

# MyGene.info R Client

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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 `getGene`

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

```
> gene <- getGene("1017", fields="all")
> length(gene)

[1] 1

> gene["name"]

[[1]]
NULL

> gene["taxid"]

[[1]]
NULL

> gene["uniprot"]

[[1]]
NULL

> gene["refseq"]

[[1]]
NULL
```

### 2.2 `getGenes`

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

```
> getGenes(c("1017", "1018", "ENSG00000148795"))

DataFrame with 3 rows and 7 columns
```

```

      query      _id X_version  entrezgene      name
      <character> <character> <integer> <character>      <character>
1         1017      1017      1         1017 cyclin dependent kin..
2         1018      1018      1         1018 cyclin dependent kin..
3 ENSG00000148795      1586      1         1586 cytochrome P450 fami..
      symbol      taxid
      <character> <integer>
1         CDK2      9606
2         CDK3      9606
3        CYP17A1      9606

```

## 3 Gene Query Service

### 3.1 query

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

```

> query(q="cdk2", size=5)

$took
[1] 34

$total
[1] 1906

$max_score
[1] 139.4469

$hits
      _id  _score  entrezgene      name  symbol  taxid
1     1017 139.44691      1017 cyclin dependent kinase 2  CDK2  9606
2     12566 116.95548      12566 cyclin dependent kinase 2  Cdk2  10090
3     362817 98.96233      362817 cyclin dependent kinase 2  Cdk2  10116
4  115647898 89.96575  115647898 cyclin dependent kinase 2  CDK2  1825980
5  100529062 89.96575  100529062 cyclin dependent kinase 2  CDK2  9031

```

```

> query(q="NM_013993")

$took
[1] 14

```

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```
$total
[1] 1

$max_score
[1] 1.693442

$hits
  _id  _score entrezgene          name symbol
1 780 1.693442      780 discoidin domain receptor tyrosine kinase 1  DDR1
  taxid
1 9606
```

### 3.2 queryMany

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

```
> queryMany(c('1053_at', '117_at', '121_at', '1255_g_at', '1294_at'),
+           scopes="reporter", species="human")

Finished
Pass returnall=TRUE to return lists of duplicate or missing query terms.
DataFrame with 6 rows and 7 columns
```

	query	_id	X_score	entrezgene	name	
	<character>	<character>	<numeric>	<character>	<character>	
1	1053_at	5982	19.0124	5982	replication factor C..	
2	117_at	3310	19.0124	3310	heat shock protein f..	
3	121_at	7849	19.0124	7849	paired box 8	
4	1255_g_at	2978	19.0124	2978	guanylate cyclase ac..	
5	1294_at	7318	17.9989	7318	ubiquitin like modif..	
6	1294_at	100847079	17.9989	100847079	microRNA 5193	
	symbol	taxid				
	<character>	<integer>				
1	RFC2	9606				
2	HSPA6	9606				
3	PAX8	9606				
4	GUCA1A	9606				
5	UBA7	9606				
6	MIR5193	9606				

## 4 makeTxDbFromMyGene

TxDb is a container for storing transcript annotations. `makeTxDbFromMyGene` allows the user to make a TxDb object in the Genomic Features package from a mygene "exons" query using a default mygene object.

```
> xli <- c('CCDC83',
+         'MAST3',
+         'RPL11',
+         'ZDHHC20',
+         'LUC7L3',
+         'SNORD49A',
+         'CTSH',
+         'ACOT8')
> txdb <- makeTxDbFromMyGene(xli,
+                            scopes="symbol", species="human")
> transcripts(txdb)
```

GRanges object with 17 ranges and 2 metadata columns:

	seqnames	ranges	strand	tx_id	tx_name
	<Rle>	<IRanges>	<Rle>	<integer>	<character>
[1]	11	85855382-85920013	+	1	NM_001286159
[2]	11	85855382-85920013	+	2	NM_173556
[3]	19	18097777-18151686	+	3	NM_015016
[4]	1	23691805-23696835	+	4	NM_000975
[5]	1	23691778-23696426	+	5	NM_001199802
...	...	...	...	...	...
[13]	17	50719602-50756215	+	13	NM_016424
[14]	17	16440035-16440106	+	14	NR_002744
[15]	15	78921749-78945098	-	15	NM_001319137
[16]	15	78921059-78945046	-	16	NM_004390
[17]	20	45841720-45857392	-	17	NM_005469

-----  
seqinfo: 7 sequences from an unspecified genome; no seqlengths

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

## 5 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.

### 5.1 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 `queryMany` method, telling it your input is `symbol`, and you want `entrezgene` (Entrez gene ids) back.

