values, either a list or a comma-separated string:

```
> out<-mg.querymany(xli, scopes=c("symbol","reporter","accession"),
+ fields=c("entrezgene","uniprot"), species="human")
```

Finished

Pass returnall=TRUE to return lists of duplicate or missing query terms.

```
> out
```

DataFrame with 9 rows and 4 columns

	query	entrezgene	uniprot	X_id
	<CharacterList>	<NumericList>	<List>	<CharacterList>
1	DDX26B	203522	#####	203522
2	CCDC83	220047	#####	220047
3	MAST3	23031	#####	23031
4	FLOT1	10211	#####	10211
5	RPL11	6135	#####	6135
6	Gm10494		#####	
7	1007_s_at	100616237	#####	100616237
8	1007_s_at	780	#####	780
9	AK125780	2978	#####	2978

```
> out$uniprot[[5]]
```



```
$`Swiss-Prot`
[1] "P62913"
```

```
$TrEMBL
[1] "Q5VVD0"
```

## 4.5 When an input id has multiple matching genes

From the previous result, you may have noticed that query term 1007\_s\_at matches two genes. In that case, you will be notified from the output, and the returned result will include both matching genes.

By passing `returnall=TRUE`, you will get both duplicate or missing query terms, together with the mapping output, from the returned result:

```
> mg.querymany(xli, scopes=c("symbol","reporter","accession"),
+             fields=c("entrezgene","uniprot"), species="human", returnall=TRUE)
```

```
Finished
```

```
$out
```

```
DataFrame with 9 rows and 4 columns
```

	query	entrezgene	uniprot	X_id
	<CharacterList>	<NumericList>	<List>	<CharacterList>
1	DDX26B	203522	#####	203522
2	CCDC83	220047	#####	220047
3	MAST3	23031	#####	23031
4	FLOT1	10211	#####	10211
5	RPL11	6135	#####	6135
6	Gm10494		#####	
7	1007_s_at	100616237	#####	100616237
8	1007_s_at	780	#####	780
9	AK125780	2978	#####	2978

```
$dup
```

```
$dup$`1007_s_at`
[1] 2
```

```
$dup$`1007_s_at`
[1] 2
```

```
$dup$`1007_s_at`
[1] 2
```

```
$dup$`1007_s_at`
[1] 2
```

```
$dup$`1007_s_at`  
[1] 2
```

```
$dup$`1007_s_at`  
[1] 2
```

```
$missing  
$missing[[1]]  
[1] "Gm10494"
```

The returned result above contains out for mapping output, missing for missing query terms (a list), and dup for query terms with multiple matches (including the number of matches).

## 4.6 Can I convert a very large list of ids?

Yes, you can. If you pass an id list (i.e., `xli` above) larger than 1000 ids, we will do the id mapping in-batch with 1000 ids at a time, and then concatenate the results all together for you. So, from the user-end, it's exactly the same as passing a shorter list. You don't need to worry about saturating our backend servers.

## 5 References

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