

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

> gene[[1]]$taxid
[1] 9606

> gene[[1]]$uniprot
$`Swiss-Prot`
[1] "P24941"

$TrEMBL
[1] "A0A024RB10" "G3V5T9"      "E7ESI2"      "A0A024RB77" "B4DDL9"
[6] "G3V317"

> gene[[1]]$refseq

$genomic
[1] "NC_000012.12" "NC_018923.2"  "NG_034014.1"

$protein
[1] "NP_001277159.1" "NP_001789.2"   "NP_439892.2"   "XP_011536034.1"

$rna
```

```
[1] "NM_001290230.1" "NM_001798.4"      "NM_052827.3"      "XM_011537732.1"

$translation
$translation[[1]]
$translation[[1]]$protein
[1] "XP_011536034.1"

$translation[[1]]$rna
[1] "XM_011537732.1"

$translation[[2]]
$translation[[2]]$protein
[1] "NP_001789.2"

$translation[[2]]$rna
[1] "NM_001798.4"

$translation[[3]]
$translation[[3]]$protein
[1] "NP_439892.2"

$translation[[3]]$rna
[1] "NM_052827.3"

$translation[[4]]
$translation[[4]]$protein
[1] "NP_001277159.1"

$translation[[4]]$rna
[1] "NM_001290230.1"
```

## 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

	_id	X_score	entrezgene			
	<character>	<numeric>	<integer>			
1	1017	21.17630	1017			
2	1018	22.36355	1018			
3	1586	22.75776	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

  

	query
	<character>
1	1017
2	1018
3	ENSG00000148795

### 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] 429.18

$took
[1] 6

$total
[1] 32

$hits
  _id  _score entrezgene      name  symbol  taxid
1  1017 429.18002      1017 cyclin dependent kinase 2    CDK2   9606
```

```

2 12566 330.22882      12566      cyclin-dependent kinase 2      Cdk2 10090
3 362817 279.42440     362817     cyclin dependent kinase 2      Cdk2 10116
4 143384 22.93534      143384 CDK2 associated cullin domain 1 CACUL1 9606
5 52004 20.56219       52004      CDK2-associated protein 2 Cdk2ap2 10090

```

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

```
$max_score
```

```
[1] 4.130858
```

```
$took
```

```
[1] 22
```

```
$total
```

```
[1] 1
```

```
$hits
```

	_id	_score	entrezgene	name	symbol
1	780	4.130858	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
```

	_id	X_score	entrezgene	name
	<character>	<numeric>	<integer>	<character>
1	5982	22.36242	5982	replication factor C subunit 2
2	3310	13.97494	3310	heat shock protein family A (Hsp70) member 6
3	7849	13.23512	7849	paired box 8
4	2978	11.18164	2978	guanylate cyclase activator 1A
5	7318	22.36288	7318	ubiquitin like modifier activating enzyme 7
6	100847079	22.36200	100847079	microRNA 5193

	symbol	taxid	query
	<character>	<integer>	<character>
1	RFC2	9606	1053_at
2	HSPA6	9606	117_at
3	PAX8	9606	121_at
4	GUCA1A	9606	1255_g_at
5	UBA7	9606	1294_at
6	MIR5193	9606	1294_at

## 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('DDX26B',
+         '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	[23691778, 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")
```

## MyGene.info R Client

```
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>	<integer>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	97.07443	220047
3	MAST3	NA	23031	98.35180	23031
4	FL0T1	NA	10211	99.91871	10211
5	RPL11	NA	6135	92.48695	6135
6	ZDHHC20	NA	253832	97.69475	253832
7	LUC7L3	NA	51747	95.93771	51747
8	SNORD49A	NA	26800	116.94720	26800
9	CTSH	NA	1512	97.69569	1512
10	AC0T8	NA	10005	95.21461	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
```

	notfound	query	_id	X_score
	<logical>	<character>	<character>	<numeric>
1	TRUE	DDX26B	NA	NA
2	NA	CCDC83	220047	97.06707
3	NA	MAST3	23031	98.35671
4	NA	FL0T1	10211	99.92080
5	NA	RPL11	6135	92.48695
6	NA	ZDHHC20	253832	97.68740
7	NA	LUC7L3	51747	95.93771
8	NA	SNORD49A	26800	116.94929
9	NA	CTSH	1512	97.69569
10	NA	AC0T8	10005	95.21461

```
ensembl
<list>
```



```

1
2                               ENSG00000150676
3                               ENSG00000099308
4  ENSG00000230143, ENSG00000206379, ENSG00000232280
5                               ENSG00000142676
6                               ENSG00000180776
7                               ENSG00000108848
8                               ENSG00000277370
9                               ENSG00000103811
10                              ENSG00000101473

> out$ensembl[[4]]$gene

[1] "ENSG00000230143" "ENSG00000206379" "ENSG00000232280" "ENSG00000206480"
[5] "ENSG00000223654" "ENSG00000236271" "ENSG00000224740" "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>	<integer>
1	DDX26B	TRUE	NA	NA	NA
2	CCDC83	NA	220047	97.07277	220047
3	MAST3	NA	23031	98.35671	23031
4	FLOT1	NA	10211	99.91927	10211
5	RPL11	NA	6135	92.48653	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	77.03105	220047	Q8IWF9
3	MAST3	NA	23031	79.08824	23031	060307
4	FLOT1	NA	10211	81.62164	10211	075955
5	RPL11	NA	6135	69.92639	6135	P62913
6	Gm10494	TRUE	NA	NA	NA	NA
7	1007_s_at	NA	100616237	13.97647	100616237	NA
8	1007_s_at	NA	780	13.23610	780	Q08345
9	AK125780	NA	2978	5.59050	2978	P43080

  

	uniprot.TrEMBL
	<list>
1	
2	H0YDV3
3	V9GYV0
4	A2AB12, Q5ST80, A2AB10, ...

```

5           Q5VVC9,Q5VVD0,Q5VVC8
6
7
8 A0A024RCJ0,A0A024RCQ1,A0A024RCL1,...
9           A6PVH5,B2R9P6,A0A0A0MTF5

> 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
  notfound      query      _id  X_score entrezgene uniprot.Swiss.Prot
  <logical> <character> <character> <numeric> <integer>      <character>
1      TRUE      DDX26B         NA         NA         NA              NA
2       NA      CCDC83      220047  77.034730      220047      Q8IWF9
3       NA      MAST3       23031  79.088240      23031      060307
4       NA      FLOT1      10211  81.622550      10211      075955
5       NA      RPL11       6135  69.926800       6135      P62913
6      TRUE      Gm10494         NA         NA         NA              NA
7       NA  1007_s_at  100616237  13.976403  100616237              NA
8       NA  1007_s_at       780  13.235414       780      Q08345
9       NA  AK125780       2978  5.590448       2978      P43080

              uniprot.TrEMBL
              <list>
1
2              H0YDV3
3              V9GYV0
4      A2AB12,Q5ST80,A2AB10,...
5      Q5VVC9,Q5VVD0,Q5VVC8

```

```
6
7
8 A0A024RCJ0,A0A024RCQ1,A0A024RCL1,...
9          A6PVH5,B2R9P6,A0A0A0MTF5

$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)