```
> 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 5 columns

	query	notfound	_id	X_score	entrezgene
	<character>	<logical>	<character>	<numeric>	<character>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	17.9209	220047
3	MAST3	NA	23031	18.1249	23031
4	FLOT1	NA	10211	18.4342	10211
5	RPL11	NA	6135	16.3041	6135
6	ZDHHC20	NA	253832	18.1500	253832
7	LUC7L3	NA	51747	17.6485	51747
8	SNORD49A	NA	26800	22.4523	26800

9	CTSH	NA	1512	17.6101	1512
10	ACOT8	NA	10005	17.6190	10005

## 5.2 Mapping gene symbols to Ensembl gene ids

Now if you want Ensembl gene ids back:

```

> out <- 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 5 columns
  query notfound _id X_score
<character> <logical> <character> <numeric>
1 DDX26B TRUE NA NA
2 CCDC83 NA 220047 17.9209
3 MAST3 NA 23031 18.1249
4 FLOT1 NA 10211 18.4342
5 RPL11 NA 6135 16.3041
6 ZDHHC20 NA 253832 18.1500
7 LUC7L3 NA 51747 17.6485
8 SNORD49A NA 26800 22.4523
9 CTSH NA 1512 17.6101
10 ACOT8 NA 10005 17.6190

ensembl
<list>
1
2 ENSG00000150676
3 ENSG00000099308
4 ENSG00000137312, ENSG00000206480, ENSG00000230143
5 ENSG00000142676
6 ENSG00000180776
7 ENSG00000108848
8 ENSG00000277370
9 ENSG00000103811
10 ENSG00000101473

> out$ensembl[[4]]$gene
[1] "ENSG00000137312" "ENSG00000206480" "ENSG00000230143" "ENSG00000223654"
[5] "ENSG00000236271" "ENSG00000224740" "ENSG00000206379" "ENSG00000232280"

```

### 5.3 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')
> 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 5 columns

	query	notfound	_id	X_score	entrezgene
	<character>	<logical>	<character>	<numeric>	<character>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	17.9209	220047
3	MAST3	NA	23031	18.1249	23031
4	FLOT1	NA	10211	18.4342	10211
5	RPL11	NA	6135	16.3041	6135
6	Gm10494	TRUE	NA	NA	NA

### 5.4 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 <- 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 7 columns
  query  notfound  _id  X_score  entrezgene  uniprot.Swiss.Prot
<character> <logical> <character> <numeric> <character> <character>
1 DDX26B      TRUE      NA      NA      NA      NA
2 CCDC83      NA      220047  17.9209  220047  Q8IWF9
3 MAST3      NA      23031  18.1249  23031  060307
4 FLOT1      NA      10211  18.4342  10211  075955
5 RPL11      NA      6135  16.3041  6135  P62913
6 Gm10494    TRUE      NA      NA      NA      NA
7 1007_s_at  NA      780  17.9989  780  Q08345
8 1007_s_at  NA      100616237  17.9989  100616237  NA
9 AK125780   NA      118142757  21.2542  118142757  P43080
  uniprot.TrEMBL
  <list>
1
2 H0YDV3
3 A0A8V8TLL8,A0A994J700,V9GYV0,...
4 A2ABJ5,Q5ST80,A2AB10,...
5 A0A2R8Y447,Q5VVD0,Q5VVC8
6
7 A0A024RCQ1,A0A0A0MSX3,Q96T62,...
8
9 A0A7I2V6E2,B2R9P6

> out$uniprot.Swiss.Prot[[5]]

[1] "P62913"

```

## 5.5 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

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```

> queryMany(xli, scopes=c("symbol", "reporter", "accession"),
+           fields=c("entrezgene", "uniprot"), species='human', returnall=TRUE)

Finished
$response
DataFrame with 9 rows and 7 columns
  query  notfound  _id  X_score  entrezgene  uniprot.Swiss.Prot
  <character> <logical> <character> <numeric> <character> <character>
1  DDX26B      TRUE      NA      NA      NA      NA
2  CCDC83      NA    220047  17.9209  220047  Q8IWF9
3  MAST3      NA    23031  18.1249  23031  060307
4  FL0T1      NA    10211  18.4342  10211  075955
5  RPL11      NA    6135  16.3041  6135  P62913
6  Gm10494    TRUE      NA      NA      NA      NA
7  1007_s_at  NA      780  17.9989  780  Q08345
8  1007_s_at  NA  100616237  17.9989  100616237  NA
9  AK125780   NA  118142757  21.2542  118142757  P43080
  uniprot.TrEMBL
  <list>
1
2
3  H0YDV3
4  A0A8V8TLL8, A0A994J700, V9GYV0, ...
5  A2ABJ5, Q5ST80, A2AB10, ...
6  A0A2R8Y447, Q5VVD0, Q5VVC8
7  A0A024RCQ1, A0A0A0MSX3, Q96T62, ...
8
9  A0A7I2V6E2, B2R9P6

$duplicates
  X1007_s_at
1          2

$missing
[1] "DDX26B" "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).

### 5.6 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. Large lists, however, may take a while longer to query, so please wait patiently.

## 6 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)