

# 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_score	entrezgene
	<character>	<character>	<numeric>	<integer>
1	1017	1017	1.55	1017
2	1018	1018	1.55	1018
3	ENSG00000148795	1586	17.838215	1586

  

	name	symbol	taxid
	<character>	<character>	<integer>
1	cyclin dependent kinase 2	CDK2	9606
2	cyclin dependent kinase 3	CDK3	9606
3	cytochrome P450 family 17 subfamily A member 1	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)
```

\$max\_score

```
[1] 437.4619
```

\$took

```
[1] 27
```

\$total

```
[1] 629
```

\$hits

	_id	_score	entrezgene	name	symbol	taxid
1	1017	437.4619	1017	cyclin dependent kinase 2	CDK2	9606
2	12566	365.6756	12566	cyclin-dependent kinase 2	Cdk2	10090
3	362817	304.3092	362817	cyclin dependent kinase 2	Cdk2	10116
4	100117828	293.8990	100117828	cyclin dependent kinase 2	Cdk2	7425
5	100925631	293.8990	100925631	cyclin dependent kinase 2	CDK2	9305

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

$max_score
[1] 6.37591

$took
[1] 34

$total
[1] 1

$hits
  _id _score entrezgene name symbol
1 780 6.37591      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		
	<character>	<character>	<numeric>	<integer>		
1	1053_at	5982	12.079607	5982		
2	117_at	3310	11.900158	3310		
3	121_at	7849	9.058544	7849		
4	1255_g_at	2978	10.533326	2978		
5	1294_at	100847079	12.910442	100847079		
6	1294_at	7318	12.041411	7318		

  

	name	symbol	taxid
	<character>	<character>	<integer>
1	replication factor C subunit 2	RFC2	9606
2	heat shock protein family A (Hsp70) member 6	HSPA6	9606
3	paired box 8	PAX8	9606

4	guanylate cyclase activator 1A	GUCA1A	9606
5	microRNA 5193	MIR5193	9606
6	ubiquitin like modifier activating enzyme 7	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	85855100-85920020	+	1	NM_001286159
[2]	11	85855100-85920020	+	2	NM_173556
[3]	19	18097792-18151689	+	3	NM_015016
[4]	1	23691805-23696835	+	4	NM_000975
[5]	1	23691778-23696426	+	5	NM_001199802
...	...	...	...	...	...
[13]	17	50719564-50752711	+	13	NM_016424
[14]	17	16440035-16440106	+	14	NR_002744
[15]	15	78921749-78945098	-	15	NM_001319137
[16]	15	78921749-78945098	-	16	NM_004390
[17]	20	45841720-45857409	-	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 11 rows and 5 columns

	query	notfound	_id	X_score	entrezgene
	<character>	<logical>	<character>	<numeric>	<integer>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	88.309685	220047

3	MAST3	NA	23031	88.46118	23031
4	FL0T1	NA	10211	90.70244	10211
5	RPL11	NA	6135	83.38305	6135
6	ZDHHC20	NA	253832	88.32353	253832
7	LUC7L3	NA	51747	84.82646	51747
8	SNORD49A	NA	ENSG00000277370	100.46342	NA
9	SNORD49A	NA	26800	100.46342	26800
10	CTSH	NA	1512	86.92721	1512
11	AC0T8	NA	10005	84.816475	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 11 rows and 5 columns

	query	notfound	_id	X_score
	<character>	<logical>	<character>	<numeric>
1	DDX26B	TRUE	NA	NA
2	CCDC83	NA	220047	88.295006
3	MAST3	NA	23031	88.27785
4	FL0T1	NA	10211	90.70244
5	RPL11	NA	6135	83.02654
6	ZDHHC20	NA	253832	88.6078
7	LUC7L3	NA	51747	85.03112
8	SNORD49A	NA	ENSG00000277370	100.46342
9	SNORD49A	NA	26800	100.46342
10	CTSH	NA	1512	86.992386
11	AC0T8	NA	10005	84.749565

1

2

3

```
4 list(gene = c("ENSG00000232280", "ENSG00000206379", "ENSG00000224740", "ENSG00000230143"
```

5

```

6
7
8
9
10
11

> out$ensembl[[4]]$gene

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

```

## 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>	<integer>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	88.320045	220047
3	MAST3	NA	23031	88.512405	23031
4	FLOT1	NA	10211	91.445595	10211
5	RPL11	NA	6135	83.117355	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>	<integer>	<character>
1	DDX26B	TRUE	NA	NA	NA	NA
2	CCDC83	NA	220047	88.24525	220047	Q8IWF9
3	MAST3	NA	23031	88.512405	23031	060307
4	FLOT1	NA	10211	90.68685	10211	075955
5	RPL11	NA	6135	82.84542	6135	P62913
6	Gm10494	TRUE	NA	NA	NA	NA
7	1007_s_at	NA	100616237	9.141225	100616237	NA
8	1007_s_at	NA	780	8.32051	780	Q08345
9	AK125780	NA	2978	9.951746	2978	P43080

```
1
2
3
4
```

```

5
6
7
8 c("A0A024RCJ0", "A0A024RCL1", "A0A0A0MSX3", "A0A024RCQ1", "Q96T61", "Q96T62", "A0A0G2JIA")
9
> 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

```

> 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>	<integer>	<character>
1	DDX26B	TRUE	NA	NA	NA	NA
2	CCDC83	NA	220047	88.32353	220047	Q8IWF9
3	MAST3	NA	23031	88.523926	23031	060307
4	FLT1	NA	10211	90.65452	10211	075955
5	RPL11	NA	6135	83.117355	6135	P62913
6	Gm10494	TRUE	NA	NA	NA	NA
7	1007_s_at	NA	780	8.645208	780	Q08345
8	1007_s_at	NA	100616237	8.623732	100616237	NA
9	AK125780	NA	2978	9.96164	2978	P43080

```

1
2
3
4
5

```

```
6
7 c("A0A024RCJ0", "A0A024RCL1", "A0A0A0MSX3", "A0A024RCQ1", "Q96T61", "Q96T62", "A0A0G2JIA")
8
9
$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., `qli` 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)