

# MyGene.info R Client

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November 6, 2019

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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>	<character>			
1	1017	1017	21.237915	1017			
2	1018	1018	21.232512	1018			
3	ENSG00000148795	1586	19.56498	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] 434.6757
```

\$took

```
[1] 69
```

\$total

```
[1] 833
```

\$hits

	_id	_score	entrezgene	name	symbol
1	1017	434.6757	1017	cyclin dependent kinase 2	CDK2
2	12566	365.5176	12566	cyclin-dependent kinase 2	Cdk2
3	362817	306.5625	362817	cyclin dependent kinase 2	Cdk2
4	100117828	290.2917	100117828	cyclin dependent kinase 2	Cdk2
5	ENSPMGG00000020139	290.2917	<NA>	cyclin-dependent kinase 2	cdk2

taxid

```
1 9606
2 10090
3 10116
4 7425
5 409849
```

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

```
$max_score
[1] 6.515819
```

```
$took
[1] 51
```

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

```
$hits
```

	_id	_score	entrezgene	name	symbol
1	780	6.515819	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>	<character>
1	1053_at	5982	11.272218	5982
2	117_at	3310	11.319566	3310
3	121_at	7849	11.25272	7849
4	1255_g_at	2978	10.875113	2978
5	1294_at	100847079	11.884336	100847079

6	1294_at	7318 10.8301325	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	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")
```

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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>	<character>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	88.81174	220047
3	MAST3	NA	23031	86.98322	23031
4	FL0T1	NA	10211	90.0023	10211
5	RPL11	NA	6135	83.23838	6135
6	ZDHHC20	NA	253832	84.02767	253832
7	LUC7L3	NA	51747	87.142456	51747
8	SNORD49A	NA	ENSG00000277370	97.8171	NA
9	SNORD49A	NA	26800	97.8171	26800
10	CTSH	NA	1512	83.44148	1512
11	AC0T8	NA	10005	81.657425	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	88.813034
3	MAST3	NA	23031	86.98322
4	FL0T1	NA	10211	90.00942
5	RPL11	NA	6135	83.23059
6	ZDHHC20	NA	253832	83.82062
7	LUC7L3	NA	51747	86.14656
8	SNORD49A	NA	ENSG00000277370	98.51243
9	SNORD49A	NA	26800	98.51243
10	CTSH	NA	1512	83.54539
11	AC0T8	NA	10005	81.657425

```

1
2
3
4 list(gene = c("ENSG00000224740", "ENSG00000223654", "ENSG00000230143", "ENSG00000236271"
5
6
7
8
9
10
11

> out$ensembl[[4]]$gene

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

```

## 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	88.81428	220047
3	MAST3	NA	23031	86.98322	23031
4	FLOT1	NA	10211	89.998184	10211
5	RPL11	NA	6135	83.22685	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	88.792496	220047	Q8IWF9
3	MAST3	NA	23031	86.989456	23031	060307
4	FLOT1	NA	10211	90.0005	10211	075955
5	RPL11	NA	6135	83.2219	6135	P62913
6	Gm10494	TRUE	NA	NA	NA	NA
7	1007_s_at	NA	100616237	12.547043	100616237	NA
8	1007_s_at	NA	780	10.784007	780	Q08345
9	AK125780	NA	2978	14.123204	2978	P43080

```

1
2
3
4
5
6
7
8 c("A0A024RCJ0", "A0A024RCL1", "A0A024RCQ1", "A0A0A0MSX3", "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> <character>      <character>
1   DDX26B      TRUE      NA      NA      NA      NA
2   CCDC83      NA    220047  88.81157    220047    Q8IWF9
3   MAST3      NA    23031  86.98322    23031    060307
4   FL0T1      NA    10211  90.0023    10211    075955
5   RPL11      NA    6135  83.24303    6135    P62913
6  Gm10494     TRUE      NA      NA      NA      NA
7  1007_s_at    NA  100616237  12.669042  100616237    NA
8  1007_s_at    NA    780  10.700329    780    Q08345
9  AK125780    NA    2978  14.114653    2978    P43080

```

```
2
3
4
5
6
7
8 c("A0A024RCJ0", "A0A024RCL1", "A0A024RCQ1", "A0A0A0MSX3", "Q96T61", "Q96T62", "A0A0G2JIA")
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., `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)