

# MyGene.info R Client

*Adam Mark, Ryan Thompson, Chunlei Wu*

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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	4	1017 cyclin dependent kin..	
2	1018	1018	4	1018 cyclin dependent kin..	
3	ENSG00000148795	1586	3	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] 8
```

```
$total
```

```
[1] 1442
```

```
$max_score
```

```
[1] 88.55403
```

```
$hits
```

	_id	_score	entrezgene	name	symbol	taxid
1	1017	88.55403	1017	cyclin dependent kinase 2	CDK2	9606
2	12566	74.27112	12566	cyclin dependent kinase 2	Cdk2	10090
3	5880545	63.78744	5880545	CDK2 EDI_169580	370354	
4	362817	62.84480	362817	cyclin dependent kinase 2	Cdk2	10116
5	143384	62.07590	143384	CDK2 associated cullin domain 1	CACUL1	9606

```
> query(q="NM_013993")
```

```
$took
```

```
[1] 17
```

```
$total
[1] 1

$max_score
[1] 1.67633

$hits
  _id _score entrezgene name symbol
1 780 1.67633      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	18.7276	5982	replication factor C..	
2	117_at	3310	19.5180	3310	heat shock protein f..	
3	121_at	7849	18.8706	7849	paired box 8	
4	1255_g_at	2978	19.3550	2978	guanylate cyclase ac..	
5	1294_at	100847079	19.1850	100847079	microRNA 5193	
6	1294_at	7318	19.1850	7318	ubiquitin like modif..	
	symbol	taxid				
	<character>	<integer>				
1	RFC2	9606				
2	HSPA6	9606				
3	PAX8	9606				
4	GUCA1A	9606				
5	MIR5193	9606				
6	UBA7	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	17.9017	220047
3	MAST3	NA	23031	18.0036	23031
4	FLOT1	NA	10211	18.2745	10211
5	RPL11	NA	6135	16.5740	6135
6	ZDHHC20	NA	253832	18.0857	253832
7	LUC7L3	NA	51747	17.6099	51747
8	SNORD49A	NA	26800	22.0677	26800

9	CTSH	NA	1512	17.6030	1512
10	ACOT8	NA	10005	17.5927	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	17.8991
3	MAST3	NA	23031	18.0033
4	FL0T1	NA	10211	18.2866
5	RPL11	NA	6135	16.5729
6	ZDHHC20	NA	253832	18.0919
7	LUC7L3	NA	51747	17.6110
8	SNORD49A	NA	26800	22.0677
9	CTSH	NA	1512	17.6019
10	ACOT8	NA	10005	17.5923

  

	ensembl
	<list>
1	
2	ENSG000000150676
3	ENSG000000099308
4	ENSG000000206480, ENSG000000223654, ENSG000000224740
5	ENSG000000142676
6	ENSG000000180776
7	ENSG000000108848
8	ENSG000000277370
9	ENSG000000103811
10	ENSG000000101473

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

```
[1] "ENSG000000206480" "ENSG000000223654" "ENSG000000224740" "ENSG000000137312"
[5] "ENSG000000230143" "ENSG000000232280" "ENSG000000206379" "ENSG000000236271"
```

## 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	17.8966	220047
3	MAST3	NA	23031	18.0066	23031
4	FLOT1	NA	10211	18.2866	10211
5	RPL11	NA	6135	16.5730	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    17.8976    220047      Q8IWF9
3       MAST3       NA      23031    18.0037     23031     060307
4       FLOT1       NA     10211    18.2866     10211     075955
5       RPL11       NA      6135    16.5907      6135     P62913
6     Gm10494      TRUE        NA        NA        NA            NA
7  1007_s_at       NA  100616237    18.8458  100616237          NA
8  1007_s_at       NA       780    18.8458       780     Q08345
9   AK125780       NA  118142757    21.5233  118142757     P43080

      uniprot.TrEMBL
      <list>
1
2
3      H0YDV3
4  A0A8V8TLL8, A0A994J700, V9GYV0, ...
5      A2ABJ5, Q5ST80, A2AB10, ...
6      A0A2R8Y447, Q5VVD0, Q5VVC8
7
8  A0A024RCQ1, A0A024RCL1, A0A0A0MSX3, ...
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

## MyGene.info R Client

```
> 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  17.9017    220047    Q8IWF9
3      MAST3      NA    23031  18.0070    23031    060307
4      FLOT1      NA    10211  18.2731    10211    075955
5      RPL11      NA     6135  16.5915     6135    P62913
6    Gm10494      TRUE      NA      NA      NA      NA
7  1007_s_at      NA  100616237  18.8458  100616237      NA
8  1007_s_at      NA      780  18.8458      780    Q08345
9   AK125780      NA  118142757  21.8884  118142757    P43080
      uniprot.TrEMBL
      <list>
1
2
3      A0A8V8TLL8,A0A994J700,V9GYV0,...
4      A2ABJ5,Q5ST80,A2AB10,...
5      A0A2R8Y447,Q5VVD0,Q5VVC8
6
7
8  A0A024RCQ1,A0A024RCL1,A0A0A0MSX3,...
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., `ids` 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)